

tct gct acc act gtc gat gct gaa gtc atc gcc gct gcc cct aac ttg 307
 Ser Ala Thr Thr Val Asp Ala Glu Val Ile Ala Ala Ala Pro Asn Leu
 55 60 65
 aag atc gtc ggt cgt gcc ggc gtg ggc ttg gac aac gtt gac atc cct 355
 Lys Ile Val Gly Arg Ala Gly Val Gly Leu Asp Asn Val Asp Ile Pro
 70 75 80 85
 gct gcc act gaa gct ggc gtc atg gtt gct aac gca ccg acc tct aat 403
 Ala Ala Thr Glu Ala Gly Val Met Val Ala Asn Ala Pro Thr Ser Asn
 90 95 100
 att cac tcc gct tgt gag cac gca att tct ttg ctg ctg tct act gct 451
 Ile His Ser Ala Cys Glu His Ala Ile Ser Leu Leu Leu Ser Thr Ala
 105 110 115
 cgc cag atc ctg ctg ctg atg cga cgc tgc gtg agg gcg agt gga agc 499
 Arg Gln Ile Leu Leu Leu Met Arg Arg Cys Val Arg Ala Ser Gly Ser
 120 125 130
 ggt ctt ctt tca acg gtg tgg aaa ttt tgc gaa aaa ctg tgc gta tgc 547
 Gly Leu Leu Ser Thr Val Trp Lys Phe Ser Glu Lys Leu Ser Val Ser
 135 140 145
 tgc gtt ttg gcc aca ttg gtc agt tgt ttg ctc agc gtc ttg ctg cgt 595
 Ser Val Leu Ala Thr Leu Val Ser Cys Leu Leu Ser Val Leu Leu Arg
 150 155 160 165
 ttg aga cca cca ttg ttg ctt acg atc ctt acg cta acc ctg ctt cgt 643
 Leu Arg Pro Pro Leu Leu Leu Thr Ile Leu Thr Leu Thr Leu Leu Arg
 170 175 180
 gcg ggt 649
 Ala Gly

<210> 152
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 <212> PRT
 <213> Corynebacterium glutamicum

<400> 152
 Val Ser Gln Asn Gly Arg Pro Val Val Leu Ile Ala Asp Lys Leu Ala
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 Gln Ser Thr Val Asp Ala Leu Gly Asp Ala Val Glu Val Arg Trp Val
 20 25 30
 Asp Gly Pro Asn Arg Pro Glu Leu Leu Asp Ala Val Lys Glu Ala Asp
 35 40 45
 Ala Leu Leu Val Arg Ser Ala Thr Thr Val Asp Ala Glu Val Ile Ala
 50 55 60
 Ala Ala Pro Asn Leu Lys Ile Val Gly Arg Ala Gly Val Gly Leu Asp
 65 70 75 80
 Asn Val Asp Ile Pro Ala Ala Thr Glu Ala Gly Val Met Val Ala Asn
 85 90 95

Ala Pro Thr Ser Asn Ile His Ser Ala Cys Glu His Ala Ile Ser Leu
 100 105 110

Leu Leu Ser Thr Ala Arg Gln Ile Leu Leu Leu Met Arg Arg Cys Val
 115 120 125

Arg Ala Ser Gly Ser Gly Leu Leu Ser Thr Val Trp Lys Phe Ser Glu
 130 135 140

Lys Leu Ser Val Ser Ser Val Leu Ala Thr Leu Val Ser Cys Leu Leu
 145 150 155 160

Ser Val Leu Leu Arg Leu Arg Pro Pro Leu Leu Leu Thr Ile Leu Thr
 165 170 175

Leu Thr Leu Leu Arg Ala Gly
 180

<210> 153
 <211> 1011
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(988)
 <223> RXN00871

<400> 153
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gtttcccaca gaacgattaa ttgaaggaga gcacaggact atg cgt tgg ttc cat 115
 Met Arg Trp Phe His
 1 5

aag aag ggc gaa ctg gcc cga gat ggt tgg caa agc gtt gtc gat gcc 163
 Lys Lys Gly Glu Leu Ala Arg Asp Gly Trp Gln Ser Val Val Asp Ala
 10 15 20

acc acc cca ggt tgg gaa tat acc ggc atc cgc att gcc gaa ctg ggc 211
 Thr Thr Pro Gly Trp Glu Tyr Thr Gly Ile Arg Ile Ala Glu Leu Gly
 25 30 35

agt ggt gaa tcg ctt gaa ctg aat gac act ggt gtg gaa cgc atc ttc 259
 Ser Gly Glu Ser Leu Glu Leu Asn Asp Thr Gly Val Glu Arg Ile Phe
 40 45 50

att cca ctt cag ggc agc ttc gat gtt gcc cac cat ggt cag gtg acc 307
 Ile Pro Leu Gln Gly Ser Phe Asp Val Ala His His Gly Gln Val Thr
 55 60 65

cat ctt cac gga aga aag tca gtc ttt gat gga cca acc gat gtg ctc 355
 His Leu His Gly Arg Lys Ser Val Phe Asp Gly Pro Thr Asp Val Leu
 70 75 80 85

tac ctc ccc act gga caa aca gca acg ctc agt ggt cag gga cga gtc 403
 Tyr Leu Pro Thr Gly Gln Thr Ala Thr Leu Ser Gly Gln Gly Arg Val
 90 95 100

gcc gtg gcg gaa gct ccc act cag gaa ccc aag gag tgg aag tac atc 451

Ala Val Ala Glu Ala Pro Thr Gln Glu Pro Lys Glu Trp Lys Tyr Ile
105 110 115

gct cca gca gaa act cct gtg gag ttg cgt gga gct ggc cgc tcg agc 499
Ala Pro Ala Glu Thr Pro Val Glu Leu Arg Gly Ala Gly Arg Ser Ser
120 125 130

cga caa gtc cac aac ttt ggc acc ccg gaa gct ctc gat gct gct cga 547
Arg Gln Val His Asn Phe Gly Thr Pro Glu Ala Leu Asp Ala Ala Arg
135 140 145

cta atc gtg tgt gaa gta atc acc cca ggt gaa aac tgg agc tct tac 595
Leu Ile Val Cys Glu Val Ile Thr Pro Gly Glu Asn Trp Ser Ser Tyr
150 155 160 165

cct cca cac aag cat gat gag cac atc cca gga cac gag tcc aag ctg 643
Pro Pro His Lys His Asp Glu His Ile Pro Gly His Glu Ser Lys Leu
170 175 180

gag gaa atc tac tac ttc gaa agc gcc cca tcg cga gtt ggt ggc agg 691
Glu Glu Ile Tyr Tyr Phe Glu Ser Ala Pro Ser Arg Val Gly Gly Arg
185 190 195

gcc gaa gca gca gaa gga gct ttc gga atg ttt tcc acc tac tcc tca 739
Ala Glu Ala Ala Glu Gly Ala Phe Gly Met Phe Ser Thr Tyr Ser Ser
200 205 210

cca gcg ggg gag atc gat atc aac gcc atg gtg tac agc ggc gat atc 787
Pro Ala Gly Glu Ile Asp Ile Asn Ala Met Val Tyr Ser Gly Asp Ile
215 220 225

gcg cta gtt cct ttc gga tac cac ggc cct gcc gtg gca gca cct ggc 835
Ala Leu Val Pro Phe Gly Tyr His Gly Pro Ala Val Ala Ala Pro Gly
230 235 240 245

tat gac ttg tac tac ctc aac gtc atg gca gga cct gat ccg gag aga 883
Tyr Asp Leu Tyr Tyr Leu Asn Val Met Ala Gly Pro Asp Pro Glu Arg
250 255 260

atc tgg ctg att aac gat gac cca gcg cac gcc tgg gtt cga gat aca 931
Ile Trp Leu Ile Asn Asp Asp Pro Ala His Ala Trp Val Arg Asp Thr
265 270 275

tgg acc ggg caa gca ttt gat gat cgc ttg cca tat gag aac gca aac 979
Trp Thr Gly Gln Ala Phe Asp Asp Arg Leu Pro Tyr Glu Asn Ala Asn
280 285 290

aag gag gga taaaatttca tggctgaaac gaa 1011
Lys Glu Gly
295

<210> 154

<211> 296

<212> PRT

<213> Corynebacterium glutamicum

<400> 154

Met Arg Trp Phe His Lys Lys Gly Glu Leu Ala Arg Asp Gly Trp Gln
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Ser Val Val Asp Ala Thr Thr Pro Gly Trp Glu Tyr Thr Gly Ile Arg
 20 25 30
 Ile Ala Glu Leu Gly Ser Gly Glu Ser Leu Glu Leu Asn Asp Thr Gly
 35 40 45
 Val Glu Arg Ile Phe Ile Pro Leu Gln Gly Ser Phe Asp Val Ala His
 50 55 60
 His Gly Gln Val Thr His Leu His Gly Arg Lys Ser Val Phe Asp Gly
 65 70 75 80
 Pro Thr Asp Val Leu Tyr Leu Pro Thr Gly Gln Thr Ala Thr Leu Ser
 85 90 95
 Gly Gln Gly Arg Val Ala Val Ala Glu Ala Pro Thr Gln Glu Pro Lys
 100 105 110
 Glu Trp Lys Tyr Ile Ala Pro Ala Glu Thr Pro Val Glu Leu Arg Gly
 115 120 125
 Ala Gly Arg Ser Ser Arg Gln Val His Asn Phe Gly Thr Pro Glu Ala
 130 135 140
 Leu Asp Ala Ala Arg Leu Ile Val Cys Glu Val Ile Thr Pro Gly Glu
 145 150 155 160
 Asn Trp Ser Ser Tyr Pro Pro His Lys His Asp Glu His Ile Pro Gly
 165 170 175
 His Glu Ser Lys Leu Glu Glu Ile Tyr Tyr Phe Glu Ser Ala Pro Ser
 180 185 190
 Arg Val Gly Gly Arg Ala Glu Ala Ala Glu Gly Ala Phe Gly Met Phe
 195 200 205
 Ser Thr Tyr Ser Ser Pro Ala Gly Glu Ile Asp Ile Asn Ala Met Val
 210 215 220
 Tyr Ser Gly Asp Ile Ala Leu Val Pro Phe Gly Tyr His Gly Pro Ala
 225 230 235 240
 Val Ala Ala Pro Gly Tyr Asp Leu Tyr Tyr Leu Asn Val Met Ala Gly
 245 250 255
 Pro Asp Pro Glu Arg Ile Trp Leu Ile Asn Asp Asp Pro Ala His Ala
 260 265 270
 Trp Val Arg Asp Thr Trp Thr Gly Gln Ala Phe Asp Asp Arg Leu Pro
 275 280 285
 Tyr Glu Asn Ala Asn Lys Glu Gly
 290 295

<210> 155

<211> 964

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(964)

<223> FRXA00871

<400> 155

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gggaaaaggc gatcaccagc cgttggctcg acccagcaac ccacggtggc attaacctcg 60

gtttcccaca gaacgattaa ttgaaggaga gcacaggact atg cgt tgg ttc cat 115
                                         Met Arg Trp Phe His
                                         1 5

aag aag ggc gaa ctg gcc cga gat ggt tgg caa agc gtt gtc gat gcc 163
Lys Lys Gly Glu Leu Ala Arg Asp Gly Trp Gln Ser Val Val Asp Ala
                        10 15 20

acc acc cca ggt tgg gaa tat acc ggc atc cgc att gcc gaa ctg ggc 211
Thr Thr Pro Gly Trp Glu Tyr Thr Gly Ile Arg Ile Ala Glu Leu Gly
                        25 30 35

agt ggt gaa tcg ctt gaa ctg aat gac act ggt gtg gaa cgc atc ttc 259
Ser Gly Glu Ser Leu Glu Leu Asn Asp Thr Gly Val Glu Arg Ile Phe
                        40 45 50

att cca ctt cag ggc agc ttc gat gtt gcc cac cat ggt cag gtg acc 307
Ile Pro Leu Gln Gly Ser Phe Asp Val Ala His His Gly Gln Val Thr
                        55 60 65

cat ctt cac gga aga aag tca gtc ttt gat gga cca acc gat gtg ctc 355
His Leu His Gly Arg Lys Ser Val Phe Asp Gly Pro Thr Asp Val Leu
                        70 75 80 85

tac ctc ccc act gga caa aca gca acg ctc agt ggt cag gga cga gtc 403
Tyr Leu Pro Thr Gly Gln Thr Ala Thr Leu Ser Gly Gln Gly Arg Val
                        90 95 100

gcc gtg gcg gaa gct ccc act cag gaa ccc aag gag tgg aag tac atc 451
Ala Val Ala Glu Ala Pro Thr Gln Glu Pro Lys Glu Trp Lys Tyr Ile
                        105 110 115

gct cca gca gaa act cct gtg gag ttg cgt gga gct ggc cgc tcg agc 499
Ala Pro Ala Glu Thr Pro Val Glu Leu Arg Gly Ala Gly Arg Ser Ser
                        120 125 130

cga caa gtc cac aac ttt ggc acc ccg gaa gct ctc gat gct gct cga 547
Arg Gln Val His Asn Phe Gly Thr Pro Glu Ala Leu Asp Ala Ala Arg
                        135 140 145

cta atc gtg tgt gaa gta atc acc cca ggt gaa aac tgg agc tct tac 595
Leu Ile Val Cys Glu Val Ile Thr Pro Gly Glu Asn Trp Ser Ser Tyr
                        150 155 160 165

cct cca cac aag cat gat gag cac atc cca gga cac gag tcc aag ctg 643
Pro Pro His Lys His Asp Glu His Ile Pro Gly His Glu Ser Lys Leu
                        170 175 180

gag gaa atc tac tac ttc gaa agc gcc cca tcg cga gtt ggt ggc agg 691
Glu Glu Ile Tyr Tyr Phe Glu Ser Ala Pro Ser Arg Val Gly Gly Arg
                        185 190 195

gcc gaa gca gca gaa gga gct ttc gga atg ttt tcc acc tac tcc tca 739
Ala Glu Ala Ala Glu Gly Ala Phe Gly Met Phe Ser Thr Tyr Ser Ser

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200	205	210	
cca gcg ggg gag atc gat	atc aac gcc atg gtg tac	agc ggc gat atc	787
Pro Ala Gly Glu Ile Asp	Ile Asn Ala Met Val Tyr	Ser Gly Asp Ile	
215	220	225	
gcg cta gtt cct ttc gga	tac cac ggc cct gcc	gtg gca gca cct ggc	835
Ala Leu Val Pro Phe Gly	Tyr His Gly Pro Ala	Val Ala Ala Pro Gly	
230	235	240 245	
tat gac ttg tac tac ctc	aac gtc atg gca gga	cct gat ccg gag aga	883
Tyr Asp Leu Tyr Tyr Leu	Asn Val Met Ala Gly	Pro Asp Pro Glu Arg	
250	255	260	
atc tgg ctg att aac gat	gac cca gcg cac gcc	tgg gtt cga gat aca	931
Ile Trp Leu Ile Asn Asp	Asp Pro Ala His Ala	Trp Val Arg Asp Thr	
265	270	275	
tgg acc ggg caa gca ttt	gat gat cgc ttg cca		964
Trp Thr Gly Gln Ala Phe	Asp Asp Arg Leu Pro		
280	285		

<210> 156

<211> 288

<212> PRT

<213> Corynebacterium glutamicum

<400> 156

Met Arg Trp Phe His Lys	Lys Gly Glu Leu Ala Arg	Asp Gly Trp Gln
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Ser Val Val Asp Ala Thr	Thr Pro Gly Trp Glu Tyr	Thr Gly Ile Arg
20	25	30

Ile Ala Glu Leu Gly Ser	Gly Glu Ser Leu Glu Leu	Asn Asp Thr Gly
35	40	45

Val Glu Arg Ile Phe Ile	Pro Leu Gln Gly Ser	Phe Asp Val Ala His
50	55	60

His Gly Gln Val Thr His	Leu His Gly Arg Lys	Ser Val Phe Asp Gly
65	70	75 80

Pro Thr Asp Val Leu Tyr	Leu Pro Thr Gly Gln Thr	Ala Thr Leu Ser
85	90	95

Gly Gln Gly Arg Val Ala	Val Ala Glu Ala Pro Thr	Gln Glu Pro Lys
100	105	110

Glu Trp Lys Tyr Ile Ala	Pro Ala Glu Thr Pro Val	Glu Leu Arg Gly
115	120	125

Ala Gly Arg Ser Ser Arg	Gln Val His Asn Phe Gly	Thr Pro Glu Ala
130	135	140

Leu Asp Ala Ala Arg Leu	Ile Val Cys Glu Val Ile	Thr Pro Gly Glu
145	150	155 160

Asn Trp Ser Ser Tyr Pro	Pro His Lys His Asp Glu	His Ile Pro Gly
165	170	175

His Glu Ser Lys Leu Glu Glu Ile Tyr Tyr Phe Glu Ser Ala Pro Ser
 180 185 190

Arg Val Gly Gly Arg Ala Glu Ala Ala Glu Gly Ala Phe Gly Met Phe
 195 200 205

Ser Thr Tyr Ser Ser Pro Ala Gly Glu Ile Asp Ile Asn Ala Met Val
 210 215 220

Tyr Ser Gly Asp Ile Ala Leu Val Pro Phe Gly Tyr His Gly Pro Ala
 225 230 235 240

Val Ala Ala Pro Gly Tyr Asp Leu Tyr Tyr Leu Asn Val Met Ala Gly
 245 250 255

Pro Asp Pro Glu Arg Ile Trp Leu Ile Asn Asp Asp Pro Ala His Ala
 260 265 270

Trp Val Arg Asp Thr Trp Thr Gly Gln Ala Phe Asp Asp Arg Leu Pro
 275 280 285

<210> 157
 <211> 373
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(373)
 <223> RXN02829

<400> 157
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ctgaattcgt cagttaaagt gtatcgaaag gagactggac atg caa aaa aat att 115
 Met Gln Lys Asn Ile
 1 5

cta aaa agt ggc atc gaa att tct gaa ctt ggg tta ggt tgc atg agt 163
 Leu Lys Ser Gly Ile Glu Ile Ser Glu Leu Gly Leu Gly Cys Met Ser
 10 15 20

tta ggc aca gat tat aaa aaa gcg caa cca att att gaa agt gca att 211
 Leu Gly Thr Asp Tyr Lys Lys Ala Gln Pro Ile Ile Glu Ser Ala Ile
 25 30 35

gat aat ggt att acg tat ttt gat act gca gat att tac gat caa gga 259
 Asp Asn Gly Ile Thr Tyr Phe Asp Thr Ala Asp Ile Tyr Asp Gln Gly
 40 45 50

gtt aat gaa gaa att gtt ggt aaa gcc tta aaa aaa tat caa aat cgt 307
 Val Asn Glu Glu Ile Val Gly Lys Ala Leu Lys Lys Tyr Gln Asn Arg
 55 60 65

gat gac atc gtt atc gga act aaa gtt gga aat cga tta act gac gat 355
 Asp Asp Ile Val Ile Gly Thr Lys Val Gly Asn Arg Leu Thr Asp Asp

ggt aat gaa gaa att gtt ggt aaa gcc tta aaa aaa tat caa aat cgt 307
Val Asn Glu Glu Ile Val Gly Lys Ala Leu Lys Lys Tyr Gln Asn Arg
55 60 65

gat gac atc gtt atc gga act aaa gtt gga aat cga tta act gac gat 355
Asp Asp Ile Val Ile Gly Thr Lys Val Gly Asn Arg Leu Thr Asp Asp
70 75 80 85

gga cat atg acg tgg gga tcc 376
Gly His Met Thr Trp Gly Ser
90

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<210> 160
<211> 92
<212> PRT
<213> Corynebacterium glutamicum
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<400> 160
Met Gln Lys Asn Ile Leu Lys Ser Gly Ile Glu Ile Ser Glu Leu Gly
  1             5             10             15
Leu Gly Cys Met Ser Leu Gly Thr Asp Tyr Lys Lys Ala Gln Pro Ile
      20             25             30
Ile Glu Ser Ala Ile Asp Asn Gly Ile Thr Tyr Phe Asp Thr Ala Asp
      35             40             45
Ile Tyr Asp Gln Gly Val Asn Glu Glu Ile Val Gly Lys Ala Leu Lys
      50             55             60
Lys Tyr Gln Asn Arg Asp Asp Ile Val Ile Gly Thr Lys Val Gly Asn
      65             70             75             80
Arg Leu Thr Asp Asp Gly His Met Thr Trp Gly Ser
      85             90

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<210> 161
<211> 948
<212> DNA
<213> Corynebacterium glutamicum
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<220>
<221> CDS
<222> (101)..(925)
<223> RXN01468
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<400> 161
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ttagcgggaa aatttcgccc aaaacaggga caatggtggt atg aca gtg aac att 115
                                         Met Thr Val Asn Ile
                                         1                               5

tca tat ctg acc gac atg gac ggc gtc ctc atc aaa gag ggc gag ata 163
Ser Tyr Leu Thr Asp Met Asp Gly Val Leu Ile Lys Glu Gly Glu Ile
                        10                               15                               20

att ccg ggt gca gat cgt ttt ctt cag tct ctc acc gat aac aat gtg 211
Ile Pro Gly Ala Asp Arg Phe Leu Gln Ser Leu Thr Asp Asn Asn Val

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239

tagtattctg taggtcatgg cat

948

<210> 162

<211> 275

<212> PRT

<213> Corynebacterium glutamicum

<400> 162

Met Thr Val Asn Ile Ser Tyr Leu Thr Asp Met Asp Gly Val Leu Ile
 1 5 10 15

Lys Glu Gly Glu Ile Ile Pro Gly Ala Asp Arg Phe Leu Gln Ser Leu
 20 25 30

Thr Asp Asn Asn Val Glu Phe Met Val Leu Thr Asn Asn Ser Ile Phe
 35 40 45

Thr Pro Arg Asp Leu Ser Ala Arg Leu Lys Thr Ser Gly Leu Asp Ile
 50 55 60

Pro Pro Glu Arg Ile Trp Thr Ser Ala Thr Ala Thr Ala His Phe Leu
 65 70 75 80

Lys Ser Gln Val Lys Glu Gly Thr Ala Tyr Val Val Gly Glu Ser Gly
 85 90 95

Leu Thr Thr Ala Leu His Thr Ala Gly Trp Ile Leu Thr Asp Ala Asn
 100 105 110

Pro Glu Phe Val Val Leu Gly Glu Thr Arg Thr Tyr Ser Phe Glu Ala
 115 120 125

Ile Thr Thr Ala Ile Asn Leu Ile Leu Gly Gly Ala Arg Phe Ile Cys
 130 135 140

Thr Asn Pro Asp Val Thr Gly Pro Ser Pro Ser Gly Ile Leu Pro Ala
 145 150 155 160

Thr Gly Ser Val Ala Ala Leu Ile Thr Ala Ala Thr Gly Ala Glu Pro
 165 170 175

Tyr Tyr Ile Gly Lys Pro Asn Pro Val Met Met Arg Ser Ala Leu Asn
 180 185 190

Thr Ile Gly Ala His Ser Glu His Thr Val Met Ile Gly Asp Arg Met
 195 200 205

Asp Thr Asp Val Lys Ser Gly Leu Glu Ala Gly Leu Ser Thr Val Leu
 210 215 220

Val Arg Ser Gly Ile Ser Asp Asp Ala Glu Ile Arg Arg Tyr Pro Phe
 225 230 235 240

Arg Pro Thr His Val Ile Asn Ser Ile Ala Asp Leu Ala Asp Cys Trp
 245 250 255

Asp Asp Pro Phe Gly Asp Gly Ala Phe His Val Pro Asp Glu Gln Gln
 260 265 270

Phe Thr Asp
275

<210> 163
<211> 948
<212> DNA
<213> Corynebacterium glutamicum

<220>
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<223> FRXA01468

<400> 163
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ttagcgggaa aatttcgccc aaaacaggga caatggtgtt atg aca gtg aac att 115
Met Thr Val Asn Ile
1 5

tca tat ctg acc gac atg gac ggc gtc ctc atc aaa gag ggc gag ata 163
Ser Tyr Leu Thr Asp Met Asp Gly Val Leu Ile Lys Glu Gly Glu Ile
10 15 20

att ccg ggt gca gat cgt ttt ctt cag tct ctc acc gat aac aat gtg 211
Ile Pro Gly Ala Asp Arg Phe Leu Gln Ser Leu Thr Asp Asn Asn Val
25 30 35

gag ttt atg gtt ttg acc aac aac tcc att ttc acc ccg agg gat ctt 259
Glu Phe Met Val Leu Thr Asn Asn Ser Ile Phe Thr Pro Arg Asp Leu
40 45 50

tct gca cgt ctt aag act tcc ggt ttg gat atc ccg ccg gag cgt att 307
Ser Ala Arg Leu Lys Thr Ser Ser Gly Leu Asp Ile Pro Pro Glu Arg Ile
55 60 65

tgg act tct gca acc gcc act gct cac ttc ctg aaa tcc cag gtc aag 355
Trp Thr Ser Ala Thr Ala Thr Ala His Phe Leu Lys Ser Gln Val Lys
70 75 80 85

gag ggc aca gcc tat gtt gtt ggc gag tcc ggt ctg acc act gcg ttg 403
Glu Gly Thr Ala Tyr Val Val Gly Glu Ser Gly Leu Thr Thr Ala Leu
90 95 100

cat acc gcg ggt tgg att ttg acg gat gca aat cct gag ttt gtt gtc 451
His Thr Ala Gly Trp Ile Leu Thr Asp Ala Asn Pro Glu Phe Val Val
105 110 115

ctg ggc gaa acc cgc aca tat tcc ttc gag gca atc act act gcg ata 499
Leu Gly Glu Thr Arg Thr Tyr Ser Phe Glu Ala Ile Thr Thr Ala Ile
120 125 130

aat ctg att ttg ggt ggc gct cgc ttt att tgc acc aac ccg gat gtc 547
Asn Leu Ile Leu Gly Gly Ala Arg Phe Ile Cys Thr Asn Pro Asp Val
135 140 145

act gga cct tca cca agt ggc att ttg cct gct act ggc tct gtc gcc 595
Thr Gly Pro Ser Pro Ser Gly Ile Leu Pro Ala Thr Gly Ser Val Ala
150 155 160 165

gca ctt att acc gca gct act ggc gct gag cct tat tac atc ggc aag 643
 Ala Leu Ile Thr Ala Ala Thr Gly Ala Glu Pro Tyr Tyr Ile Gly Lys
 170 175 180

cca aac cct gtg atg atg cgc agt gcg ctg aac acc atc ggg gcg cat 691
 Pro Asn Pro Val Met Met Arg Ser Ala Leu Asn Thr Ile Gly Ala His
 185 190 195

tcc gag cac act gtc atg atc ggc gac cgc atg gac acc gac gtg aaa 739
 Ser Glu His Thr Val Met Ile Gly Asp Arg Met Asp Thr Asp Val Lys
 200 205 210

tct ggt ttg gaa gcc gcc ctg agc acc gtg ctg gtt cga agc gga att 787
 Ser Gly Leu Glu Ala Gly Leu Ser Thr Val Leu Val Arg Ser Gly Ile
 215 220 225

tcc gac gac gcc gag atc cgc cgc tac ccc ttc cgc cca act cac gtg 835
 Ser Asp Asp Ala Glu Ile Arg Arg Tyr Pro Phe Arg Pro Thr His Val
 230 235 240 245

atc aat tcc atc gcc gat ctt gcc gat tgc tgg gac gat cct ttc ggt 883
 Ile Asn Ser Ile Ala Asp Leu Ala Asp Cys Trp Asp Asp Pro Phe Gly
 250 255 260

gac ggt gca ttt cac gta cca gat gag cag cag ttc act gac 925
 Asp Gly Ala Phe His Val Pro Asp Glu Gln Gln Phe Thr Asp
 265 270 275

tagtattctg taggtcatgg cat 948

<210> 164

<211> 275

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 164

Met Thr Val Asn Ile Ser Tyr Leu Thr Asp Met Asp Gly Val Leu Ile
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Lys Glu Gly Glu Ile Ile Pro Gly Ala Asp Arg Phe Leu Gln Ser Leu
 20 25 30

Thr Asp Asn Asn Val Glu Phe Met Val Leu Thr Asn Asn Ser Ile Phe
 35 40 45

Thr Pro Arg Asp Leu Ser Ala Arg Leu Lys Thr Ser Gly Leu Asp Ile
 50 55 60

Pro Pro Glu Arg Ile Trp Thr Ser Ala Thr Ala Thr Ala His Phe Leu
 65 70 75 80

Lys Ser Gln Val Lys Glu Gly Thr Ala Tyr Val Val Gly Glu Ser Gly
 85 90 95

Leu Thr Thr Ala Leu His Thr Ala Gly Trp Ile Leu Thr Asp Ala Asn
 100 105 110

Pro Glu Phe Val Val Leu Gly Glu Thr Arg Thr Tyr Ser Phe Glu Ala
 115 120 125

Ile Thr Thr Ala Ile Asn Leu Ile Leu Gly Gly Ala Arg Phe Ile Cys
 130 135 140

Thr Asn Pro Asp Val Thr Gly Pro Ser Pro Ser Gly Ile Leu Pro Ala
 145 150 155 160

Thr Gly Ser Val Ala Ala Leu Ile Thr Ala Ala Thr Gly Ala Glu Pro
 165 170 175

Tyr Tyr Ile Gly Lys Pro Asn Pro Val Met Met Arg Ser Ala Leu Asn
 180 185 190

Thr Ile Gly Ala His Ser Glu His Thr Val Met Ile Gly Asp Arg Met
 195 200 205

Asp Thr Asp Val Lys Ser Gly Leu Glu Ala Gly Leu Ser Thr Val Leu
 210 215 220

Val Arg Ser Gly Ile Ser Asp Asp Ala Glu Ile Arg Arg Tyr Pro Phe
 225 230 235 240

Arg Pro Thr His Val Ile Asn Ser Ile Ala Asp Leu Ala Asp Cys Trp
 245 250 255

Asp Asp Pro Phe Gly Asp Gly Ala Phe His Val Pro Asp Glu Gln Gln
 260 265 270

Phe Thr Asp
 275

<210> 165
 <211> 1128
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(1105)
 <223> RXA00794

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 cgtaaccagg tcagatcaag tgccccagga ggcccttcag atg aac cta aag aac 115
 Met Asn Leu Lys Asn
 1 5

ccc gaa acg cca gac cgt aac ctt gct atg gag ctg gtg cga gtt acg 163
 Pro Glu Thr Pro Asp Arg Asn Leu Ala Met Glu Leu Val Arg Val Thr
 10 15 20

gaa gca gct gca ctg gct tct gga cgt tgg gtt gga cgt ggc atg aag 211
 Glu Ala Ala Ala Leu Ala Ser Gly Arg Trp Val Gly Arg Gly Met Lys
 25 30 35

aat gaa ggc gac ggt gcc gct gtt gac gcc atg cgc cag ctc atc aac 259
 Asn Glu Gly Asp Gly Ala Ala Val Asp Ala Met Arg Gln Leu Ile Asn
 40 45 50

tca gtg acc atg aag ggc gtc gtt gtt atc ggc gag ggc gaa aaa gac 307

Ser	Val	Thr	Met	Lys	Gly	Val	Val	Val	Ile	Gly	Glu	Gly	Glu	Lys	Asp		
55						60					65						
gaa	gct	cca	atg	ctg	tac	aac	ggc	gaa	gag	gtc	gga	acc	ggc	ttt	gga	355	
Glu	Ala	Pro	Met	Leu	Tyr	Asn	Gly	Glu	Glu	Val	Gly	Thr	Gly	Phe	Gly		
70					75					80					85		
cct	gag	gtt	gat	atc	gca	gtt	gac	cca	gtt	gac	ggc	acc	acc	ctg	atg	403	
Pro	Glu	Val	Asp	Ile	Ala	Val	Asp	Pro	Val	Asp	Gly	Thr	Thr	Leu	Met		
				90					95					100			
gct	gag	ggc	cgc	ccc	aac	gca	att	tcc	att	ctc	gca	gct	gca	gag	cgt	451	
Ala	Glu	Gly	Arg	Pro	Asn	Ala	Ile	Ser	Ile	Leu	Ala	Ala	Ala	Glu	Arg		
			105					110					115				
ggc	acc	atg	tac	gat	cca	tcc	tcc	gtc	ttc	tac	atg	aag	aag	atc	gcc	499	
Gly	Thr	Met	Tyr	Asp	Pro	Ser	Ser	Val	Phe	Tyr	Met	Lys	Lys	Ile	Ala		
		120					125					130					
gtg	gga	cct	gag	gcc	gca	ggc	aag	atc	gac	atc	gaa	gct	cca	gtt	gcc	547	
Val	Gly	Pro	Glu	Ala	Ala	Gly	Lys	Ile	Asp	Ile	Glu	Ala	Pro	Val	Ala		
	135					140					145						
cac	aac	atc	aac	gcg	gtg	gca	aag	tcc	aag	gga	atc	aac	cct	tcc	gac	595	
His	Asn	Ile	Asn	Ala	Val	Ala	Lys	Ser	Lys	Gly	Ile	Asn	Pro	Ser	Asp		
150					155					160					165		
gtc	acc	gtt	gtc	gtg	ctt	gac	cgt	cct	cgc	cac	atc	gaa	ctg	atc	gca	643	
Val	Thr	Val	Val	Val	Leu	Asp	Arg	Pro	Arg	His	Ile	Glu	Leu	Ile	Ala		
				170					175					180			
gac	att	cgt	cgt	gca	ggc	gca	aag	gtt	cgt	ctc	atc	tcc	gac	ggc	gac	691	
Asp	Ile	Arg	Arg	Ala	Gly	Ala	Lys	Val	Arg	Leu	Ile	Ser	Asp	Gly	Asp		
			185					190					195				
gtt	gca	ggc	gca	gtt	gca	gca	gct	cag	gat	tcc	aac	tcc	gtg	gac	atc	739	
Val	Ala	Gly	Ala	Val	Ala	Ala	Ala	Gln	Asp	Ser	Asn	Ser	Val	Asp	Ile		
		200					205					210					
atg	atg	ggc	acc	ggc	gga	acc	cca	gaa	ggc	atc	atc	act	gcg	tgc	gcc	787	
Met	Met	Gly	Thr	Gly	Gly	Thr	Pro	Glu	Gly	Ile	Ile	Thr	Ala	Cys	Ala		
	215					220					225						
atg	aag	tgc	atg	ggc	ggc	gaa	atc	cag	ggc	atc	ctg	gcc	cca	atg	aac	835	
Met	Lys	Cys	Met	Gly	Gly	Glu	Ile	Gln	Gly	Ile	Leu	Ala	Pro	Met	Asn		
230					235					240					245		
gat	ttc	gag	cgc	cag	aag	gca	cac	gac	gct	ggc	ctg	gtt	ctt	gat	cag	883	
Asp	Phe	Glu	Arg	Gln	Lys	Ala	His	Asp	Ala	Gly	Leu	Val	Leu	Asp	Gln		
				250					255					260			
gtt	ctg	cac	acc	aac	gat	ctg	gtg	agc	tcc	gac	aac	tgc	tac	ttc	gtg	931	
Val	Leu	His	Thr	Asn	Asp	Leu	Val	Ser	Ser	Asp	Asn	Cys	Tyr	Phe	Val		
			265					270					275				
gca	acc	ggc	gtg	acc	aac	ggc	gac	atg	ctc	cgt	ggc	gtt	tcc	tac	cgc	979	
Ala	Thr	Gly	Val	Thr	Asn	Gly	Asp	Met	Leu	Arg	Gly	Val	Ser	Tyr	Arg		
		280				285						290					
gca	aac	ggc	gca	acc	acc	cgt	tcc	ctg	gtt	atg	cgc	gca	aag	tca	ggc	1027	
Ala	Asn	Gly	Ala	Thr	Thr	Arg	Ser	Leu	Val	Met	Arg	Ala	Lys	Ser	Gly		

295 300 305
 acc atc cgc cac atc gag tct gtc cac cag ctg tcc aag ctg cag gaa 1075
 Thr Ile Arg His Ile Glu Ser Val His Gln Leu Ser Lys Leu Gln Glu
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 tac tcc gtg gtt gac tac acc acc gcg acc taagagctct tagttcgaaa 1125
 Tyr Ser Val Val Asp Tyr Thr Thr Ala Thr
 330 335
 aac 1128

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 <212> PRT
 <213> *Corynebacterium glutamicum*

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 35 40 45
 Arg Gln Leu Ile Asn Ser Val Thr Met Lys Gly Val Val Val Ile Gly
 50 55 60
 Glu Gly Glu Lys Asp Glu Ala Pro Met Leu Tyr Asn Gly Glu Glu Val
 65 70 75 80
 Gly Thr Gly Phe Gly Pro Glu Val Asp Ile Ala Val Asp Pro Val Asp
 85 90 95
 Gly Thr Thr Leu Met Ala Glu Gly Arg Pro Asn Ala Ile Ser Ile Leu
 100 105 110
 Ala Ala Ala Glu Arg Gly Thr Met Tyr Asp Pro Ser Ser Val Phe Tyr
 115 120 125
 Met Lys Lys Ile Ala Val Gly Pro Glu Ala Ala Gly Lys Ile Asp Ile
 130 135 140
 Glu Ala Pro Val Ala His Asn Ile Asn Ala Val Ala Lys Ser Lys Gly
 145 150 155 160
 Ile Asn Pro Ser Asp Val Thr Val Val Val Leu Asp Arg Pro Arg His
 165 170 175
 Ile Glu Leu Ile Ala Asp Ile Arg Arg Ala Gly Ala Lys Val Arg Leu
 180 185 190
 Ile Ser Asp Gly Asp Val Ala Gly Ala Val Ala Ala Ala Gln Asp Ser
 195 200 205
 Asn Ser Val Asp Ile Met Met Gly Thr Gly Gly Thr Pro Glu Gly Ile
 210 215 220

Ile Thr Ala Cys Ala Met Lys Cys Met Gly Gly Glu Ile Gln Gly Ile
 225 230 235 240

Leu Ala Pro Met Asn Asp Phe Glu Arg Gln Lys Ala His Asp Ala Gly
 245 250 255

Leu Val Leu Asp Gln Val Leu His Thr Asn Asp Leu Val Ser Ser Asp
 260 265 270

Asn Cys Tyr Phe Val Ala Thr Gly Val Thr Asn Gly Asp Met Leu Arg
 275 280 285

Gly Val Ser Tyr Arg Ala Asn Gly Ala Thr Thr Arg Ser Leu Val Met
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Arg Ala Lys Ser Gly Thr Ile Arg His Ile Glu Ser Val His Gln Leu
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Ser Lys Leu Gln Glu Tyr Ser Val Val Asp Tyr Thr Thr Ala Thr
 325 330 335

<210> 167
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 <222> (101)..(1012)
 <223> RXN02920

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 Met Lys Phe Val Met
 1 5

tat ccg cat ttg tgg gag tcc acg acc gct gtc att gag ggt ggc gga 163
 Tyr Pro His Leu Trp Glu Ser Thr Thr Ala Val Ile Glu Gly Gly Gly
 10 15 20

cat gag cgg gtt gag gat att aaa gat gca gac ttc att ttc ttt aat 211
 His Glu Arg Val Glu Asp Ile Lys Asp Ala Asp Phe Ile Phe Phe Asn
 25 30 35

ggt tca gcg ccg gag ttc ccg gat ttg ccg gag aac atc aag ttc gtg 259
 Gly Ser Ala Pro Glu Phe Pro Asp Leu Pro Glu Asn Ile Lys Phe Val
 40 45 50

cag gcc tcc atg gcg ggt att gat gcg ctg gtc aag cgt ggt gtc gtc 307
 Gln Ala Ser Met Ala Gly Ile Asp Ala Leu Val Lys Arg Gly Val Val
 55 60 65

aat gag aag gca cgt tgg gca aac gcg gct ggc ctg tac gct gac acc 355
 Asn Glu Lys Ala Arg Trp Ala Asn Ala Ala Gly Leu Tyr Ala Asp Thr
 70 75 80 85

gtt gct gag tcc acc att ggt tta att ctg gcg cag atg cac atg cat 403
 Val Ala Glu Ser Thr Ile Gly Leu Ile Leu Ala Gln Met His Met His

90										95										100										
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Ala	Thr	Thr	Arg	Leu	Ala	Lys	Ser	Trp	Ser	Val	Arg	Pro	Glu	Val	Glu															
			105				110				115																			
aac	aac	aag	tca	tgg	ctg	cat	gac	aat	aaa	act	gtc	gct	att	ttg	ggc	499														
Asn	Asn	Lys	Ser	Trp	Leu	His	Asp	Asn	Lys	Thr	Val	Ala	Ile	Leu	Gly															
			120				125				130																			
gdc	ggt	ggc	att	ggc	gtg	cgt	ctg	ctg	gaa	atg	ctc	aag	ccg	ttc	aac	547														
Ala	Gly	Gly	Ile	Gly	Val	Arg	Leu	Leu	Glu	Met	Leu	Lys	Pro	Phe	Asn															
			135				140				145																			
gtg	aag	acc	att	gcg	gtt	aat	aac	tct	ggt	cgt	ccg	gtg	gaa	ggt	gca	595														
Val	Lys	Thr	Ile	Ala	Val	Asn	Asn	Ser	Gly	Arg	Pro	Val	Glu	Gly	Ala															
			150				155				160					165														
gat	gaa	acc	ttc	gcc	atg	gat	aag	gct	gag	cac	gtg	tgg	gct	gag	gct	643														
Asp	Glu	Thr	Phe	Ala	Met	Asp	Lys	Ala	Glu	His	Val	Trp	Ala	Glu	Ala															
			170				175				180																			
gat	gtg	ttt	gtg	ctc	atc	ctg	ccg	ctg	act	gat	gcc	act	tat	cag	atc	691														
Asp	Val	Phe	Val	Leu	Ile	Leu	Pro	Leu	Thr	Asp	Ala	Thr	Tyr	Gln	Ile															
			185				190				195																			
gtc	aat	gca	gaa	act	ttg	ggc	aag	atg	aag	cct	tct	gcc	gtg	gtg	gtc	739														
Val	Asn	Ala	Glu	Thr	Leu	Gly	Lys	Met	Lys	Pro	Ser	Ala	Val	Val	Val															
			200				205				210																			
aat	gtg	ggg	cgt	ggc	ccg	ctg	atc	aac	acc	gat	gat	ctg	gtg	gat	gca	787														
Asn	Val	Gly	Arg	Gly	Pro	Leu	Ile	Asn	Thr	Asp	Asp	Leu	Val	Asp	Ala															
			215				220				225																			
ttg	aac	aac	ggc	acc	att	gcg	ggt	gct	gcg	ctg	gac	gtt	acc	gat	cct	835														
Leu	Asn	Asn	Gly	Thr	Ile	Ala	Gly	Ala	Ala	Leu	Asp	Val	Thr	Asp	Pro															
			230				235				240					245														
gag	cca	ctt	cct	gac	agc	cac	ccg	ctg	tgg	gag	atg	gac	aat	gtg	gtt	883														
Glu	Pro	Leu	Pro	Asp	Ser	His	Pro	Leu	Trp	Glu	Met	Asp	Asn	Val	Val															
			250				255				260																			
atc	act	cct	cat	act	gca	aac	acg	aat	gag	agg	att	cgt	gct	ttg	acc	931														
Ile	Thr	Pro	His	Thr	Ala	Asn	Thr	Asn	Glu	Arg	Ile	Arg	Ala	Leu	Thr															
			265				270				275																			
ggc	gaa	ctc	acc	ttg	cgc	aac	att	gag	ttg	ttt	gag	gca	ggc	gag	cag	979														
Gly	Glu	Leu	Thr	Leu	Arg	Asn	Ile	Glu	Leu	Phe	Glu	Ala	Gly	Glu	Gln															
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Met	Ala	Thr	Glu	Val	Asp	Val	Val	Ala	Gly	Tyr																				
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ccg															1035															

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<211> 304

<212> PRT

<213> Corynebacterium glutamicum

<400> 168

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Met Lys Phe Val Met Tyr Pro His Leu Trp Glu Ser Thr Thr Ala Val
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Ile Glu Gly Gly Gly His Glu Arg Val Glu Asp Ile Lys Asp Ala Asp
      20           25           30

Phe Ile Phe Phe Asn Gly Ser Ala Pro Glu Phe Pro Asp Leu Pro Glu
      35           40           45

Asn Ile Lys Phe Val Gln Ala Ser Met Ala Gly Ile Asp Ala Leu Val
 50           55           60

Lys Arg Gly Val Val Asn Glu Lys Ala Arg Trp Ala Asn Ala Ala Gly
 65           70           75           80

Leu Tyr Ala Asp Thr Val Ala Glu Ser Thr Ile Gly Leu Ile Leu Ala
      85           90           95

Gln Met His Met His Ala Thr Thr Arg Leu Ala Lys Ser Trp Ser Val
      100           105           110

Arg Pro Glu Val Glu Asn Asn Lys Ser Trp Leu His Asp Asn Lys Thr
      115           120           125

Val Ala Ile Leu Gly Ala Gly Gly Ile Gly Val Arg Leu Leu Glu Met
      130           135           140

Leu Lys Pro Phe Asn Val Lys Thr Ile Ala Val Asn Asn Ser Gly Arg
145           150           155           160

Pro Val Glu Gly Ala Asp Glu Thr Phe Ala Met Asp Lys Ala Glu His
      165           170           175

Val Trp Ala Glu Ala Asp Val Phe Val Leu Ile Leu Pro Leu Thr Asp
      180           185           190

Ala Thr Tyr Gln Ile Val Asn Ala Glu Thr Leu Gly Lys Met Lys Pro
      195           200           205

Ser Ala Val Val Val Asn Val Gly Arg Gly Pro Leu Ile Asn Thr Asp
      210           215           220

Asp Leu Val Asp Ala Leu Asn Asn Gly Thr Ile Ala Gly Ala Ala Leu
225           230           235           240

Asp Val Thr Asp Pro Glu Pro Leu Pro Asp Ser His Pro Leu Trp Glu
      245           250           255

Met Asp Asn Val Val Ile Thr Pro His Thr Ala Asn Thr Asn Glu Arg
      260           265           270

Ile Arg Ala Leu Thr Gly Glu Leu Thr Leu Arg Asn Ile Glu Leu Phe
      275           280           285

Glu Ala Gly Glu Gln Met Ala Thr Glu Val Asp Val Val Ala Gly Tyr
      290           295           300

```


ctt cct gac agc cac ccg ctg tgg gag atg gac aat gtg gtt atc act 633
 Leu Pro Asp Ser His Pro Leu Trp Glu Met Asp Asn Val Val Ile Thr
 180 185 190

 cct cat act gca aac acg aat gag agg att cgt gct ttg acc ggc gaa 681
 Pro His Thr Ala Asn Thr Asn Glu Arg Ile Arg Ala Leu Thr Gly Glu
 195 200 205 210

 ctc acc ttg cgc aac att gag ttg ttt gag gca ggc gag cag atg gcc 729
 Leu Thr Leu Arg Asn Ile Glu Leu Phe Glu Ala Gly Glu Gln Met Ala
 215 220 225

 acc gag gtc gat gtg gtg gct ggc tac taggcctttt atggtgtgat 776
 Thr Glu Val Asp Val Val Ala Gly Tyr
 230 235

 ccg 779

<210> 170
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 <213> Corynebacterium glutamicum

<400> 170
 Met Arg Lys His Arg Trp Ala Asn Ala Ala Gly Leu Tyr Ala Asp Thr
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 Val Ala Glu Ser Thr Ile Gly Leu Ile Leu Ala Gln Met His Met His
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 Ala Thr Thr Arg Leu Ala Lys Ser Trp Ser Val Arg Pro Glu Val Glu
 35 40 45

 Asn Asn Lys Ser Trp Leu His Asp Asn Lys Thr Val Ala Ile Leu Gly
 50 55 60

 Ala Gly Gly Ile Gly Val Arg Leu Leu Glu Met Leu Lys Pro Phe Asn
 65 70 75 80

 Val Lys Thr Ile Ala Val Asn Asn Ser Gly Arg Pro Val Glu Gly Ala
 85 90 95

 Asp Glu Thr Phe Ala Met Asp Lys Ala Glu His Val Trp Ala Glu Ala
 100 105 110

 Asp Val Phe Val Leu Ile Leu Pro Leu Thr Asp Ala Thr Tyr Gln Ile
 115 120 125

 Val Asn Ala Glu Thr Leu Gly Lys Met Lys Pro Ser Ala Val Val Val
 130 135 140

 Asn Val Gly Arg Gly Pro Leu Ile Asn Thr Asp Asp Leu Val Asp Ala
 145 150 155 160

 Leu Asn Asn Gly Thr Ile Ala Gly Ala Ala Leu Asp Val Thr Asp Pro
 165 170 175

 Glu Pro Leu Pro Asp Ser His Pro Leu Trp Glu Met Asp Asn Val Val
 180 185 190

Ile Thr Pro His Thr Ala Asn Thr Asn Glu Arg Ile Arg Ala Leu Thr
 195 200 205

Gly Glu Leu Thr Leu Arg Asn Ile Glu Leu Phe Glu Ala Gly Glu Gln
 210 215 220

Met Ala Thr Glu Val Asp Val Val Ala Gly Tyr
 225 230 235

<210> 171

<211> 792

<212> DNA

<213> Corynebacterium glutamicum

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<222> (101)..(769)

<223> RXN02688

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gggttcgcgc agcaagcgaa ggaaggaaac ttaactagcc atg gcc ggc cgg att 115
 Met Ala Gly Arg Ile
 1 5

att ttg cta cga cac ggg cag act cac aac aac gtc aaa cac ctc ctg 163
 Ile Leu Leu Arg His Gly Gln Thr His Asn Asn Val Lys His Leu Leu
 10 15 20

gac acc cgc cca cca gga gct gaa ctc acc gac ctg ggc cgt aaa caa 211
 Asp Thr Arg Pro Pro Gly Ala Glu Leu Thr Asp Leu Gly Arg Lys Gln
 25 30 35

gcc ctt gaa gtt ggc cac gaa cta gcc acc tac tcc ggt gag cgc ctc 259
 Ala Leu Glu Val Gly His Glu Leu Ala Thr Tyr Ser Gly Glu Arg Leu
 40 45 50

gcc cat gtg tac agc tcc atc gtg ttg cgc gcc caa caa acc gcc gtg 307
 Ala His Val Tyr Ser Ser Ile Val Leu Arg Ala Gln Gln Thr Ala Val
 55 60 65

ctt gcc acc tct acc ttt gaa aaa gct cgc gac atg cag tcc ggt gcg 355
 Leu Ala Thr Ser Thr Phe Glu Lys Ala Arg Asp Met Gln Ser Gly Ala
 70 75 80 85

att cca ctc gac gtt gtg gaa ggc att cag gaa atc aac gtc ggc gac 403
 Ile Pro Leu Asp Val Val Glu Gly Ile Gln Glu Ile Asn Val Gly Asp
 90 95 100

ttt gaa atg cgc ggc gat gaa gaa gcc cac atg aat tac tcc cgc gca 451
 Phe Glu Met Arg Gly Asp Glu Glu Ala His Met Asn Tyr Ser Arg Ala
 105 110 115

ctc aac ggc tgg ctt cac ggg gat cct gcc gct ggt ctt ccc ggc ggt 499
 Leu Asn Gly Trp Leu His Gly Asp Pro Ala Ala Gly Leu Pro Gly Gly
 120 125 130

gag acc tac aaa gac gtg ctg aac cgc tac cag ccg act ctt gat cga 547
 Glu Thr Tyr Lys Asp Val Leu Asn Arg Tyr Gln Pro Thr Leu Asp Arg

135	140	145	
atc atg gac agc cac gac ctt gac gac gac cgc gac gtt gcc gtt gtc			595
Ile Met Asp Ser His Asp Leu Asp Asp Asp Arg Asp Val Ala Val Val			
150	155	160	165
agc cac ggc gcc gtc atc cgc atc gtg gca aca cac gca act ggt gtg			643
Ser His Gly Ala Val Ile Arg Ile Val Ala Thr His Ala Thr Gly Val			
	170	175	180
gat ccc aac ttt gcg ttc aac acc tac ctg ggc aac tgc cgc ttc gtg			691
Asp Pro Asn Phe Ala Phe Asn Thr Tyr Leu Gly Asn Cys Arg Phe Val			
	185	190	195
gtg ctg gag cca aac ggt aag aaa ttc agc caa tgg gat gtt gtg cgc			739
Val Leu Glu Pro Asn Gly Lys Lys Phe Ser Gln Trp Asp Val Val Arg			
	200	205	210
tgg act gac agc cca ctg cca tgg cag gag taattgagac caaaggctcg			789
Trp Thr Asp Ser Pro Leu Pro Trp Gln Glu			
	215	220	
gat			792
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<213> Corynebacterium glutamicum			
<400> 172			
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Val Lys His Leu Leu Asp Thr Arg Pro Pro Gly Ala Glu Leu Thr Asp			
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Leu Gly Arg Lys Gln Ala Leu Glu Val Gly His Glu Leu Ala Thr Tyr			
	35	40	45
Ser Gly Glu Arg Leu Ala His Val Tyr Ser Ser Ile Val Leu Arg Ala			
	50	55	60
Gln Gln Thr Ala Val Leu Ala Thr Ser Thr Phe Glu Lys Ala Arg Asp			
	65	70	75
Met Gln Ser Gly Ala Ile Pro Leu Asp Val Val Glu Gly Ile Gln Glu			
	85	90	95
Ile Asn Val Gly Asp Phe Glu Met Arg Gly Asp Glu Glu Ala His Met			
	100	105	110
Asn Tyr Ser Arg Ala Leu Asn Gly Trp Leu His Gly Asp Pro Ala Ala			
	115	120	125
Gly Leu Pro Gly Gly Glu Thr Tyr Lys Asp Val Leu Asn Arg Tyr Gln			
	130	135	140
Pro Thr Leu Asp Arg Ile Met Asp Ser His Asp Leu Asp Asp Asp Arg			
	145	150	155
			160

Asp Val Ala Val Val Ser His Gly Ala Val Ile Arg Ile Val Ala Thr
 165 170 175

His Ala Thr Gly Val Asp Pro Asn Phe Ala Phe Asn Thr Tyr Leu Gly
 180 185 190

Asn Cys Arg Phe Val Val Leu Glu Pro Asn Gly Lys Lys Phe Ser Gln
 195 200 205

Trp Asp Val Val Arg Trp Thr Asp Ser Pro Leu Pro Trp Gln Glu
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<211> 336

<212> DNA

<213> Corynebacterium glutamicum

<220>

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<222> (101)..(313)

<223> RXN03087

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gaataacctgg aaaagagctg atattgatag ggtttaagtc atg aag atc tac gca 115
 Met Lys Ile Tyr Ala
 1 5

cct ttt gct gga atc gtc cac tat ttt gtc gat gaa ggc gat ccc gtg 163
 Pro Phe Ala Gly Ile Val His Tyr Phe Val Asp Glu Gly Asp Pro Val
 10 15 20

gaa acc ggc atg caa ctg gga acg gta gaa acc atc aaa ctc gag gca 211
 Glu Thr Gly Met Gln Leu Gly Thr Val Glu Thr Ile Lys Leu Glu Ala
 25 30 35

cca atc atg gca ccg gga cct ggc atc gta gct aag gtt tct ttt gat 259
 Pro Ile Met Ala Pro Gly Pro Gly Ile Val Ala Lys Val Ser Phe Asp
 40 45 50

gat ttc tcc gac gtc acc ggc ggc gat gaa ctc ctc gaa ttg gag gca 307
 Asp Phe Ser Asp Val Thr Gly Gly Asp Glu Leu Leu Glu Leu Glu Ala
 55 60 65

aag aac taatgggtca aaccgcgcatc att 336
 Lys Asn
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<210> 174

<211> 71

<212> PRT

<213> Corynebacterium glutamicum

<400> 174

Met Lys Ile Tyr Ala Pro Phe Ala Gly Ile Val His Tyr Phe Val Asp
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Glu Gly Asp Pro Val Glu Thr Gly Met Gln Leu Gly Thr Val Glu Thr

20 25 30
 Ile Lys Leu Glu Ala Pro Ile Met Ala Pro Gly Pro Gly Ile Val Ala
 35 40 45
 Lys Val Ser Phe Asp Asp Phe Ser Asp Val Thr Gly Gly Asp Glu Leu
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 Leu Glu Leu Glu Ala Lys Asn
 65 70

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 <212> DNA
 <213> Corynebacterium glutamicum

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 <223> RXN03186

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 Met Ala Asp Gln Ala
 1 5

 aaa ctt ggt ggc aag ccc tcg gat gac tct aac ttc gcg atg atc cgc 163
 Lys Leu Gly Gly Lys Pro Ser Asp Asp Ser Asn Phe Ala Met Ile Arg
 10 15 20

 gat ggc gtg gca tct tat ttg aac gac tca gat ccg gag gag acc aac 211
 Asp Gly Val Ala Ser Tyr Leu Asn Asp Ser Asp Pro Glu Glu Thr Asn
 25 30 35

 gag tgg atg gat tca ctc gac gga tta ctc cag gag tct tct cca gaa 259
 Glu Trp Met Asp Ser Leu Asp Gly Leu Leu Gln Glu Ser Ser Pro Glu
 40 45 50

 cgt gct cgt tac ctc atg ctt cgt ttg ctt gag cgt gca tct gca aag 307
 Arg Ala Arg Tyr Leu Met Leu Arg Leu Leu Glu Arg Ala Ser Ala Lys
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 Arg
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<210> 176
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 <212> PRT
 <213> Corynebacterium glutamicum

<400> 176
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Pro Glu Glu Thr Asn Glu Trp Met Asp Ser Leu Asp Gly Leu Leu Gln
 35 40 45
 Glu Ser Ser Pro Glu Arg Ala Arg Tyr Leu Met Leu Arg Leu Leu Glu
 50 55 60
 Arg Ala Ser Ala Lys Arg
 65 70

<210> 177
 <211> 302
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (1)..(279)
 <223> RXN03187

<400> 177
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 Val Ala Val Ser Asp Phe Ser Thr Asp Leu Pro Asn Gln Ile Arg Glu
 1 5 10 15
 tgg gtc cca ggc gac tac acc gtt ctc ggt gca gat ggc ttc ggt ttc 96
 Trp Val Pro Gly Asp Tyr Thr Val Leu Gly Ala Asp Gly Phe Gly Phe
 20 25 30
 tct gat acc cgc cca gct gct cgt cgc ttc ttc aac atc gac gct gag 144
 Ser Asp Thr Arg Pro Ala Ala Arg Arg Phe Phe Asn Ile Asp Ala Glu
 35 40 45
 tcc att gtt gtt gca gtg ctg aac tcc ctg gca cgc gaa ggc aag atc 192
 Ser Ile Val Val Ala Val Leu Asn Ser Leu Ala Arg Glu Gly Lys Ile
 50 55 60
 gac gtc tcc gtt gct gct cag gct gct gag aag ttc aag ttg gat gat 240
 Asp Val Ser Val Ala Ala Gln Ala Ala Glu Lys Phe Lys Leu Asp Asp
 65 70 75 80
 cct acg agt gtt tcc gta gat cca aac gct cct gag gaa taaatcacct 289
 Pro Thr Ser Val Ser Val Asp Pro Asn Ala Pro Glu Glu
 85 90
 caagggacag ata 302

<210> 178
 <211> 93
 <212> PRT
 <213> Corynebacterium glutamicum

<400> 178
 Val Ala Val Ser Asp Phe Ser Thr Asp Leu Pro Asn Gln Ile Arg Glu
 1 5 10 15
 Trp Val Pro Gly Asp Tyr Thr Val Leu Gly Ala Asp Gly Phe Gly Phe
 20 25 30

<400> 179															
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ggcgagaact ctgtcgaatg acacaaaatc tggagaagta atg act act gct gca															115
Met Thr Thr Ala Ala															
1 5															
atc agg ggc ctt cag ggc gag gcg ccg acc aag aat aag gaa ctg ctg															163
Ile Arg Gly Leu Gln Gly Glu Ala Pro Thr Lys Asn Lys Glu Leu Leu															
10 15 20															
aac tgg atc gca gac gcc gtc gag ctc ttc cag cct gag gct gtt gtg															211
Asn Trp Ile Ala Asp Ala Val Glu Leu Phe Gln Pro Glu Ala Val Val															
25 30 35															
ttc gtt gat gga tcc cag gct gag tgg gat cgc atg gcg gag gat ctt															259
Phe Val Asp Gly Ser Gln Ala Glu Trp Asp Arg Met Ala Glu Asp Leu															
40 45 50															
gtt gaa gcc ggt acc ctc atc aag ctc aac gag gaa aag cgt ccg aac															307
Val Glu Ala Gly Thr Leu Ile Lys Leu Asn Glu Glu Lys Arg Pro Asn															
55 60 65															
agc tac cta gct cgt tcc aac cca tct gac gtt gcg cgc gtt gag tcc															355
Ser Tyr Leu Ala Arg Ser Asn Pro Ser Asp Val Ala Arg Val Glu Ser															
70 75 80 85															
cgc acc ttc atc tgc tcc gag aag gaa gaa gat gct ggc cca acc aac															403
Arg Thr Phe Ile Cys Ser Glu Lys Glu Glu Asp Ala Gly Pro Thr Asn															
90 95 100															
aac tgg gct cca cca cag gca atg aag gac gaa atg tcc aag cat tac															451
Asn Trp Ala Pro Pro Gln Ala Met Lys Asp Glu Met Ser Lys His Tyr															
105 110 115															
gct ggt tcc atg aag ggg cgc acc atg tac gtc gtg cct ttc tgc atg															499
Ala Gly Ser Met Lys Gly Arg Thr Met Tyr Val Val Pro Phe Cys Met															
120 125 130															

ggt cca atc agc gat ccg gac cct aag ctt ggt gtg cag ctc act gac	547
Gly Pro Ile Ser Asp Pro Asp Pro Lys Leu Gly Val Gln Leu Thr Asp	
135 140 145	
tcc gag tac gtt gtc atg tcc atg cgc atc atg acc cgc atg ggt att	595
Ser Glu Tyr Val Val Met Ser Met Arg Ile Met Thr Arg Met Gly Ile	
150 155 160 165	
gaa gcg ctg gac aag atc ggc gcg aac ggc agc ttc gtc agg tgc ctc	643
Glu Ala Leu Asp Lys Ile Gly Ala Asn Gly Ser Phe Val Arg Cys Leu	
170 175 180	
cac tcc gtt ggt gct cct ttg gag cca ggc cag gaa gac gtt gca tgg	691
His Ser Val Gly Ala Pro Leu Glu Pro Gly Gln Glu Asp Val Ala Trp	
185 190 195	
cct tgc aac gac acc aag tac atc acc cag ttc cca gag acc aag gaa	739
Pro Cys Asn Asp Thr Lys Tyr Ile Thr Gln Phe Pro Glu Thr Lys Glu	
200 205 210	
att tgg tcc tac ggt tcc ggc tac ggc gga aac gca atc ctg gca aag	787
Ile Trp Ser Tyr Gly Ser Gly Tyr Gly Gly Asn Ala Ile Leu Ala Lys	
215 220 225	
aag tgc tac gca ctg cgt atc gca tct gtc atg gct cgc gaa gaa gga	835
Lys Cys Tyr Ala Leu Arg Ile Ala Ser Val Met Ala Arg Glu Glu Gly	
230 235 240 245	
tgg atg gct gag cac atg ctc atc ctg aag ctg atc aac cca gag ggc	883
Trp Met Ala Glu His Met Leu Ile Leu Lys Leu Ile Asn Pro Glu Gly	
250 255 260	
aag gcg tac cac atc gca gca gca ttc cca tct gct tgt ggc aag acc	931
Lys Ala Tyr His Ile Ala Ala Ala Phe Pro Ser Ala Cys Gly Lys Thr	
265 270 275	
aac ctc gcc atg atc act cca acc atc cca ggc tgg acc gct cag gtt	979
Asn Leu Ala Met Ile Thr Pro Thr Ile Pro Gly Trp Thr Ala Gln Val	
280 285 290	
gtt ggc gac gac atc gct tgg ctg aag ctg cgc gag gac ggc ctc tac	1027
Val Gly Asp Asp Ile Ala Trp Leu Lys Leu Arg Glu Asp Gly Leu Tyr	
295 300 305	
gca gtt aac cca gaa aat ggt ttc ttc ggt gtt gct cca ggc acc aac	1075
Ala Val Asn Pro Glu Asn Gly Phe Phe Gly Val Ala Pro Gly Thr Asn	
310 315 320 325	
tac gca tcc aac cca atc gcg atg aag acc atg gaa cca ggc aac acc	1123
Tyr Ala Ser Asn Pro Ile Ala Met Lys Thr Met Glu Pro Gly Asn Thr	
330 335 340	
ctg ttc acc aac gtg gca ctc acc gac gac ggc gac atc tgg tgg gaa	1171
Leu Phe Thr Asn Val Ala Leu Thr Asp Asp Gly Asp Ile Trp Trp Glu	
345 350 355	
ggc atg gac ggc gac gcc cca gct cac ctc att gac tgg atg ggc aac	1219
Gly Met Asp Gly Asp Ala Pro Ala His Leu Ile Asp Trp Met Gly Asn	
360 365 370	

gac tgg acc cca gag tcc gac gaa aac gct gct cac cct aac tcc cgt Asp Trp Thr Pro Glu Ser Asp Glu Asn Ala Ala His Pro Asn Ser Arg 375 380 385	1267
tac tgc gta gca atc gac cag tcc cca gca gca gca cct gag ttc aac Tyr Cys Val Ala Ile Asp Gln Ser Pro Ala Ala Ala Pro Glu Phe Asn 390 395 400 405	1315
gac tgg gaa ggc gtc aag atc gac gca atc ctc ttc ggt gga cgt cgc Asp Trp Glu Gly Val Lys Ile Asp Ala Ile Leu Phe Gly Gly Arg Arg 410 415 420	1363
gca gac acc gtc cca ctg gtt acc cag acc tac gac tgg gag cac ggc Ala Asp Thr Val Pro Leu Val Thr Gln Thr Tyr Asp Trp Glu His Gly 425 430 435	1411
acc atg gtt ggt gca ctg ctc gca tcc ggt cag acc gca gct tcc gca Thr Met Val Gly Ala Leu Leu Ala Ser Gly Gln Thr Ala Ala Ser Ala 440 445 450	1459
gaa gca aag gtc ggc aca ctc cgc cac gac cca atg gca atg ctc cca Glu Ala Lys Val Gly Thr Leu Arg His Asp Pro Met Ala Met Leu Pro 455 460 465	1507
ttc att ggc tac aac gct ggt gaa tac ctg cag aac tgg att gac atg Phe Ile Gly Tyr Asn Ala Gly Glu Tyr Leu Gln Asn Trp Ile Asp Met 470 475 480 485	1555
ggt aac aag ggt ggc gac aag atg cca tcc atc ttc ctg gtc aac tgg Gly Asn Lys Gly Gly Asp Lys Met Pro Ser Ile Phe Leu Val Asn Trp 490 495 500	1603
ttc cgc cgt ggc gaa gat gga cgc ttc ctg tgg cct ggc ttc ggc gac Phe Arg Arg Gly Glu Asp Gly Arg Phe Leu Trp Pro Gly Phe Gly Asp 505 510 515	1651
aac tct cgc gtt ctg aag tgg gtc atc gac cgc atc gaa ggc cac gtt Asn Ser Arg Val Leu Lys Trp Val Ile Asp Arg Ile Glu Gly His Val 520 525 530	1699
ggc gca gac gag acc gtt gtt gga cac acc gct aag gcc gaa gac ctc Gly Ala Asp Glu Thr Val Val Gly His Thr Ala Lys Ala Glu Asp Leu 535 540 545	1747
gac ctc gac ggc ctc gac acc cca att gag gat gtc aag gaa gca ctg Asp Leu Asp Gly Leu Asp Thr Pro Ile Glu Asp Val Lys Glu Ala Leu 550 555 560 565	1795
acc gct cct gca gag cag tgg gca aac gac gtt gaa gac aac gcc gag Thr Ala Pro Ala Glu Gln Trp Ala Asn Asp Val Glu Asp Asn Ala Glu 570 575 580	1843
tac ctc act ttc ctc gga cca cgt gtt cct gca gag gtt cac agc cag Tyr Leu Thr Phe Leu Gly Pro Arg Val Pro Ala Glu Val His Ser Gln 585 590 595	1891
ttc gat gct ctg aag gcc cgc att tca gca gct cac gct taaagttcac Phe Asp Ala Leu Lys Ala Arg Ile Ser Ala Ala His Ala 600 605 610	1940
gcttaagaac tgc	1953

<210> 180

<211> 610

<212> PRT

<213> Corynebacterium glutamicum

<400> 180

Met Thr Thr Ala Ala Ile Arg Gly Leu Gln Gly Glu Ala Pro Thr Lys
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Asn Lys Glu Leu Leu Asn Trp Ile Ala Asp Ala Val Glu Leu Phe Gln
 20 25 30

Pro Glu Ala Val Val Phe Val Asp Gly Ser Gln Ala Glu Trp Asp Arg
 35 40 45

Met Ala Glu Asp Leu Val Glu Ala Gly Thr Leu Ile Lys Leu Asn Glu
 50 55 60

Glu Lys Arg Pro Asn Ser Tyr Leu Ala Arg Ser Asn Pro Ser Asp Val
 65 70 75 80

Ala Arg Val Glu Ser Arg Thr Phe Ile Cys Ser Glu Lys Glu Glu Asp
 85 90 95

Ala Gly Pro Thr Asn Asn Trp Ala Pro Pro Gln Ala Met Lys Asp Glu
 100 105 110

Met Ser Lys His Tyr Ala Gly Ser Met Lys Gly Arg Thr Met Tyr Val
 115 120 125

Val Pro Phe Cys Met Gly Pro Ile Ser Asp Pro Asp Pro Lys Leu Gly
 130 135 140

Val Gln Leu Thr Asp Ser Glu Tyr Val Val Met Ser Met Arg Ile Met
 145 150 155 160

Thr Arg Met Gly Ile Glu Ala Leu Asp Lys Ile Gly Ala Asn Gly Ser
 165 170 175

Phe Val Arg Cys Leu His Ser Val Gly Ala Pro Leu Glu Pro Gly Gln
 180 185 190

Glu Asp Val Ala Trp Pro Cys Asn Asp Thr Lys Tyr Ile Thr Gln Phe
 195 200 205

Pro Glu Thr Lys Glu Ile Trp Ser Tyr Gly Ser Gly Tyr Gly Gly Asn
 210 215 220

Ala Ile Leu Ala Lys Lys Cys Tyr Ala Leu Arg Ile Ala Ser Val Met
 225 230 235 240

Ala Arg Glu Glu Gly Trp Met Ala Glu His Met Leu Ile Leu Lys Leu
 245 250 255

Ile Asn Pro Glu Gly Lys Ala Tyr His Ile Ala Ala Ala Phe Pro Ser
 260 265 270

Ala Cys Gly Lys Thr Asn Leu Ala Met Ile Thr Pro Thr Ile Pro Gly
 275 280 285

Trp Thr Ala Gln Val Val Gly Asp Asp Ile Ala Trp Leu Lys Leu Arg
 290 295 300
 Glu Asp Gly Leu Tyr Ala Val Asn Pro Glu Asn Gly Phe Phe Gly Val
 305 310 315 320
 Ala Pro Gly Thr Asn Tyr Ala Ser Asn Pro Ile Ala Met Lys Thr Met
 325 330 335
 Glu Pro Gly Asn Thr Leu Phe Thr Asn Val Ala Leu Thr Asp Asp Gly
 340 345 350
 Asp Ile Trp Trp Glu Gly Met Asp Gly Asp Ala Pro Ala His Leu Ile
 355 360 365
 Asp Trp Met Gly Asn Asp Trp Thr Pro Glu Ser Asp Glu Asn Ala Ala
 370 375 380
 His Pro Asn Ser Arg Tyr Cys Val Ala Ile Asp Gln Ser Pro Ala Ala
 385 390 395 400
 Ala Pro Glu Phe Asn Asp Trp Glu Gly Val Lys Ile Asp Ala Ile Leu
 405 410 415
 Phe Gly Gly Arg Arg Ala Asp Thr Val Pro Leu Val Thr Gln Thr Tyr
 420 425 430
 Asp Trp Glu His Gly Thr Met Val Gly Ala Leu Leu Ala Ser Gly Gln
 435 440 445
 Thr Ala Ala Ser Ala Glu Ala Lys Val Gly Thr Leu Arg His Asp Pro
 450 455 460
 Met Ala Met Leu Pro Phe Ile Gly Tyr Asn Ala Gly Glu Tyr Leu Gln
 465 470 475 480
 Asn Trp Ile Asp Met Gly Asn Lys Gly Gly Asp Lys Met Pro Ser Ile
 485 490 495
 Phe Leu Val Asn Trp Phe Arg Arg Gly Glu Asp Gly Arg Phe Leu Trp
 500 505 510
 Pro Gly Phe Gly Asp Asn Ser Arg Val Leu Lys Trp Val Ile Asp Arg
 515 520 525
 Ile Glu Gly His Val Gly Ala Asp Glu Thr Val Val Gly His Thr Ala
 530 535 540
 Lys Ala Glu Asp Leu Asp Leu Asp Gly Leu Asp Thr Pro Ile Glu Asp
 545 550 555 560
 Val Lys Glu Ala Leu Thr Ala Pro Ala Glu Gln Trp Ala Asn Asp Val
 565 570 575
 Glu Asp Asn Ala Glu Tyr Leu Thr Phe Leu Gly Pro Arg Val Pro Ala
 580 585 590
 Glu Val His Ser Gln Phe Asp Ala Leu Lys Ala Arg Ile Ser Ala Ala
 595 600 605

His Ala
610

<210> 181
<211> 1305
<212> DNA
<213> *Corynebacterium glutamicum*

<220>
<221> CDS
<222> (101)..(1282)
<223> RXS01260

<400> 181
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ctttacccat gagaagaaga ccttcggcat caatggcgaa gtg acc ttc aac tat 115
Val Thr Phe Asn Tyr
1 5
gag gat gct cac aag cgt tcc cgt ggc gtt tcc gac aag atc gtt gga 163
Glu Asp Ala His Lys Arg Ser Arg Gly Val Ser Asp Lys Ile Val Gly
10 15 20
ggc gtt cat tac ttg atg aag aag aac aag atc atc gaa att cat ggt 211
Gly Val His Tyr Leu Met Lys Lys Asn Lys Ile Ile Glu Ile His Gly
25 30 35
ctt gga aac ttc aag gat gct aag act ctt gag gtc acc gac ggt aag 259
Leu Gly Asn Phe Lys Asp Ala Lys Thr Leu Glu Val Thr Asp Gly Lys
40 45 50
gat gct ggc aag acc atc acc ttt gat gac tgc atc atc gca acc ggt 307
Asp Ala Gly Lys Thr Ile Thr Phe Asp Asp Cys Ile Ile Ala Thr Gly
55 60 65
tcg gta gtc aac acc ctc cgt ggc gtt gac ttc tca gag aac gtt gtg 355
Ser Val Val Asn Thr Leu Arg Gly Val Asp Phe Ser Glu Asn Val Val
70 75 80 85
tct ttt gaa gag cag att ctt aac cct gtt gcg cca aag aag atg gtc 403
Ser Phe Glu Glu Gln Ile Leu Asn Pro Val Ala Pro Lys Lys Met Val
90 95 100
att gtt ggt gca ggc gca att gga atg gaa ttc gcc tac gtt ctt ggt 451
Ile Val Gly Ala Gly Ala Ile Gly Met Glu Phe Ala Tyr Val Leu Gly
105 110 115
aac tac ggt gta gat gta acc gtc atc gag ttc atg gat cgt gtg ctt 499
Asn Tyr Gly Val Asp Val Thr Val Ile Glu Phe Met Asp Arg Val Leu
120 125 130
cca aat gaa gat gct gaa gtc tcc aag gtt att gca aag gcc tac aag 547
Pro Asn Glu Asp Ala Glu Val Ser Lys Val Ile Ala Lys Ala Tyr Lys
135 140 145
aag atg ggc gtt aag ctt ctt cct ggc cat gca acc act gct gtt cgg 595
Lys Met Gly Val Lys Leu Leu Pro Gly His Ala Thr Thr Ala Val Arg
150 155 160 165

gac aac ggt gac ttt gtc gag gtt gat tac cag aag aag ggc tct gac	643
Asp Asn Gly Asp Phe Val Glu Val Asp Tyr Gln Lys Lys Gly Ser Asp	
170 175 180	
aag aca gag act ctt act gtt gat cga gtc atg gtt tcc gtt ggt ttc	691
Lys Thr Glu Thr Leu Thr Val Asp Arg Val Met Val Ser Val Gly Phe	
185 190 195	
cgt cca cgc gtt gag gga ttt ggt ctt gaa aac act ggc gtt aag ctc	739
Arg Pro Arg Val Glu Gly Phe Gly Leu Glu Asn Thr Gly Val Lys Leu	
200 205 210	
acc gag cgt ggc gca atc gag atc gat gat tac atg cgt acc aac gtc	787
Thr Glu Arg Gly Ala Ile Glu Ile Asp Asp Tyr Met Arg Thr Asn Val	
215 220 225	
gat ggc att tac gcc atc ggt gac gtg acc gcc aag ctt cag ctt gct	835
Asp Gly Ile Tyr Ala Ile Gly Asp Val Thr Ala Lys Leu Gln Leu Ala	
230 235 240 245	
cac gtc gca gaa gca cag ggc att gtt gcc gca gag act att gct ggt	883
His Val Ala Glu Ala Gln Gly Ile Val Ala Ala Glu Thr Ile Ala Gly	
250 255 260	
gca gaa act cag act ctt ggt gat tac atg atg atg cca cgt gca acc	931
Ala Glu Thr Gln Thr Leu Gly Asp Tyr Met Met Met Pro Arg Ala Thr	
265 270 275	
ttc tgc aac cca cag gtt tct tcc ttt ggt tac acc gaa gag cag gcc	979
Phe Cys Asn Pro Gln Val Ser Ser Phe Gly Tyr Thr Glu Glu Gln Ala	
280 285 290	
aag gag aag tgg cca gat cgt gag atc aag gtt gct tcc ttc cca ttc	1027
Lys Glu Lys Trp Pro Asp Arg Glu Ile Lys Val Ala Ser Phe Pro Phe	
295 300 305	
tct gca aac ggt aaa gca gtt ggc ctg gca gaa act gat ggt ttc gca	1075
Ser Ala Asn Gly Lys Ala Val Gly Leu Ala Glu Thr Asp Gly Phe Ala	
310 315 320 325	
aag atc gtt gct gat gca gaa ttc ggt gag ctg ctc ggt gca cac ctg	1123
Lys Ile Val Ala Asp Ala Glu Phe Gly Glu Leu Leu Gly Ala His Leu	
330 335 340	
gtt gga gca aat gca tca gag ctc atc aat gaa ttg gtg ctt gct cag	1171
Val Gly Ala Asn Ala Ser Glu Leu Ile Asn Glu Leu Val Leu Ala Gln	
345 350 355	
aac tgg gat ctc acc act gaa gag atc tct cgt agc gtc cat att cac	1219
Asn Trp Asp Leu Thr Thr Glu Glu Ile Ser Arg Ser Val His Ile His	
360 365 370	
cca acg cta tct gag gca gtt aag gaa gct gca cac ggt atc tct gga	1267
Pro Thr Leu Ser Glu Ala Val Lys Glu Ala Ala His Gly Ile Ser Gly	
375 380 385	
cac atg atc aac ttc tagaatccac ctgcttggtgcc ctg	1305
His Met Ile Asn Phe	
390	

<210> 182
 <211> 394
 <212> PRT
 <213> Corynebacterium glutamicum

<400> 182

Val	Thr	Phe	Asn	Tyr	Glu	Asp	Ala	His	Lys	Arg	Ser	Arg	Gly	Val	Ser
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Asp	Lys	Ile	Val	Gly	Gly	Val	His	Tyr	Leu	Met	Lys	Lys	Asn	Lys	Ile
			20					25					30		
Ile	Glu	Ile	His	Gly	Leu	Gly	Asn	Phe	Lys	Asp	Ala	Lys	Thr	Leu	Glu
		35					40					45			
Val	Thr	Asp	Gly	Lys	Asp	Ala	Gly	Lys	Thr	Ile	Thr	Phe	Asp	Asp	Cys
	50					55					60				
Ile	Ile	Ala	Thr	Gly	Ser	Val	Val	Asn	Thr	Leu	Arg	Gly	Val	Asp	Phe
65					70					75					80
Ser	Glu	Asn	Val	Val	Ser	Phe	Glu	Glu	Gln	Ile	Leu	Asn	Pro	Val	Ala
			85						90					95	
Pro	Lys	Lys	Met	Val	Ile	Val	Gly	Ala	Gly	Ala	Ile	Gly	Met	Glu	Phe
			100					105					110		
Ala	Tyr	Val	Leu	Gly	Asn	Tyr	Gly	Val	Asp	Val	Thr	Val	Ile	Glu	Phe
		115					120					125			
Met	Asp	Arg	Val	Leu	Pro	Asn	Glu	Asp	Ala	Glu	Val	Ser	Lys	Val	Ile
	130					135					140				
Ala	Lys	Ala	Tyr	Lys	Lys	Met	Gly	Val	Lys	Leu	Leu	Pro	Gly	His	Ala
145					150					155					160
Thr	Thr	Ala	Val	Arg	Asp	Asn	Gly	Asp	Phe	Val	Glu	Val	Asp	Tyr	Gln
			165						170					175	
Lys	Lys	Gly	Ser	Asp	Lys	Thr	Glu	Thr	Leu	Thr	Val	Asp	Arg	Val	Met
			180					185					190		
Val	Ser	Val	Gly	Phe	Arg	Pro	Arg	Val	Glu	Gly	Phe	Gly	Leu	Glu	Asn
		195					200					205			
Thr	Gly	Val	Lys	Leu	Thr	Glu	Arg	Gly	Ala	Ile	Glu	Ile	Asp	Asp	Tyr
	210					215					220				
Met	Arg	Thr	Asn	Val	Asp	Gly	Ile	Tyr	Ala	Ile	Gly	Asp	Val	Thr	Ala
225				230						235					240
Lys	Leu	Gln	Leu	Ala	His	Val	Ala	Glu	Ala	Gln	Gly	Ile	Val	Ala	Ala
			245						250					255	
Glu	Thr	Ile	Ala	Gly	Ala	Glu	Thr	Gln	Thr	Leu	Gly	Asp	Tyr	Met	Met
		260						265					270		
Met	Pro	Arg	Ala	Thr	Phe	Cys	Asn	Pro	Gln	Val	Ser	Ser	Phe	Gly	Tyr
		275					280					285			
Thr	Glu	Glu	Gln	Ala	Lys	Glu	Lys	Trp	Pro	Asp	Arg	Glu	Ile	Lys	Val

290 295 300

Ala Ser Phe Pro Phe Ser Ala Asn Gly Lys Ala Val Gly Leu Ala Glu
 305 310 315 320

Thr Asp Gly Phe Ala Lys Ile Val Ala Asp Ala Glu Phe Gly Glu Leu
 325 330 335

Leu Gly Ala His Leu Val Gly Ala Asn Ala Ser Glu Leu Ile Asn Glu
 340 345 350

Leu Val Leu Ala Gln Asn Trp Asp Leu Thr Thr Glu Glu Ile Ser Arg
 355 360 365

Ser Val His Ile His Pro Thr Leu Ser Glu Ala Val Lys Glu Ala Ala
 370 375 380

His Gly Ile Ser Gly His Met Ile Asn Phe
 385 390

<210> 183
 <211> 294
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(271)
 <223> RXS01261

<400> 183
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atgcacgaca atgaccact aaacacgtat ccttgaatgc gtg act gaa cat tat 115
 Val Thr Glu His Tyr
 1 5

gac gta gta gta ctc gga gcc ggc ccc ggt ggc tat gtc tcc gcc atc 163
 Asp Val Val Val Leu Gly Ala Gly Pro Gly Gly Tyr Val Ser Ala Ile
 10 15 20

cgt gca gcg cag ctt ggc aag aag gtt gct gta att gag aag cag tac 211
 Arg Ala Ala Gln Leu Gly Lys Lys Val Ala Val Ile Glu Lys Gln Tyr
 25 30 35

tgg ggt ggt gtt tgc cta aac gtg ggc tgc att cct tcc aaa gtc tct 259
 Trp Gly Gly Val Cys Leu Asn Val Gly Cys Ile Pro Ser Lys Val Ser
 40 45 50

gat caa aaa cgc tgaagttgcc cataccttta ccc 294
 Asp Gln Lys Arg
 55

<210> 184
 <211> 57
 <212> PRT
 <213> Corynebacterium glutamicum

<400> 184

Val Thr Glu His Tyr Asp Val Val Val Leu Gly Ala Gly Pro Gly Gly
 1 5 10 15
 Tyr Val Ser Ala Ile Arg Ala Ala Gln Leu Gly Lys Lys Val Ala Val
 20 25 30
 Ile Glu Lys Gln Tyr Trp Gly Gly Val Cys Leu Asn Val Gly Cys Ile
 35 40 45
 Pro Ser Lys Val Ser Asp Gln Lys Arg
 50 55

<210> 185
 <211> 1650
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(1627)
 <223> RXA02640

<400> 185
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 aaacactgct tagtggccca atacgtgcaa aaataaggcc atg aga atc tca aag 115
 Met Arg Ile Ser Lys
 1 5
 gcc aat gcg tat gtt gca gcg att gac caa ggc acc act tcc act cgg 163
 Ala Asn Ala Tyr Val Ala Ala Ile Asp Gln Gly Thr Thr Ser Thr Arg
 10 15 20
 tgc atc ttc att gat gcc caa gga aaa gtg gtg tct tct gct tcc aag 211
 Cys Ile Phe Ile Asp Ala Gln Gly Lys Val Val Ser Ser Ala Ser Lys
 25 30 35
 gag cac cgc caa atc ttc cca caa cag ggc tgg gta gag cac gat cct 259
 Glu His Arg Gln Ile Phe Pro Gln Gln Gly Trp Val Glu His Asp Pro
 40 45 50
 gaa gaa att tgg gac aac att cga tct gtc gtc agc cag gcg atg gtc 307
 Glu Glu Ile Trp Asp Asn Ile Arg Ser Val Val Ser Gln Ala Met Val
 55 60 65
 tcc att gac atc acc cca cac gag gtt gca tcg ctg gga gtc acc aac 355
 Ser Ile Asp Ile Thr Pro His Glu Val Ala Ser Leu Gly Val Thr Asn
 70 75 80 85
 cag cgc gaa acc acc gtg gtg tgg gac aag cac acc ggc gaa cct gtc 403
 Gln Arg Glu Thr Thr Val Val Trp Asp Lys His Thr Gly Glu Pro Val
 90 95 100
 tac aac gca atc gtg tgg caa gac acc cgc acc tct gac att tgc cta 451
 Tyr Asn Ala Ile Val Trp Gln Asp Thr Arg Thr Ser Asp Ile Cys Leu
 105 110 115
 gag atc gcg ggc gaa gaa ggc cag gaa aag tgg ctt gac cgc acc ggc 499
 Glu Ile Ala Gly Glu Glu Gly Gln Glu Lys Trp Leu Asp Arg Thr Gly
 120 125 130

ctg ctg atc aac tcc tac cca tcg ggg ccc aaa atc aag tgg att ctc	547
Leu Leu Ile Asn Ser Tyr Pro Ser Gly Pro Lys Ile Lys Trp Ile Leu	
135 140 145	
gac aac gtt gag gga gct cgc gaa cgc gcc gaa aag ggc gac ctt ttg	595
Asp Asn Val Glu Gly Ala Arg Glu Arg Ala Glu Lys Gly Asp Leu Leu	
150 155 160 165	
ttt ggc acc atg gat acc tgg gtg ctg tgg aac ctg acc ggc ggt gtc	643
Phe Gly Thr Met Asp Thr Trp Val Leu Trp Asn Leu Thr Gly Gly Val	
170 175 180	
cgc ggc gac gac ggt gat gat gcc atc cac gtc acc gat gtc acc aac	691
Arg Gly Asp Asp Gly Asp Asp Ala Ile His Val Thr Asp Val Thr Asn	
185 190 195	
gca tcc cgc aca cta ttg atg gat ctc cgc acg caa cag tgg gat cca	739
Ala Ser Arg Thr Leu Leu Met Asp Leu Arg Thr Gln Gln Trp Asp Pro	
200 205 210	
gaa cta tgc gaa gcc cta gac att ccg atg tcc atg ctc cct gag att	787
Glu Leu Cys Glu Ala Leu Asp Ile Pro Met Ser Met Leu Pro Glu Ile	
215 220 225	
cgt ccc tcc gtc gga gaa ttc cgc tcc gtg cgc cac cgc gga acc cta	835
Arg Pro Ser Val Gly Gln Phe Arg Ser Val Arg His Arg Gly Thr Leu	
230 235 240 245	
gcc gac gtc ccg att act ggc gtg ctc ggc gac cag caa gcg gcc ctt	883
Ala Asp Val Pro Ile Thr Gly Val Leu Gly Asp Gln Gln Ala Ala Leu	
250 255 260	
ttt ggt cag ggc gga ttc cac gaa ggt gct gct aaa aat acc tac ggc	931
Phe Gly Gln Gly Gly Phe His Glu Gly Ala Ala Lys Asn Thr Tyr Gly	
265 270 275	
acc ggc ctc ttc ctg ctg atg aac acc ggc acc tcg ttg aag att tcc	979
Thr Gly Leu Phe Leu Leu Met Asn Thr Gly Thr Ser Leu Lys Ile Ser	
280 285 290	
gag cac ggc ctg ctg tcc acc atc gcc tat caa cgg gaa gga tcc gct	1027
Glu His Gly Leu Leu Ser Thr Ile Ala Tyr Gln Arg Glu Gly Ser Ala	
295 300 305	
ccg gtc tac gcg ctg gaa ggt tcc gta tcc atg ggc ggt tcc ttg gtg	1075
Pro Val Tyr Ala Leu Glu Gly Ser Val Ser Met Gly Gly Ser Leu Val	
310 315 320 325	
cag tgg ctg cgc gac aac cta cag cta atc ccc aac gca cca gcg att	1123
Gln Trp Leu Arg Asp Asn Leu Gln Leu Ile Pro Asn Ala Pro Ala Ile	
330 335 340	
gaa aac ctc gcc cga gaa gtc gaa gac aac ggt ggc gtt cat gtt gtc	1171
Glu Asn Leu Ala Arg Glu Val Glu Asp Asn Gly Gly Val His Val Val	
345 350 355	
cca gca ttc acc gga ctg ttc gca cca cgt tgg cgc ccc gat gct cgt	1219
Pro Ala Phe Thr Gly Leu Phe Ala Pro Arg Trp Arg Pro Asp Ala Arg	
360 365 370	

ggc gtc att aca ggc ctc acc cgt ttt gcc aac cgc aaa cac atc gcc 1267
 Gly Val Ile Thr Gly Leu Thr Arg Phe Ala Asn Arg Lys His Ile Ala
 375 380 385
 cgc gca gtc ctt gaa gcc aac gcc ttc caa acc cgc gaa gtt gtg gac 1315
 Arg Ala Val Leu Glu Ala Asn Ala Phe Gln Thr Arg Glu Val Val Asp
 390 395 400 405
 gcc atg gcc aaa gac gca ggc aaa gcc ctc gaa tcc ctc cgc gtc gac 1363
 Ala Met Ala Lys Asp Ala Gly Lys Ala Leu Glu Ser Leu Arg Val Asp
 410 415 420
 ggt gcg atg gtg gaa aat gac ctc ctc atg caa atg caa gcc gac ttc 1411
 Gly Ala Met Val Glu Asn Asp Leu Leu Met Gln Met Gln Ala Asp Phe
 425 430 435
 ctc ggc atc gac gtc caa cgt ctc gag gac gta gaa acc acc gcc gtc 1459
 Leu Gly Ile Asp Val Gln Arg Leu Glu Asp Val Glu Thr Thr Ala Val
 440 445 450
 ggc gtc gca ttc gct gca ggt ctc ggc tct gga ttc ttc aaa aca act 1507
 Gly Val Ala Phe Ala Ala Gly Leu Gly Ser Gly Phe Phe Lys Thr Thr
 455 460 465
 gac gag atc gaa aaa ctt att gca gtg aag aaa gtc tgg aac cct gac 1555
 Asp Glu Ile Glu Lys Leu Ile Ala Val Lys Lys Val Trp Asn Pro Asp
 470 475 480 485
 atg agc gaa gaa gag cgc gaa cgt cgc tat gcc gaa tgg aat agg gca 1603
 Met Ser Glu Glu Glu Arg Glu Arg Arg Tyr Ala Glu Trp Asn Arg Ala
 490 495 500
 gtg gag cat tct tat gac cag gcc tagctgattt gggtcggcct tta 1650
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<210> 186

<211> 509

<212> PRT

<213> Corynebacterium glutamicum

<400> 186

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 20 25 30
 Ser Ser Ala Ser Lys Glu His Arg Gln Ile Phe Pro Gln Gln Gly Trp
 35 40 45
 Val Glu His Asp Pro Glu Glu Ile Trp Asp Asn Ile Arg Ser Val Val
 50 55 60
 Ser Gln Ala Met Val Ser Ile Asp Ile Thr Pro His Glu Val Ala Ser
 65 70 75 80
 Leu Gly Val Thr Asn Gln Arg Glu Thr Thr Val Val Trp Asp Lys His
 85 90 95

Thr Gly Glu Pro Val Tyr Asn Ala Ile Val Trp Gln Asp Thr Arg Thr
 100 105 110
 Ser Asp Ile Cys Leu Glu Ile Ala Gly Glu Glu Gly Gln Glu Lys Trp
 115 120 125
 Leu Asp Arg Thr Gly Leu Leu Ile Asn Ser Tyr Pro Ser Gly Pro Lys
 130 135 140
 Ile Lys Trp Ile Leu Asp Asn Val Glu Gly Ala Arg Glu Arg Ala Glu
 145 150 155 160
 Lys Gly Asp Leu Leu Phe Gly Thr Met Asp Thr Trp Val Leu Trp Asn
 165 170 175
 Leu Thr Gly Gly Val Arg Gly Asp Asp Gly Asp Asp Ala Ile His Val
 180 185 190
 Thr Asp Val Thr Asn Ala Ser Arg Thr Leu Leu Met Asp Leu Arg Thr
 195 200 205
 Gln Gln Trp Asp Pro Glu Leu Cys Glu Ala Leu Asp Ile Pro Met Ser
 210 215 220
 Met Leu Pro Glu Ile Arg Pro Ser Val Gly Glu Phe Arg Ser Val Arg
 225 230 235 240
 His Arg Gly Thr Leu Ala Asp Val Pro Ile Thr Gly Val Leu Gly Asp
 245 250 255
 Gln Gln Ala Ala Leu Phe Gly Gln Gly Gly Phe His Glu Gly Ala Ala
 260 265 270
 Lys Asn Thr Tyr Gly Thr Gly Leu Phe Leu Leu Met Asn Thr Gly Thr
 275 280 285
 Ser Leu Lys Ile Ser Glu His Gly Leu Leu Ser Thr Ile Ala Tyr Gln
 290 295 300
 Arg Glu Gly Ser Ala Pro Val Tyr Ala Leu Glu Gly Ser Val Ser Met
 305 310 315 320
 Gly Gly Ser Leu Val Gln Trp Leu Arg Asp Asn Leu Gln Leu Ile Pro
 325 330 335
 Asn Ala Pro Ala Ile Glu Asn Leu Ala Arg Glu Val Glu Asp Asn Gly
 340 345 350
 Gly Val His Val Val Pro Ala Phe Thr Gly Leu Phe Ala Pro Arg Trp
 355 360 365
 Arg Pro Asp Ala Arg Gly Val Ile Thr Gly Leu Thr Arg Phe Ala Asn
 370 375 380
 Arg Lys His Ile Ala Arg Ala Val Leu Glu Ala Asn Ala Phe Gln Thr
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 Arg Glu Val Val Asp Ala Met Ala Lys Asp Ala Gly Lys Ala Leu Glu
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 Ser Leu Arg Val Asp Gly Ala Met Val Glu Asn Asp Leu Leu Met Gln

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ctgagacggt	taaatatcgt	tttcgaaagg	tgggtttcgc	gtg	gtt	tct	gta	agc											115	
				Val	Val	Ser	Val	Ser												
									1											5
gtg	atg	ggt	gca	ggt	tcc	tgg	gga	acc	acg	ttg	gcc	aag	gtc	ttc	tct	163				
Val	Met	Gly	Ala	Gly	Ser	Trp	Gly	Thr	Thr	Leu	Ala	Lys	Val	Phe	Ser					
				10											15	20				
gat	gct	ggc	aac	gct	gtg	acg	ttg	tgg	gcg	agg	cgg	gaa	gag	ttg	gca	211				
Asp	Ala	Gly	Asn	Ala	Val	Thr	Leu	Trp	Ala	Arg	Arg	Glu	Glu	Leu	Ala					
			25											30	35					
agc	acc	atc	cgt	gac	agc	cat	gaa	aac	cgt	gat	tac	ctt	ccg	ggg	att	259				
Ser	Thr	Ile	Arg	Asp	Ser	His	Glu	Asn	Arg	Asp	Tyr	Leu	Pro	Gly	Ile					
		40											45	50						
acg	ttg	ccg	gag	tcg	ctg	cag	gtc	aca	tca	tcg	gca	acg	gag	gct	tta	307				
Thr	Leu	Pro	Glu	Ser	Leu	Gln	Val	Thr	Ser	Ser	Ala	Thr	Glu	Ala	Leu					
	55												60	65						
gag	ggc	gca	gcc	att	gtg	gtg	ttg	gcg	att	cct	tcg	cag	gcg	ttg	cgt	355				
Glu	Gly	Ala	Ala	Ile	Val	Val	Leu	Ala	Ile	Pro	Ser	Gln	Ala	Leu	Arg					
70											75	80		85						
ggc	aat	ttg	gcg	gag	tgg	aaa	gag	acg	atc	ccg	cag	gat	gcg	acc	ttg	403				
Gly	Asn	Leu	Ala	Glu	Trp	Lys	Glu	Thr	Ile	Pro	Gln	Asp	Ala	Thr	Leu					
				90											95	100				
gtg	tcc	ttg	gct	aaa	ggt	att	gaa	aag	ggc	acg	cac	ctg	cgg	atg	agt	451				
Val	Ser	Leu	Ala	Lys	Gly	Ile	Glu	Lys	Gly	Thr	His	Leu	Arg	Met	Ser					

105							110							115							
gaa	gtg	atc	gcg	gag	gtg	acg	gaa	gcg	gat	cct	tca	cgc	atc	gcg	gtg	499					
Glu	Val	Ile	Ala	Glu	Val	Thr	Glu	Ala	Asp	Pro	Ser	Arg	Ile	Ala	Val						
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ttg	tcg	ggg	cca	aac	ctt	gct	gag	atc	gcg	gag	ggg	cag	cct	gca	547						
Leu	Ser	Gly	Pro	Asn	Leu	Ala	Glu	Ile	Ala	Glu	Gly	Gln	Pro	Ala							
135							140							145							
gct	acg	gtg	att	gct	tgc	cct	gat	gaa	aac	cga	gcg	aaa	ctt	gtg	595						
Ala	Thr	Val	Ile	Ala	Cys	Pro	Asp	Glu	Asn	Arg	Ala	Lys	Leu	Val							
150							155							160							
gct	gca	gtg	gct	gcg	ccg	tat	ttc	cgc	ccg	tac	acc	aac	act	gat	643						
Ala	Ala	Val	Ala	Ala	Pro	Tyr	Phe	Arg	Pro	Tyr	Thr	Asn	Thr	Asp							
170							175							180							
gtg	ggc	act	gaa	atc	ggt	ggt	gcg	tgt	aag	aac	gtc	atc	gcg	ctg	691						
Val	Gly	Thr	Glu	Ile	Gly	Gly	Ala	Cys	Lys	Asn	Val	Ile	Ala	Leu							
185							190							195							
tgt	ggt	att	tcc	cat	ggt	tac	ggc	ctg	ggt	gag	aac	acc	aat	gca	739						
Cys	Gly	Ile	Ser	His	Gly	Tyr	Gly	Leu	Gly	Glu	Asn	Thr	Asn	Ala							
200							205							210							
ttg	att	act	cgt	ggc	ctt	gca	gag	atc	gca	cgc	ctc	ggt	gcc	aca	787						
Leu	Ile	Thr	Arg	Gly	Leu	Ala	Glu	Ile	Ala	Arg	Leu	Gly	Ala	Thr							
215							220							225							
ggt	gcg	gat	gcg	aag	act	ttt	tct	ggc	ctt	gcg	gga	atg	ggc	gac	835						
Gly	Ala	Asp	Ala	Lys	Thr	Phe	Ser	Gly	Leu	Ala	Gly	Met	Gly	Asp							
230							235							240							
gtg	gct	acg	tgt	tca	tca	ccg	ctg	tcg	cgt	aac	cgc	agc	ttc	ggt	883						
Val	Ala	Thr	Cys	Ser	Ser	Pro	Leu	Ser	Arg	Asn	Arg	Ser	Phe	Gly							
250							255							260							
cgt	ttg	ggt	cag	ggt	gaa	tcc	cta	gag	aag	gct	cgc	gag	gca	acc	931						
Arg	Leu	Gly	Gln	Gly	Glu	Ser	Leu	Glu	Lys	Ala	Arg	Glu	Ala	Thr							
265							270							275							
ggt	cag	gtt	gcg	gag	ggt	gtt	att	tcc	tcg	cag	tcg	att	ttt	gat	979						
Gly	Gln	Val	Ala	Glu	Gly	Val	Ile	Ser	Ser	Gln	Ser	Ile	Phe	Asp							
280							285							290							
gcc	acc	aag	ctt	ggt	gtg	gag	atg	ccg	atc	acc	cag	gct	gtc	tac	1027						
Ala	Thr	Lys	Leu	Gly	Val	Glu	Met	Pro	Ile	Thr	Gln	Ala	Val	Tyr							
295							300							305							
gtg	tgc	cac	cga	gat	atg	aaa	gta	act	gac	atg	att	gtg	gct	ctc	1075						
Val	Cys	His	Arg	Asp	Met	Lys	Val	Thr	Asp	Met	Ile	Val	Ala	Leu							
310							315							320							
ggc	agg	tct	aag	aag	gct	gag	tagtcttagg	ttgtaagctt	caa						1119						
Gly	Arg	Ser	Lys	Lys	Ala	Glu															
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<211> 332

<212> PRT

<213> Corynebacterium glutamicum

<400> 188

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 20 25 30
 Arg Glu Glu Leu Ala Ser Thr Ile Arg Asp Ser His Glu Asn Arg Asp
 35 40 45
 Tyr Leu Pro Gly Ile Thr Leu Pro Glu Ser Leu Gln Val Thr Ser Ser
 50 55 60
 Ala Thr Glu Ala Leu Glu Gly Ala Ala Ile Val Val Leu Ala Ile Pro
 65 70 75 80
 Ser Gln Ala Leu Arg Gly Asn Leu Ala Glu Trp Lys Glu Thr Ile Pro
 85 90 95
 Gln Asp Ala Thr Leu Val Ser Leu Ala Lys Gly Ile Glu Lys Gly Thr
 100 105 110
 His Leu Arg Met Ser Glu Val Ile Ala Glu Val Thr Glu Ala Asp Pro
 115 120 125
 Ser Arg Ile Ala Val Leu Ser Gly Pro Asn Leu Ala Arg Glu Ile Ala
 130 135 140
 Glu Gly Gln Pro Ala Ala Thr Val Ile Ala Cys Pro Asp Glu Asn Arg
 145 150 155 160
 Ala Lys Leu Val Gln Ala Ala Val Ala Ala Pro Tyr Phe Arg Pro Tyr
 165 170 175
 Thr Asn Thr Asp Val Val Gly Thr Glu Ile Gly Gly Ala Cys Lys Asn
 180 185 190
 Val Ile Ala Leu Ala Cys Gly Ile Ser His Gly Tyr Gly Leu Gly Glu
 195 200 205
 Asn Thr Asn Ala Ser Leu Ile Thr Arg Gly Leu Ala Glu Ile Ala Arg
 210 215 220
 Leu Gly Ala Thr Leu Gly Ala Asp Ala Lys Thr Phe Ser Gly Leu Ala
 225 230 235 240
 Gly Met Gly Asp Leu Val Ala Thr Cys Ser Ser Pro Leu Ser Arg Asn
 245 250 255
 Arg Ser Phe Gly Glu Arg Leu Gly Gln Gly Glu Ser Leu Glu Lys Ala
 260 265 270
 Arg Glu Ala Thr Asn Gly Gln Val Ala Glu Gly Val Ile Ser Ser Gln
 275 280 285
 Ser Ile Phe Asp Leu Ala Thr Lys Leu Gly Val Glu Met Pro Ile Thr
 290 295 300

Gln Ala Val Tyr Gly Val Cys His Arg Asp Met Lys Val Thr Asp Met
 305 310 315 320

Ile Val Ala Leu Met Gly Arg Ser Lys Lys Ala Glu
 325 330

<210> 189
 <211> 1015
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
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 <222> (101)..(1015)
 <223> FRXA01025

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 ctgaracggt taaatatcgt tttcgaaagg tgggtttcgc gtg gtt tct gta agc 115
 Val Val Ser Val Ser
 1 5
 gtg atg ggt gca ggt tcc tgg gga acc acg ttg gcc aag gtc ttc tct 163
 Val Met Gly Ala Gly Ser Trp Gly Thr Thr Leu Ala Lys Val Phe Ser
 10 15 20
 gat gct ggc aac gct gtg acg ttg tgg gcg agg cgg gaa gag ttg gca 211
 Asp Ala Gly Asn Ala Val Thr Leu Trp Ala Arg Arg Glu Glu Leu Ala
 25 30 35
 agc acc atc cgt gac agc cat gaa aac cgt gat tac ctt ccg ggg att 259
 Ser Thr Ile Arg Asp Ser His Glu Asn Arg Asp Tyr Leu Pro Gly Ile
 40 45 50
 acg ttg ccg gag tcg ctg cag gtc aca tca tcg gca acg gag gct tta 307
 Thr Leu Pro Glu Ser Leu Gln Val Thr Ser Ser Ala Thr Glu Ala Leu
 55 60 65
 gag ggc gca gcc att gtg gtg ttg gcg att cct tcg cag gcg ttg cgt 355
 Glu Gly Ala Ala Ile Val Val Leu Ala Ile Pro Ser Gln Ala Leu Arg
 70 75 80 85
 ggc aat ttg gcg gag tgg aaa gag acg atc ccg cag gat gcg acc ttg 403
 Gly Asn Leu Ala Glu Trp Lys Glu Thr Ile Pro Gln Asp Ala Thr Leu
 90 95 100
 gtg tcc ttg gct aaa ggt att gaa aag ggc acg cac ctg cgg atg agt 451
 Val Ser Leu Ala Lys Gly Ile Glu Lys Gly Thr His Leu Arg Met Ser
 105 110 115
 gaa gtg atc gcg gag gtg acg gaa gcg gat cct tca cgc atc gcg gtg 499
 Glu Val Ile Ala Glu Val Thr Glu Ala Asp Pro Ser Arg Ile Ala Val
 120 125 130
 ttg tcg ggg cca aac ctt gct cgt gag atc gcg gag ggg cag cct gca 547
 Leu Ser Gly Pro Asn Leu Ala Arg Glu Ile Ala Glu Gly Gln Pro Ala
 135 140 145
 gct acg gtg att gct tgc cct gat gaa aac cga gcg aaa ctt gtg cag 595

Ala Thr Val Ile Ala Cys Pro Asp Glu Asn Arg Ala Lys Leu Val Gln
 150 155 160 165

gct gca gtg gct gcg ccg tat ttc cgc ccg tac acc aac act gat gtg 643
 Ala Ala Val Ala Ala Pro Tyr Phe Arg Pro Tyr Thr Asn Thr Asp Val
 170 175 180

gtg ggc act gaa atc ggt ggt gcg tgt aag aac gtc atc gcg ctg gcc 691
 Val Gly Thr Glu Ile Gly Gly Ala Cys Lys Asn Val Ile Ala Leu Ala
 185 190 195

tgt ggt att tcc cat ggt tac ggc ctg ggt gag aac acc aat gca tcg 739
 Cys Gly Ile Ser His Gly Tyr Gly Leu Gly Glu Asn Thr Asn Ala Ser
 200 205 210

ttg att act cgt ggc ctt gca gag atc gca cgc ctc ggt gcc aca ttg 787
 Leu Ile Thr Arg Gly Leu Ala Glu Ile Ala Arg Leu Gly Ala Thr Leu
 215 220 225

ggt gcg gat gcg aag act ttt tct ggc ctt gcg gga atg ggc gac ttg 835
 Gly Ala Asp Ala Lys Thr Phe Ser Gly Leu Ala Gly Met Gly Asp Leu
 230 235 240 245

gtg gct acg tgt tca tca ccg ctg tcg cgt aac cgc agc ttc ggt gag 883
 Val Ala Thr Cys Ser Ser Pro Leu Ser Arg Asn Arg Ser Phe Gly Glu
 250 255 260

cgt ttg ggt cag ggt gaa tcc cta gag aag gct cgc gag gca acc aat 931
 Arg Leu Gly Gln Gly Glu Ser Leu Glu Lys Ala Arg Glu Ala Thr Asn
 265 270 275

ggt cag gtt gcg gag ggt gtt att tcc tcg cag tcg att ttt gat ctt 979
 Gly Gln Val Ala Glu Gly Val Ile Ser Ser Gln Ser Ile Phe Asp Leu
 280 285 290

gcc acc aag ctt ggt gtg gag atg ccg atc acc cag 1015
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<210> 190

<211> 305

<212> PRT

<213> Corynebacterium glutamicum

<400> 190

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 20 25 30

Arg Glu Glu Leu Ala Ser Thr Ile Arg Asp Ser His Glu Asn Arg Asp
 35 40 45

Tyr Leu Pro Gly Ile Thr Leu Pro Glu Ser Leu Gln Val Thr Ser Ser
 50 55 60

Ala Thr Glu Ala Leu Glu Gly Ala Ala Ile Val Val Leu Ala Ile Pro
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<210> 191
<211> 1809
<212> DNA
<213> Corynebacterium glutamicum
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<223> RXA01851
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                Met Thr Ser Ala His
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Phe Glu Ser Arg Arg Ile Gly Pro Pro Leu Arg Asp Asn Tyr Asp Val			
10 15 20			
att gtg att ggc ggt ggt atc tca ggt gta cag att gcg cga cat gct	211		
Ile Val Ile Gly Gly Gly Ile Ser Gly Val Gln Ile Ala Arg His Ala			
25 30 35			
caa ggc cgc ggt tta cgc act gtg atg ttt gag gcc aga gat tat tct	259		
Gln Gly Arg Gly Leu Arg Thr Val Met Phe Glu Ala Arg Asp Tyr Ser			
40 45 50			
tct gga aca tca tcg aca acc tcc aag atg att cat ggt ggt ttg cgc	307		
Ser Gly Thr Ser Ser Thr Thr Ser Lys Met Ile His Gly Gly Leu Arg			
55 60 65			
tat ttg gag cag tac gat ttc ggc gtg gtc cag gaa gcc gtg aag gaa	355		
Tyr Leu Glu Gln Tyr Asp Phe Gly Val Val Gln Glu Ala Val Lys Glu			
70 75 80 85			
cgc cgg tac cta ggt atc gcc gct ccg cat ttg gtg gct cca cgc agt	403		
Arg Arg Tyr Leu Gly Ile Ala Ala Pro His Leu Val Ala Pro Arg Ser			
90 95 100			
ttc atg ctc acg gcg ttt gat tgg tca gag ccg aaa gcc cct atg ttg	451		
Phe Met Leu Thr Ala Phe Asp Trp Ser Glu Pro Lys Ala Pro Met Leu			
105 110 115			
ggt gct ggt gtg gcg ttg tat gaa acg atg gcg tgg cag cgt aac cag	499		
Gly Ala Gly Val Ala Leu Tyr Glu Thr Met Ala Trp Gln Arg Asn Gln			
120 125 130			
ggg caa tcg aag gaa aac cac tcg ccg cgt ttc cgg tgg att cct aaa	547		
Gly Gln Ser Lys Glu Asn His Ser Pro Arg Phe Arg Trp Ile Pro Lys			
135 140 145			
aat gca ctg ctc aag gaa gtc ccg tgg ctt gac ccg gag ggc ttg aag	595		
Asn Ala Leu Leu Lys Glu Val Pro Trp Leu Asp Pro Glu Gly Leu Lys			
150 155 160 165			
gga gcg tgg cgc cac gat gat acg ttg aat ctc cat gca gaa cga ctc	643		
Gly Ala Trp Arg His Asp Asp Thr Leu Asn Leu His Ala Glu Arg Leu			
170 175 180			
ctc ctc gcg gtg att aaa gct ttt gcg gca gat ggc gga acg gcg atc	691		
Leu Leu Ala Val Ile Lys Ala Phe Ala Ala Asp Gly Gly Thr Ala Ile			
185 190 195			
aac cac gcc aaa gtc act cgc att ctc cgg aac gtg gaa gaa ggc cgc	739		
Asn His Ala Lys Val Thr Arg Ile Leu Arg Asn Val Glu Glu Gly Arg			
200 205 210			
gtc aag ggt gta gaa gtg act gat cag gtc acc aac acc acg cat gag	787		
Val Lys Gly Val Glu Val Thr Asp Gln Val Thr Asn Thr Thr His Glu			
215 220 225			
gtg aat gcc cct gtg gtg atc aac gct gcg ggt ccg tgg gtt gcg cag	835		
Val Asn Ala Pro Val Val Ile Asn Ala Ala Gly Pro Trp Val Ala Gln			
230 235 240 245			

gcg ttg ggt gat ttg gcg gag gta acc aag ttg aag gtg cgc caa tcc	883
Ala Leu Gly Asp Leu Ala Glu Val Thr Lys Leu Lys Val Arg Gln Ser	
250 255 260	
aag gga gtg cat ttg ctc act ggt gat ttg ggc agc cag agt ggc gtg	931
Lys Gly Val His Leu Leu Thr Gly Asp Leu Gly Ser Gln Ser Gly Val	
265 270 275	
ttt gtg cgt ggc aaa aac ggc aag cat gtg atc gtg aat ccg tgg atg	979
Phe Val Arg Gly Lys Asn Gly Lys His Val Ile Val Asn Pro Trp Met	
280 285 290	
ggg cgc acc ctt att ggt cca acc gac acc atg att gac ggt gac gct	1027
Gly Arg Thr Leu Ile Gly Pro Thr Asp Thr Met Ile Asp Gly Asp Ala	
295 300 305	
gat gat gcg gct gca gat gaa agc gat atc gat ttg ctg ctt gag acc	1075
Asp Asp Ala Ala Ala Asp Glu Ser Asp Ile Asp Leu Leu Leu Glu Thr	
310 315 320 325	
atc gat tcg gta cgc gct aca ccg ctt gat cgc aaa gag atc atc tcc	1123
Ile Asp Ser Val Arg Ala Thr Pro Leu Asp Arg Lys Glu Ile Ile Ser	
330 335 340	
acg ctg gtg ggt gtg cgc ccg ctt gtt gat gac ggc acc gac acc tac	1171
Thr Leu Val Gly Val Arg Pro Leu Val Asp Asp Gly Thr Asp Thr Tyr	
345 350 355	
acg tcc tct cgc cgt ttc gat att tcc gat cac gcc aac gtc ggc att	1219
Thr Ser Ser Arg Arg Phe Asp Ile Ser Asp His Ala Asn Val Gly Ile	
360 365 370	
gat ggt ttg gtg tct gtc tct ggc ggc aag tgg acc act tcc cgc gtg	1267
Asp Gly Leu Val Ser Val Ser Gly Gly Lys Trp Thr Thr Ser Arg Val	
375 380 385	
atg ggg tac aag gtg att gag cat gtg gtg gag cac caa gct gcg gtg	1315
Met Gly Tyr Lys Val Ile Glu His Val Val Glu His Gln Ala Ala Val	
390 395 400 405	
tta cct ccg ctg cgc cac ttt gac tcc agg cag atg ccg ttg agt act	1363
Leu Pro Pro Leu Arg His Phe Asp Ser Arg Gln Met Pro Leu Ser Thr	
410 415 420	
tct ttt ggc gcg tat gag tcc gtg gct gat tcc ttt gag tca gcg ctt	1411
Ser Phe Gly Ala Tyr Glu Ser Val Ala Asp Ser Phe Glu Ser Ala Leu	
425 430 435	
cgc agc cac ccc gag ctg gat gtg gat gat gaa atc cgc gtg cat ctg	1459
Arg Ser His Pro Glu Leu Asp Val Asp Asp Glu Ile Arg Val His Leu	
440 445 450	
gcc aga ctg tat gga act gag cat gaa aaa gtg ctg gat ctc gtc gca	1507
Ala Arg Leu Tyr Gly Thr Glu His Glu Lys Val Leu Asp Leu Val Ala	
455 460 465	
aag caa ccc gac ctg ggg cgc cga ctt gac cca gac aac ctt gat atc	1555
Lys Gln Pro Asp Leu Gly Arg Arg Leu Asp Pro Asp Asn Leu Asp Ile	
470 475 480 485	

gcg gcg cag gcc gtt ttt gct gtc gcc gag gag gcg gcc gtc gac ctg 1603
 Ala Ala Gln Ala Val Phe Ala Val Ala Glu Glu Ala Ala Val Asp Leu
 490 495 500

gcg gac gtg ctg gat cgt cgc atc gtg ctc ggc acg ctg ggt tat gtg 1651
 Ala Asp Val Leu Asp Arg Arg Ile Val Leu Gly Thr Leu Gly Tyr Val
 505 510 515

caa ccg gct gcc gtg cgt gcg acg gcc gaa gca atg gcg cag gtc acc 1699
 Gln Pro Ala Ala Val Arg Ala Thr Ala Glu Ala Met Ala Gln Val Thr
 520 525 530

ggg tgg tca gct gag ctt atc gac gcc cag tgc cag tcc tac ctc gcc 1747
 Gly Trp Ser Ala Glu Leu Ile Asp Ala Gln Cys Gln Ser Tyr Leu Ala
 535 540 545

aag caa gac aaa atc caa gcc gtg tta aag ccg tac cgc taacactccg 1796
 Lys Gln Asp Lys Ile Gln Ala Val Leu Lys Pro Tyr Arg
 550 555 560

tcacgcacac cgg 1809

<210> 192
 <211> 562
 <212> PRT
 <213> Corynebacterium glutamicum

<400> 192
 Met Thr Ser Ala His Phe Glu Ser Arg Arg Ile Gly Pro Pro Leu Arg
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Asp Asn Tyr Asp Val Ile Val Ile Gly Gly Gly Ile Ser Gly Val Gln
 20 25 30

Ile Ala Arg His Ala Gln Gly Arg Gly Leu Arg Thr Val Met Phe Glu
 35 40 45

Ala Arg Asp Tyr Ser Ser Gly Thr Ser Ser Thr Thr Ser Lys Met Ile
 50 55 60

His Gly Gly Leu Arg Tyr Leu Glu Gln Tyr Asp Phe Gly Val Val Gln
 65 70 75 80

Glu Ala Val Lys Glu Arg Arg Tyr Leu Gly Ile Ala Ala Pro His Leu
 85 90 95

Val Ala Pro Arg Ser Phe Met Leu Thr Ala Phe Asp Trp Ser Glu Pro
 100 105 110

Lys Ala Pro Met Leu Gly Ala Gly Val Ala Leu Tyr Glu Thr Met Ala
 115 120 125

Trp Gln Arg Asn Gln Gly Gln Ser Lys Glu Asn His Ser Pro Arg Phe
 130 135 140

Arg Trp Ile Pro Lys Asn Ala Leu Leu Lys Glu Val Pro Trp Leu Asp
 145 150 155 160

Pro Glu Gly Leu Lys Gly Ala Trp Arg His Asp Asp Thr Leu Asn Leu
 165 170 175

His Ala Glu Arg Leu Leu Leu Ala Val Ile Lys Ala Phe Ala Ala Asp
 180 185 190
 Gly Gly Thr Ala Ile Asn His Ala Lys Val Thr Arg Ile Leu Arg Asn
 195 200 205
 Val Glu Glu Gly Arg Val Lys Gly Val Glu Val Thr Asp Gln Val Thr
 210 215 220
 Asn Thr Thr His Glu Val Asn Ala Pro Val Val Ile Asn Ala Ala Gly
 225 230 235 240
 Pro Trp Val Ala Gln Ala Leu Gly Asp Leu Ala Glu Val Thr Lys Leu
 245 250 255
 Lys Val Arg Gln Ser Lys Gly Val His Leu Leu Thr Gly Asp Leu Gly
 260 265 270
 Ser Gln Ser Gly Val Phe Val Arg Gly Lys Asn Gly Lys His Val Ile
 275 280 285
 Val Asn Pro Trp Met Gly Arg Thr Leu Ile Gly Pro Thr Asp Thr Met
 290 295 300
 Ile Asp Gly Asp Ala Asp Asp Ala Ala Ala Asp Glu Ser Asp Ile Asp
 305 310 315 320
 Leu Leu Leu Glu Thr Ile Asp Ser Val Arg Ala Thr Pro Leu Asp Arg
 325 330 335
 Lys Glu Ile Ile Ser Thr Leu Val Gly Val Arg Pro Leu Val Asp Asp
 340 345 350
 Gly Thr Asp Thr Tyr Thr Ser Ser Arg Arg Phe Asp Ile Ser Asp His
 355 360 365
 Ala Asn Val Gly Ile Asp Gly Leu Val Ser Val Ser Gly Gly Lys Trp
 370 375 380
 Thr Thr Ser Arg Val Met Gly Tyr Lys Val Ile Glu His Val Val Glu
 385 390 395 400
 His Gln Ala Ala Val Leu Pro Pro Leu Arg His Phe Asp Ser Arg Gln
 405 410 415
 Met Pro Leu Ser Thr Ser Phe Gly Ala Tyr Glu Ser Val Ala Asp Ser
 420 425 430
 Phe Glu Ser Ala Leu Arg Ser His Pro Glu Leu Asp Val Asp Asp Glu
 435 440 445
 Ile Arg Val His Leu Ala Arg Leu Tyr Gly Thr Glu His Glu Lys Val
 450 455 460
 Leu Asp Leu Val Ala Lys Gln Pro Asp Leu Gly Arg Arg Leu Asp Pro
 465 470 475 480
 Asp Asn Leu Asp Ile Ala Ala Gln Ala Val Phe Ala Val Ala Glu Glu
 485 490 495

Ala Ala Val Asp Leu Ala Asp Val Leu Asp Arg Arg Ile Val Leu Gly
 500 505 510

Thr Leu Gly Tyr Val Gln Pro Ala Val Arg Ala Thr Ala Glu Ala
 515 520 525

Met Ala Gln Val Thr Gly Trp Ser Ala Glu Leu Ile Asp Ala Gln Cys
 530 535 540

Gln Ser Tyr Leu Ala Lys Gln Asp Lys Ile Gln Ala Val Leu Lys Pro
 545 550 555 560

Tyr Arg

<210> 193
 <211> 900
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(877)
 <223> RXA01242

<400> 193
 cgccggcaac caaatgaggc ttttgggcgt tggacagtga gacaatgggt aagaaattcg 60

gacatatatta gtaaatggc tttttgcttt aaggagtgc atg tac gca gag gag 115
 Met Tyr Ala Glu Glu
 1 5

cgc cgt cga cag att gcc tca tta acg gca gtt gag gga cgt gta aat 163
 Arg Arg Arg Gln Ile Ala Ser Leu Thr Ala Val Glu Gly Arg Val Asn
 10 15 20

gtc aca gaa tta gcg ggc cga ttc gat gtc act gca gag acg att cga 211
 Val Thr Glu Leu Ala Gly Arg Phe Asp Val Thr Ala Glu Thr Ile Arg
 25 30 35

cga gac ctt gcg gtg cta gac cgc gag gga att gtt cac cgc gtt cac 259
 Arg Asp Leu Ala Val Leu Asp Arg Glu Gly Ile Val His Arg Val His
 40 45 50

ggt ggc gca gta gcc acc caa tct ttc caa acc aca gag ttg agc ttg 307
 Gly Gly Ala Val Ala Thr Gln Ser Phe Gln Thr Thr Glu Leu Ser Leu
 55 60 65

gat act cgt ttc agg tct gca tcg tca gca aag tac tcc att gcc aag 355
 Asp Thr Arg Phe Arg Ser Ala Ser Ser Ala Lys Tyr Ser Ile Ala Lys
 70 75 80 85

gca gcg atg cag ttc ctg ccc gct gag cat ggc gga ctg ttc ctc gat 403
 Ala Ala Met Gln Phe Leu Pro Ala Glu His Gly Gly Leu Phe Leu Asp
 90 95 100

gcg gga act act gtt act gct ttg gcc gat ctc att tct gag cat cct 451
 Ala Gly Thr Thr Val Thr Ala Leu Ala Asp Leu Ile Ser Glu His Pro
 105 110 115

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agc tcc aag cag tgg tcg atc gtg acc aac tgc ctc ccc atc gca ctt 499
Ser Ser Lys Gln Trp Ser Ile Val Thr Asn Cys Leu Pro Ile Ala Leu
      120                      125                      130

aat ctg gcc aac gcc ggg ctt gat gat gtc cag ctg ctt gga gga agc 547
Asn Leu Ala Asn Ala Gly Leu Asp Asp Val Gln Leu Leu Gly Gly Ser
      135                      140                      145

gtt cgc gcg atc acc cag gct gtt gtg ggt gac act gcg ctt cgt act 595
Val Arg Ala Ile Thr Gln Ala Val Val Gly Asp Thr Ala Leu Arg Thr
      150                      155                      160                      165

ctc gcg ctg atg cgt gcg gat gta gtg ttc atc ggc acc aac gcg ttg 643
Leu Ala Leu Met Arg Ala Asp Val Val Phe Ile Gly Thr Asn Ala Leu
      170                      175                      180

acg ttg gat cac gga ttg tct acg gcc gat tcc caa gag gct gcc atg 691
Thr Leu Asp His Gly Leu Ser Thr Ala Asp Ser Gln Glu Ala Ala Met
      185                      190                      195

aaa tct gcg atg atc acc aac gcc cac aag gtg gtg gtg ttg tgt gac 739
Lys Ser Ala Met Ile Thr Asn Ala His Lys Val Val Val Leu Cys Asp
      200                      205                      210

tcc acc aag atg ggc acc gac tac ctc gtg agc ttt ggc gca atc agc 787
Ser Thr Lys Met Gly Thr Asp Tyr Leu Val Ser Phe Gly Ala Ile Ser
      215                      220                      225

gat atc gat gtg gtg gtc acc gat gcg ggt gca cca gca agt ttc gtt 835
Asp Ile Asp Val Val Val Thr Asp Ala Gly Ala Pro Ala Ser Phe Val
      230                      235                      240                      245

gag cag ttg cga gaa cgc gat gta gaa gtt gtg att gca gaa 877
Glu Gln Leu Arg Glu Arg Asp Val Glu Val Val Ile Ala Glu
      250                      255

tgattcttac agtcactgca agt 900

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<210> 194

<211> 259

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 194

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Met Tyr Ala Glu Glu Arg Arg Arg Gln Ile Ala Ser Leu Thr Ala Val
  1                      5                      10                      15

```

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Glu Gly Arg Val Asn Val Thr Glu Leu Ala Gly Arg Phe Asp Val Thr
      20                      25                      30

```

```

Ala Glu Thr Ile Arg Arg Asp Leu Ala Val Leu Asp Arg Glu Gly Ile
      35                      40                      45

```

```

Val His Arg Val His Gly Gly Ala Val Ala Thr Gln Ser Phe Gln Thr
      50                      55                      60

```

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Thr Glu Leu Ser Leu Asp Thr Arg Phe Arg Ser Ala Ser Ser Ala Lys
      65                      70                      75                      80

```

```

Tyr Ser Ile Ala Lys Ala Ala Met Gln Phe Leu Pro Ala Glu His Gly

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85										90					95						
Gly	Leu	Phe	Leu	Asp	Ala	Gly	Thr	Thr	Val	Thr	Ala	Leu	Ala	Asp	Leu						
			100					105					110								
Ile	Ser	Glu	His	Pro	Ser	Ser	Lys	Gln	Trp	Ser	Ile	Val	Thr	Asn	Cys						
		115					120					125									
Leu	Pro	Ile	Ala	Leu	Asn	Leu	Ala	Asn	Ala	Gly	Leu	Asp	Asp	Val	Gln						
	130					135					140										
Leu	Leu	Gly	Gly	Ser	Val	Arg	Ala	Ile	Thr	Gln	Ala	Val	Val	Gly	Asp						
145					150					155				160							
Thr	Ala	Leu	Arg	Thr	Leu	Ala	Leu	Met	Arg	Ala	Asp	Val	Val	Phe	Ile						
				165					170					175							
Gly	Thr	Asn	Ala	Leu	Thr	Leu	Asp	His	Gly	Leu	Ser	Thr	Ala	Asp	Ser						
			180					185					190								
Gln	Glu	Ala	Ala	Met	Lys	Ser	Ala	Met	Ile	Thr	Asn	Ala	His	Lys	Val						
		195					200					205									
Val	Val	Leu	Cys	Asp	Ser	Thr	Lys	Met	Gly	Thr	Asp	Tyr	Leu	Val	Ser						
	210					215					220										
Phe	Gly	Ala	Ile	Ser	Asp	Ile	Asp	Val	Val	Val	Thr	Asp	Ala	Gly	Ala						
225					230					235				240							
Pro	Ala	Ser	Phe	Val	Glu	Gln	Leu	Arg	Glu	Arg	Asp	Val	Glu	Val	Val						
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Ile Ala Glu

<210> 195
 <211> 969
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(946)
 <223> RXA02288

<400> 195
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 agtgctggat ctaacaacat ttccgtggtg actttttcac atg tcc caa gtg att 115
 Met Ser Gln Val Ile
 1 5
 ccc gcc agc tca caa gaa aag cgt cgt gag cgc atc gtt tct tat gtc 163
 Pro Ala Ser Ser Gln Glu Lys Arg Arg Glu Arg Ile Val Ser Tyr Val
 10 15 20
 acc cgt cat gga ttc gct cgt gtt gaa gca tta gct gag ctt ttt gag 211
 Thr Arg His Gly Phe Ala Arg Val Glu Ala Leu Ala Glu Leu Phe Glu
 25 30 35

gtc agc gca atg acc att cac cgt gat ttg gag gcg ctg gct gca gac	259
Val Ser Ala Met Thr Ile His Arg Asp Leu Glu Ala Leu Ala Ala Asp	
40 45 50	
aat ttg gtg gag cgc att agg ggt ggc gcg cgt tcg gtg tcg ccg tcg	307
Asn Leu Val Glu Arg Ile Arg Gly Gly Ala Arg Ser Val Ser Pro Ser	
55 60 65	
atg agt gag ttg gca gtg gag cag cgt cgg cat ttg cat cgc act gtt	355
Met Ser Glu Leu Ala Val Glu Gln Arg Arg His Leu His Arg Thr Val	
70 75 80 85	
aaa gag gcg ttg tgt act gca gca gca cgg ttg att ccg gag ggc gct	403
Lys Glu Ala Leu Cys Thr Ala Ala Ala Arg Leu Ile Pro Glu Gly Ala	
90 95 100	
gtg gtg gcg att gat gat tcc acc acg ttg gag tct ttg gtt gag aag	451
Val Val Ala Ile Asp Asp Ser Thr Thr Leu Glu Ser Leu Val Glu Lys	
105 110 115	
ttg ccg cag cgg tca cca tcg gcg ttg att acg cat tct ttg aag aca	499
Leu Pro Gln Arg Ser Pro Ser Ala Leu Ile Thr His Ser Leu Lys Thr	
120 125 130	
atg gcg gat cat cgt gtg cgc gcc ggg atg agc gat atc cgt ttg att	547
Met Ala Asp His Arg Val Arg Ala Gly Met Ser Asp Ile Arg Leu Ile	
135 140 145	
gcg tgt gcg gga ttg tat ttc gcg gag act gat tct ttc ttg ggc aag	595
Ala Cys Ala Gly Leu Tyr Phe Ala Glu Thr Asp Ser Phe Leu Gly Lys	
150 155 160 165	
gca act tca gcg cag ttg aat gag ctg tcg gcg gat att tct ttt gtt	643
Ala Thr Ser Ala Gln Leu Asn Glu Leu Ser Ala Asp Ile Ser Phe Val	
170 175 180	
tct acg act gcg gtg cgc gct acg ggg gag gtt ccg gcg ctg ttt cat	691
Ser Thr Thr Ala Val Arg Ala Thr Gly Glu Val Pro Ala Leu Phe His	
185 190 195	
cct gat atg gag gct gct gat acg aag cgg gcg ttg att ggg att ggt	739
Pro Asp Met Glu Ala Ala Asp Thr Lys Arg Ala Leu Ile Gly Ile Gly	
200 205 210	
agc gtg cgt gtg ttg gtg gtg gat tct agt aaa ttt ggt tcg gct ggt	787
Ser Val Arg Val Leu Val Val Asp Ser Ser Lys Phe Gly Ser Ala Gly	
215 220 225	
gtg ttc aag gtt gct tcg att gag gag ttt gac cac atc atc att gat	835
Val Phe Lys Val Ala Ser Ile Glu Glu Phe Asp His Ile Ile Ile Asp	
230 235 240 245	
cag cag tgc acc cgt gag cag cgg gat ctt ttg cgt aat tcg cgc gcg	883
Gln Gln Cys Thr Arg Glu Gln Arg Asp Leu Leu Arg Asn Ser Arg Ala	
250 255 260	
cag atc cat gtg att gac cac aat ggt gat gaa att ttg gat acc cca	931
Gln Ile His Val Ile Asp His Asn Gly Asp Glu Ile Leu Asp Thr Pro	
265 270 275	
acg gaa gag gat ttt taagatggct ttggttcttg gaa	969

Thr Glu Glu Asp Phe
280

<210> 196

<211> 282

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 196

Met Ser Gln Val Ile Pro Ala Ser Ser Gln Glu Lys Arg Arg Glu Arg
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Ile Val Ser Tyr Val Thr Arg His Gly Phe Ala Arg Val Glu Ala Leu
20 25 30

Ala Glu Leu Phe Glu Val Ser Ala Met Thr Ile His Arg Asp Leu Glu
35 40 45

Ala Leu Ala Ala Asp Asn Leu Val Glu Arg Ile Arg Gly Gly Ala Arg
50 55 60

Ser Val Ser Pro Ser Met Ser Glu Leu Ala Val Glu Gln Arg Arg His
65 70 75 80

Leu His Arg Thr Val Lys Glu Ala Leu Cys Thr Ala Ala Ala Arg Leu
85 90 95

Ile Pro Glu Gly Ala Val Val Ala Ile Asp Asp Ser Thr Thr Leu Glu
100 105 110

Ser Leu Val Glu Lys Leu Pro Gln Arg Ser Pro Ser Ala Leu Ile Thr
115 120 125

His Ser Leu Lys Thr Met Ala Asp His Arg Val Arg Ala Gly Met Ser
130 135 140

Asp Ile Arg Leu Ile Ala Cys Ala Gly Leu Tyr Phe Ala Glu Thr Asp
145 150 155 160

Ser Phe Leu Gly Lys Ala Thr Ser Ala Gln Leu Asn Glu Leu Ser Ala
165 170 175

Asp Ile Ser Phe Val Ser Thr Thr Ala Val Arg Ala Thr Gly Glu Val
180 185 190

Pro Ala Leu Phe His Pro Asp Met Glu Ala Ala Asp Thr Lys Arg Ala
195 200 205

Leu Ile Gly Ile Gly Ser Val Arg Val Leu Val Val Asp Ser Ser Lys
210 215 220

Phe Gly Ser Ala Gly Val Phe Lys Val Ala Ser Ile Glu Glu Phe Asp
225 230 235 240

His Ile Ile Ile Asp Gln Gln Cys Thr Arg Glu Gln Arg Asp Leu Leu
245 250 255

Arg Asn Ser Arg Ala Gln Ile His Val Ile Asp His Asn Gly Asp Glu
260 265 270

Ile Leu Asp Thr Pro Thr Glu Glu Asp Phe
275 280

<210> 197
<211> 887
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (1)..(864)
<223> RXN01891

<400> 197
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Gly Gly His Tyr Gly Leu Pro Phe Ala Arg Ser Thr Val Leu Phe Tyr
1 5 10 15
tac aac aag gat ctg tgg gct aag gct ggc ctg gaa gat cgt ggc cca 96
Tyr Asn Lys Asp Leu Trp Ala Lys Ala Gly Leu Glu Asp Arg Gly Pro
20 25 30
gag tca tgg gaa gag ttc tcc gag tgg ggt cca aag ctg cag gaa gcg 144
Glu Ser Trp Glu Glu Phe Ser Glu Trp Gly Pro Lys Leu Gln Glu Ala
35 40 45
atg gac agt ggt ttc gca cac ggt tgg gga gat gca acc aac tac ctt 192
Met Asp Ser Gly Phe Ala His Gly Trp Gly Asp Ala Thr Asn Tyr Leu
50 55 60
tct tgg act ttc gaa ggc cca atg tgg tcc ctc ggc ggc aac tac tct 240
Ser Trp Thr Phe Glu Gly Pro Met Trp Ser Leu Gly Gly Asn Tyr Ser
65 70 75 80
gaa ggt tgg gag tcc cgt ctg act acc cca gag acc atc cgt gca gtt 288
Glu Gly Trp Glu Ser Arg Leu Thr Thr Pro Glu Thr Ile Arg Ala Val
85 90 95
gag tgg ctc aag tcc acc gtt gat gaa ggt ttc gca acc gtc tcc acc 336
Glu Trp Leu Lys Ser Thr Val Asp Glu Gly Phe Ala Thr Val Ser Thr
100 105 110
gac gtc acc aac gag ttc gca acc ggc ctg atc ggt tca tgc atc cag 384
Asp Val Thr Asn Glu Phe Ala Thr Gly Leu Ile Gly Ser Cys Ile Gln
115 120 125
tcc acc ggt gat ctg tct tcg gtt gcc ggc gct gca agc ttc gac tgg 432
Ser Thr Gly Asp Leu Ser Ser Val Ala Gly Ala Ala Ser Phe Asp Trp
130 135 140
ggc gta gca gca ctt cct aac cca acc ggc gag ggc gct tgc cca acc 480
Gly Val Ala Ala Leu Pro Asn Pro Thr Gly Glu Gly Ala Cys Pro Thr
145 150 155 160
ggt ggc gca ggc ctg gga atc cca tct ggc atc tct gag cag cgt cag 528
Gly Gly Ala Gly Leu Gly Ile Pro Ser Gly Ile Ser Glu Gln Arg Gln
165 170 175
gac aac gcc ctg aag ttc atc gac ttc ctc acc aac gcc gcg aac act 576
Asp Asn Ala Leu Lys Phe Ile Asp Phe Leu Thr Asn Ala Ala Asn Thr

180	185	190	
ggc tac tgg tcc cgc gag acc ggt tat gtt cca gtt cgt aag gat gct			624
Gly Tyr Trp Ser Arg Glu Thr Gly Tyr Val Pro Val Arg Lys Asp Ala			
195	200	205	
gca tct gat cca gat cac gca gca ttc ctc gag gag aac cct gca tac			672
Ala Ser Asp Pro Asp His Ala Ala Phe Leu Glu Glu Asn Pro Ala Tyr			
210	215	220	
aac gtt gca gtg gag cag ctt cct gat acc cgt tcc cag gac aac ttc			720
Asn Val Ala Val Glu Gln Leu Pro Asp Thr Arg Ser Gln Asp Asn Phe			
225	230	235	240
cgc gtg ctg ctg cca aac ggt gac cgc acc atc ggt gac gca ctg gag			768
Arg Val Leu Leu Pro Asn Gly Asp Arg Thr Ile Gly Asp Ala Leu Glu			
245	250	255	
aag atc tgc ctg act ggt gca gac atc gat gtc acc ctg gct gag gtt			816
Lys Ile Cys Leu Thr Gly Ala Asp Ile Asp Val Thr Leu Ala Glu Val			
260	265	270	
gag acc aag ctg aac acc atc tac acc cgc gac atc gaa cca ctt att			864
Glu Thr Lys Leu Asn Thr Ile Tyr Thr Arg Asp Ile Glu Pro Leu Ile			
275	280	285	
taatccgagc acttcagcta cac			887

<210> 198

<211> 288

<212> PRT

<213> Corynebacterium glutamicum

<400> 198

Gly Gly His Tyr Gly Leu Pro Phe Ala Arg Ser Thr Val Leu Phe Tyr			
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Tyr Asn Lys Asp Leu Trp Ala Lys Ala Gly Leu Glu Asp Arg Gly Pro			
20	25	30	
Glu Ser Trp Glu Glu Phe Ser Glu Trp Gly Pro Lys Leu Gln Glu Ala			
35	40	45	
Met Asp Ser Gly Phe Ala His Gly Trp Gly Asp Ala Thr Asn Tyr Leu			
50	55	60	
Ser Trp Thr Phe Glu Gly Pro Met Trp Ser Leu Gly Gly Asn Tyr Ser			
65	70	75	80
Glu Gly Trp Glu Ser Arg Leu Thr Thr Pro Glu Thr Ile Arg Ala Val			
85	90	95	
Glu Trp Leu Lys Ser Thr Val Asp Glu Gly Phe Ala Thr Val Ser Thr			
100	105	110	
Asp Val Thr Asn Glu Phe Ala Thr Gly Leu Ile Gly Ser Cys Ile Gln			
115	120	125	
Ser Thr Gly Asp Leu Ser Ser Val Ala Gly Ala Ala Ser Phe Asp Trp			
130	135	140	

Gly Val Ala Ala Leu Pro Asn Pro Thr Gly Glu Gly Ala Cys Pro Thr
 145 150 155 160
 Gly Gly Ala Gly Leu Gly Ile Pro Ser Gly Ile Ser Glu Gln Arg Gln
 165 170 175
 Asp Asn Ala Leu Lys Phe Ile Asp Phe Leu Thr Asn Ala Ala Asn Thr
 180 185 190
 Gly Tyr Trp Ser Arg Glu Thr Gly Tyr Val Pro Val Arg Lys Asp Ala
 195 200 205
 Ala Ser Asp Pro Asp His Ala Ala Phe Leu Glu Glu Asn Pro Ala Tyr
 210 215 220
 Asn Val Ala Val Glu Gln Leu Pro Asp Thr Arg Ser Gln Asp Asn Phe
 225 230 235 240
 Arg Val Leu Leu Pro Asn Gly Asp Arg Thr Ile Gly Asp Ala Leu Glu
 245 250 255
 Lys Ile Cys Leu Thr Gly Ala Asp Ile Asp Val Thr Leu-Ala Glu Val
 260 265 270
 Glu Thr Lys Leu Asn Thr Ile Tyr Thr Arg Asp Ile Glu Pro Leu Ile
 275 280 285

<210> 199
 <211> 842
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (1)..(819)
 <223> FRXA01891

<400> 199
 tac tac aac aag gat ctg tgg gct aag gct ggc ctg gaa gat cgt ggc 48
 Tyr Tyr Asn Lys Asp Leu Trp Ala Lys Ala Gly Leu Glu Asp Arg Gly
 1 5 10 15
 cca gag tca tgg gaa gag ttc tcc gag tgg ggt cca aag ctg cag gaa 96
 Pro Glu Ser Trp Glu Glu Phe Ser Glu Trp Gly Pro Lys Leu Gln Glu
 20 25 30
 gcg atg gac agt ggt ttc gca cac ggt tgg gga gat gca acc aac tac 144
 Ala Met Asp Ser Gly Phe Ala His Gly Trp Gly Asp Ala Thr Asn Tyr
 35 40 45
 ctt tct tgg act ttc gaa ggc cca atg tgg tcc ctc ggc ggc aac tac 192
 Leu Ser Trp Thr Phe Glu Gly Pro Met Trp Ser Leu Gly Gly Asn Tyr
 50 55 60
 tct gaa ggt tgg gag tcc cgt ctg act acc cca gag acc atc cgt gca 240
 Ser Glu Gly Trp Glu Ser Arg Leu Thr Thr Pro Glu Thr Ile Arg Ala

65	70	75	80	
ggt gag tgg ctc aag tcc acc gtt gat gaa ggt ttc gca acc gtc tcc				288
Val Glu Trp Leu Lys Ser Thr Val Asp Glu Gly Phe Ala Thr Val Ser				
	85	90	95	
acc gac gtc acc aac gag ttc gca acc ggc ctg atc ggt tca tgc atc				336
Thr Asp Val Thr Asn Glu Phe Ala Thr Gly Leu Ile Gly Ser Cys Ile				
	100	105	110	
cag tcc acc ggt gat ctg tct tcg gtt gcc ggc gct gca agc ttc gac				384
Gln Ser Thr Gly Asp Leu Ser Val Ala Gly Ala Ala Ser Phe Asp				
	115	120	125	
tgg ggc gta gca gca ctt cct aac cca acc ggc gag ggc gct tgc cca				432
Trp Gly Val Ala Ala Leu Pro Asn Pro Thr Gly Glu Gly Ala Cys Pro				
	130	135	140	
acc ggt ggc gca ggc ctg gga atc cca tct ggc atc tct gag cag cgt				480
Thr Gly Gly Ala Gly Leu Gly Ile Pro Ser Gly Ile Ser Glu Gln Arg				
	145	150	155	160
cag gac aac gcc ctg aag ttc atc gac ttc ctc acc aac gcc gcg aac				528
Gln Asp Asn Ala Leu Lys Phe Ile Asp Phe Leu Thr Asn Ala Ala Asn				
	165	170	175	
act ggc tac tgg tcc cgc gag acc ggt tat gtt cca gtt cgt aag gat				576
Thr Gly Tyr Trp Ser Arg Glu Thr Gly Tyr Val Pro Val Arg Lys Asp				
	180	185	190	
gct gca tct gat cca gat cac gca gca ttc ctc gag gag aac cct gca				624
Ala Ala Ser Asp Pro Asp His Ala Ala Phe Leu Glu Glu Asn Pro Ala				
	195	200	205	
tac aac gtt gca gtg gag cag ctt cct gat acc cgt tcc cag gac aac				672
Tyr Asn Val Ala Val Glu Gln Leu Pro Asp Thr Arg Ser Gln Asp Asn				
	210	215	220	
ttc cgc gtg ctg ctg cca aac ggt gac cgc acc atc ggt gac gca ctg				720
Phe Arg Val Leu Leu Pro Asn Gly Asp Arg Thr Ile Gly Asp Ala Leu				
	225	230	235	240
gag aag atc tgc ctg act ggt gca gac atc gat gtc acc ctg gct gag				768
Glu Lys Ile Cys Leu Thr Gly Ala Asp Ile Asp Val Thr Leu Ala Glu				
	245	250	255	
ggt gag acc aag ctg aac acc atc tac acc cgc gac atc gaa cca ctt				816
Val Glu Thr Lys Leu Asn Thr Ile Tyr Thr Arg Asp Ile Glu Pro Leu				
	260	265	270	
att taatccgagc acttcagcta cac				842
Ile				

<210> 200

<211> 273

<212> PRT

<213> Corynebacterium glutamicum

<400> 200

Tyr Tyr Asn Lys Asp Leu Trp Ala Lys Ala Gly Leu Glu Asp Arg Gly
 1 5 10 15
 Pro Glu Ser Trp Glu Glu Phe Ser Glu Trp Gly Pro Lys Leu Gln Glu
 20 25 30
 Ala Met Asp Ser Gly Phe Ala His Gly Trp Gly Asp Ala Thr Asn Tyr
 35 40 45
 Leu Ser Trp Thr Phe Glu Gly Pro Met Trp Ser Leu Gly Gly Asn Tyr
 50 55 60
 Ser Glu Gly Trp Glu Ser Arg Leu Thr Thr Pro Glu Thr Ile Arg Ala
 65 70 75 80
 Val Glu Trp Leu Lys Ser Thr Val Asp Glu Gly Phe Ala Thr Val Ser
 85 90 95
 Thr Asp Val Thr Asn Glu Phe Ala Thr Gly Leu Ile Gly Ser Cys Ile
 100 105 110
 Gln Ser Thr Gly Asp Leu Ser Ser Val Ala Gly Ala Ala Ser Phe Asp
 115 120 125
 Trp Gly Val Ala Ala Leu Pro Asn Pro Thr Gly Glu Gly Ala Cys Pro
 130 135 140
 Thr Gly Gly Ala Gly Leu Gly Ile Pro Ser Gly Ile Ser Glu Gln Arg
 145 150 155 160
 Gln Asp Asn Ala Leu Lys Phe Ile Asp Phe Leu Thr Asn Ala Ala Asn
 165 170 175
 Thr Gly Tyr Trp Ser Arg Glu Thr Gly Tyr Val Pro Val Arg Lys Asp
 180 185 190
 Ala Ala Ser Asp Pro Asp His Ala Ala Phe Leu Glu Glu Asn Pro Ala
 195 200 205
 Tyr Asn Val Ala Val Glu Gln Leu Pro Asp Thr Arg Ser Gln Asp Asn
 210 215 220
 Phe Arg Val Leu Leu Pro Asn Gly Asp Arg Thr Ile Gly Asp Ala Leu
 225 230 235 240
 Glu Lys Ile Cys Leu Thr Gly Ala Asp Ile Asp Val Thr Leu Ala Glu
 245 250 255
 Val Glu Thr Lys Leu Asn Thr Ile Tyr Thr Arg Asp Ile Glu Pro Leu
 260 265 270

Ile

<210> 201

<211> 776

<212> DNA

<213> *Corynebacterium glutamicum*

<220>

<221> CDS

<222> (7)..(753)

<223> RXA02414

<400> 201

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  Met Ser Tyr Asn Ser Pro Tyr Asn Asn Thr Asn Phe Ser Thr Thr
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ggc gcg ttc caa cct gct ggt ggg ccg gtg aag ccg tgg aat aag ccc 99
Gly Ala Phe Gln Pro Ala Gly Gly Pro Val Lys Pro Trp Asn Lys Pro
          20             25             30

gat gcc agc ctg aat cag cag ctg aaa aac aaa tcc cgt gtg cgc aca 147
Asp Ala Ser Leu Asn Gln Gln Leu Lys Asn Lys Ser Arg Val Arg Thr
          35             40             45

ggt ctt acc atc gcc atc ggt tat gta gtg gtg att tgg gcg gtg cat 195
Gly Leu Thr Ile Ala Ile Gly Tyr Val Val Val Ile Trp Ala Val His
          50             55             60

ttg gca tcc atc gtc att gcg ctg ctc act ggc ttc aac ctg acc aac 243
Leu Ala Ser Ile Val Ile Ala Leu Leu Thr Gly Phe Asn Leu Thr Asn
          65             70             75

ttt ggt att cat ccg ctg gat acc agt gca ctg tgg ggt att ttc acc 291
Phe Gly Ile His Pro Leu Asp Thr Ser Ala Leu Trp Gly Ile Phe Thr
          80             85             90             95

tca ccg ctg ttg cat gga agc ttc agc cac ctc att gga aat acc gtt 339
Ser Pro Leu Leu His Gly Ser Phe Ser His Leu Ile Gly Asn Thr Val
          100             105             110

cca ggc ttt ata ttc agt ttc ctc atc ggt atg agt ggc aag cgc gtg 387
Pro Gly Phe Ile Phe Ser Phe Leu Ile Gly Met Ser Gly Lys Arg Val
          115             120             125

ttc tgg gaa gtc acg att atc gca ggt ctc atc ggc ggt ctt ggt aca 435
Phe Trp Glu Val Thr Ile Ile Ala Gly Leu Ile Gly Gly Leu Gly Thr
          130             135             140

tgg att ttc ggt gga atc ggc acc aac cac atc ggt gcg tcc ggc ctg 483
Trp Ile Phe Gly Gly Ile Gly Thr Asn His Ile Gly Ala Ser Gly Leu
          145             150             155

att tat ggc tgg ctt ggc tac ctg atc gtg cgt gga att ttc aac aag 531
Ile Tyr Gly Trp Leu Gly Tyr Leu Ile Val Arg Gly Ile Phe Asn Lys
          160             165             170             175

gat att aaa cag ttc ctg ctt ggc ata gtt ttg gcg ttc att tac tcc 579
Asp Ile Lys Gln Phe Leu Leu Gly Ile Val Leu Ala Phe Ile Tyr Ser
          180             185             190

ggt ttg ttc tgg ggt ctg cta cct act caa atc ggt gtg tcc tgg cag 627
Gly Leu Phe Trp Gly Leu Leu Pro Thr Gln Ile Gly Val Ser Trp Gln
          195             200             205

ggc cac ctt ttc ggt gca ctt ggt gga atc ggt gcg ggt gct ttt atc 675
Gly His Leu Phe Gly Ala Leu Gly Gly Ile Gly Ala Gly Ala Phe Ile
          210             215             220

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gcc tcg gat gac ccg gca gcg ttg aaa gcg aag aag caa cag aag aaa 723
 Ala Ser Asp Asp Pro Ala Ala Leu Lys Ala Lys Lys Gln Gln Lys Lys
 225 230 235

tta gaa aag caa caa cgc caa aga ggc tta tagttttcac ctacgcgacta 773
 Leu Glu Lys Gln Gln Arg Gln Arg Gly Leu
 240 245

cac 776

<210> 202

<211> 249

<212> PRT

<213> Corynebacterium glutamicum

<400> 202

Met Ser Tyr Asn Ser Pro Tyr Asn Asn Thr Asn Phe Ser Thr Thr Gly
 1 5 10 15

Ala Phe Gln Pro Ala Gly Gly Pro Val Lys Pro Trp Asn Lys Pro Asp
 20 25 30

Ala Ser Leu Asn Gln Gln Leu Lys Asn Lys Ser Arg Val Arg Thr Gly
 35 40 45

Leu Thr Ile Ala Ile Gly Tyr Val Val Val Ile Trp Ala Val His Leu
 50 55 60

Ala Ser Ile Val Ile Ala Leu Leu Thr Gly Phe Asn Leu Thr Asn Phe
 65 70 75 80

Gly Ile His Pro Leu Asp Thr Ser Ala Leu Trp Gly Ile Phe Thr Ser
 85 90 95

Pro Leu Leu His Gly Ser Phe Ser His Leu Ile Gly Asn Thr Val Pro
 100 105 110

Gly Phe Ile Phe Ser Phe Leu Ile Gly Met Ser Gly Lys Arg Val Phe
 115 120 125

Trp Glu Val Thr Ile Ile Ala Gly Leu Ile Gly Gly Leu Gly Thr Trp
 130 135 140

Ile Phe Gly Gly Ile Gly Thr Asn His Ile Gly Ala Ser Gly Leu Ile
 145 150 155 160

Tyr Gly Trp Leu Gly Tyr Leu Ile Val Arg Gly Ile Phe Asn Lys Asp
 165 170 175

Ile Lys Gln Phe Leu Leu Gly Ile Val Leu Ala Phe Ile Tyr Ser Gly
 180 185 190

Leu Phe Trp Gly Leu Leu Pro Thr Gln Ile Gly Val Ser Trp Gln Gly
 195 200 205

His Leu Phe Gly Ala Leu Gly Gly Ile Gly Ala Gly Ala Phe Ile Ala
 210 215 220

Ser Asp Asp Pro Ala Ala Leu Lys Ala Lys Lys Gln Gln Lys Lys Leu
 225 230 235 240

Glu Lys Gln Gln Arg Gln Arg Gly Leu
245

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<212> DNA
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<222> (101)..(817)
<223> RXN01580

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tcaactttgc tccctatcct taaaaagccc acagaaaagg atg tat aag aat atg 115
Met Tyr Lys Asn Met
1 5
cac att gtt gcc cat cgc ggt gcg gaa gat ctg cac ctc gaa aac acc 163
His Ile Val Ala His Arg Gly Ala Glu Asp Leu His Leu Glu Asn Thr
10 15 20
atg acc gct ttc cag gct gcc gcg ccc gct gac gct ttt gag ctg gat 211
Met Thr Ala Phe Gln Ala Ala Pro Ala Asp Ala Phe Glu Leu Asp
25 30 35
atc cac gcc acc gct gac aat cag gtc gtc gtt atc cac gac cgc acc 259
Ile His Ala Thr Ala Asp Asn Gln Val Val Val Ile His Asp Arg Thr
40 45 50
gca gcg cgt gtt gcc gcg cca gat tcc ctg cac cgc gac acc ccg gtt 307
Ala Ala Arg Val Ala Ala Pro Asp Ser Leu His Arg Asp Thr Pro Val
55 60 65
gcg cgc tta agc gcc gcg caa atc aag gag ata acg ctt atc gac gga 355
Ala Arg Leu Ser Ala Ala Gln Ile Lys Glu Ile Thr Leu Ile Asp Gly
70 75 80 85
tcc ccc gta cca acc ctg gag gaa gtt cta ctc cag acg agc ctg ccg 403
Ser Pro Val Pro Thr Leu Glu Glu Val Leu Leu Gln Thr Ser Leu Pro
90 95 100
atc caa gtg gaa atc aaa tct gcc ggt gca gtt cca gca gcc gca gca 451
Ile Gln Val Glu Ile Lys Ser Ala Gly Ala Val Pro Ala Ala Ala Ala
105 110 115
tta ttg cag aaa tac cca gag cac ctg gag cgc ctg ctg ttc atc agt 499
Leu Leu Gln Lys Tyr Pro Glu His Leu Glu Arg Leu Leu Phe Ile Ser
120 125 130
ttc atc gat gca gca ctg gtg gaa atc gtg gat cga ctg cca gaa gct 547
Phe Ile Asp Ala Ala Leu Val Glu Ile Val Asp Arg Leu Pro Glu Ala
135 140 145
cgc gtg gga atc ttg cgc gat gcg tcc atg gat gat ctg cgc att ctt 595
Arg Val Gly Ile Leu Arg Asp Ala Ser Met Asp Asp Leu Arg Ile Leu
150 155 160 165

gat tac atc ccg cta aaa aat gtg ggc gcg atc ttg ccc tcg tgg aaa 643
Asp Tyr Ile Pro Leu Lys Asn Val Gly Ala Ile Leu Pro Ser Trp Lys
170 175 180

gca cta aac gtg gcg tca att gct gat cta cat acc aag gga atc aag 691
Ala Leu Asn Val Ala Ser Ile Ala Asp Leu His Thr Lys Gly Ile Lys
185 190 195

gtt ggc tgc tgg aca att cgg gat gaa aat gcg ttt ggg atc gca caa 739
Val Gly Cys Trp Thr Ile Arg Asp Glu Asn Ala Phe Gly Ile Ala Gln
200 205 210

caa gct ggc gtt gat tac gcc act gtt agc gat ccc tct cgt ttc ctc 787
Gln Ala Gly Val Asp Tyr Ala Thr Val Ser Asp Pro Ser Arg Phe Leu
215 220 225

gcg ccc tcc cct gct ggg gag ttg cac tgg taaataatct agtgaccaga 837
Ala Pro Ser Pro Ala Gly Glu Leu His Trp
230 235

ctg 840

<210> 204
<211> 239
<212> PRT
<213> Corynebacterium glutamicum

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20 25 30

Ala Phe Glu Leu Asp Ile His Ala Thr Ala Asp Asn Gln Val Val Val
35 40 45

Ile His Asp Arg Thr Ala Ala Arg Val Ala Ala Pro Asp Ser Leu His
50 55 60

Arg Asp Thr Pro Val Ala Arg Leu Ser Ala Ala Gln Ile Lys Glu Ile
65 70 75 80

Thr Leu Ile Asp Gly Ser Pro Val Pro Thr Leu Glu Glu Val Leu Leu
85 90 95

Gln Thr Ser Leu Pro Ile Gln Val Glu Ile Lys Ser Ala Gly Ala Val
100 105 110

Pro Ala Ala Ala Ala Leu Leu Gln Lys Tyr Pro Glu His Leu Glu Arg
115 120 125

Leu Leu Phe Ile Ser Phe Ile Asp Ala Ala Leu Val Glu Ile Val Asp
130 135 140

Arg Leu Pro Glu Ala Arg Val Gly Ile Leu Arg Asp Ala Ser Met Asp
145 150 155 160

Asp Leu Arg Ile Leu Asp Tyr Ile Pro Leu Lys Asn Val Gly Ala Ile

[illegible]

Ile	Pro	Leu	Ala	Pro	Leu	His	Asn	Pro	Ala	Asn	Val	Asp	Gly	Ile	Asp	
		120					125					130				
gtt	gct	cga	aaa	att	ctc	ccc	gat	gtc	cca	cac	gta	gct	gtc	ttt	gac	547
Val	Ala	Arg	Lys	Ile	Leu	Pro	Asp	Val	Pro	His	Val	Ala	Val	Phe	Asp	
		135				140					145					
acc	ggt	ttc	ttc	cac	tca	ctt	cca	cca	gca	gct	gcg	ctg	tat	gcc	atc	595
Thr	Gly	Phe	Phe	His	Ser	Leu	Pro	Pro	Ala	Ala	Ala	Leu	Tyr	Ala	Ile	
		150				155					160				165	
aac	aag	gat	gtc	gca	gct	gaa	cac	gga	atc	agg	cgc	tat	ggt	ttc	cac	643
Asn	Lys	Asp	Val	Ala	Ala	Glu	His	Gly	Ile	Arg	Arg	Tyr	Gly	Phe	His	
				170					175					180		
ggc	acc	tcc	cat	gaa	ttt	gtg	tcc	aag	cgc	gtg	gtg	gaa	att	ctg	gaa	691
Gly	Thr	Ser	His	Glu	Phe	Val	Ser	Lys	Arg	Val	Val	Glu	Ile	Leu	Glu	
			185					190					195			
aag	ccc	acc	gaa	gac	atc	aac	acc	atc	acc	ttc	cac	ctg	ggc	aac	ggc	739
Lys	Pro	Thr	Glu	Asp	Ile	Asn	Thr	Ile	Thr	Phe	His	Leu	Gly	Asn	Gly	
		200					205					210				
gca	tcc	atg	gct	gct	gtt	caa	ggt	ggc	cgt	gcg	gta	gat	act	tcc	atg	787
Ala	Ser	Met	Ala	Ala	Val	Gln	Gly	Gly	Arg	Ala	Val	Asp	Thr	Ser	Met	
		215				220					225					
ggt	atg	aca	cct	ctc	gcg	ggc	ctt	gtc	atg	ggt	acc	cga	agc	ggt	gac	835
Gly	Met	Thr	Pro	Leu	Ala	Gly	Leu	Val	Met	Gly	Thr	Arg	Ser	Gly	Asp	
		230				235				240					245	
att	gat	cca	ggt	atc	gtc	ttc	cac	ctt	tcc	cgc	acc	gct	ggc	atg	agc	883
Ile	Asp	Pro	Gly	Ile	Val	Phe	His	Leu	Ser	Arg	Thr	Ala	Gly	Met	Ser	
				250					255					260		
atc	gat	gag	atc	gat	aat	ctg	ctg	aac	aaa	aag	tcg	ggt	gta	aag	gga	931
Ile	Asp	Glu	Ile	Asp	Asn	Leu	Leu	Asn	Lys	Lys	Ser	Gly	Val	Lys	Gly	
			265					270					275			
ctt	tcc	ggt	gtt	aat	gat	ttc	cgt	gaa	ctg	cgg	gaa	atg	atc	gac	aac	979
Leu	Ser	Gly	Val	Asn	Asp	Phe	Arg	Glu	Leu	Arg	Glu	Met	Ile	Asp	Asn	
		280					285					290				
aat	gat	caa	gat	gcc	tgg	tcc	gcg	tac	aac	att	tac	ata	cac	caa	ctc	1027
Asn	Asp	Gln	Asp	Ala	Trp	Ser	Ala	Tyr	Asn	Ile	Tyr	Ile	His	Gln	Leu	
		295				300					305					
cgc	cgc	tac	ctc	ggt	tcc	tac	atg	gtg	gca	ctg	gga	cgg	gta	gac	acc	1075
Arg	Arg	Tyr	Leu	Gly	Ser	Tyr	Met	Val	Ala	Leu	Gly	Arg	Val	Asp	Thr	
		310			315					320					325	
atc	gtg	ttc	acc	gcc	ggt	gtc	ggt	gaa	aat	gcc	cag	ttt	gtc	cgt	gag	1123
Ile	Val	Phe	Thr	Ala	Gly	Val	Gly	Glu	Asn	Ala	Gln	Phe	Val	Arg	Glu	
				330					335					340		
gat	gcc	ttg	gca	ggt	ttg	gaa	atg	tac	gga	att	gag	atc	gat	cca	gag	1171
Asp	Ala	Leu	Ala	Gly	Leu	Glu	Met	Tyr	Gly	Ile	Glu	Ile	Asp	Pro	Glu	
			345					350					355			
cgt	aac	gca	ttg	cca	aac	gat	ggt	cct	cga	ttg	att	tcc	acc	gat	gcc	1219
Arg	Asn	Ala	Leu	Pro	Asn	Asp	Gly	Pro	Arg	Leu	Ile	Ser	Thr	Asp	Ala	

360 365 370
 tcc aag gtg aag gtg ttt gtt att cca act aat gaa gag tta gct atc 1267
 Ser Lys Val Lys Val Phe Val Ile Pro Thr Asn Glu Glu Leu Ala Ile
 375 380 385
 gct agg tac gcg gtg aag ttc gct tagctctcct ggtaggatac cac 1314
 Ala Arg Tyr Ala Val Lys Phe Ala
 390 395

 <210> 206
 <211> 397
 <212> PRT
 <213> *Corynebacterium glutamicum*

 <400> 206
 Met Ala Leu Ala Leu Val Leu Asn Ser Gly Ser Ser Ser Ile Lys Phe
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 Gln Leu Val Asn Pro Glu Asn Ser Ala Ile Asp Glu Pro Tyr Val Ser
 20 25 30
 Gly Leu Val Glu Gln Ile Gly Glu Pro Asn Gly Arg Ile Val Leu Lys
 35 40 45
 Ile Glu Gly Glu Lys Tyr Thr Leu Glu Thr Pro Ile Ala Asp His Ser
 50 55 60
 Glu Gly Leu Asn Leu Ala Phe Asp Leu Met Asp Gln His Asn Cys Gly
 65 70 75 80
 Pro Ser Gln Leu Glu Ile Thr Ala Val Gly His Arg Val Val His Gly
 85 90 95
 Gly Ile Leu Phe Ser Ala Pro Glu Leu Ile Thr Asp Glu Ile Val Glu
 100 105 110
 Met Ile Arg Asp Leu Ile Pro Leu Ala Pro Leu His Asn Pro Ala Asn
 115 120 125
 Val Asp Gly Ile Asp Val Ala Arg Lys Ile Leu Pro Asp Val Pro His
 130 135 140
 Val Ala Val Phe Asp Thr Gly Phe Phe His Ser Leu Pro Pro Ala Ala
 145 150 155 160
 Ala Leu Tyr Ala Ile Asn Lys Asp Val Ala Ala Glu His Gly Ile Arg
 165 170 175
 Arg Tyr Gly Phe His Gly Thr Ser His Glu Phe Val Ser Lys Arg Val
 180 185 190
 Val Glu Ile Leu Glu Lys Pro Thr Glu Asp Ile Asn Thr Ile Thr Phe
 195 200 205
 His Leu Gly Asn Gly Ala Ser Met Ala Ala Val Gln Gly Gly Arg Ala
 210 215 220
 Val Asp Thr Ser Met Gly Met Thr Pro Leu Ala Gly Leu Val Met Gly
 225 230 235 240

Thr Arg Ser Gly Asp Ile Asp Pro Gly Ile Val Phe His Leu Ser Arg
 245 250 255
 Thr Ala Gly Met Ser Ile Asp Glu Ile Asp Asn Leu Leu Asn Lys Lys
 260 265 270
 Ser Gly Val Lys Gly Leu Ser Gly Val Asn Asp Phe Arg Glu Leu Arg
 275 280 285
 Glu Met Ile Asp Asn Asn Asp Gln Asp Ala Trp Ser Ala Tyr Asn Ile
 290 295 300
 Tyr Ile His Gln Leu Arg Arg Tyr Leu Gly Ser Tyr Met Val Ala Leu
 305 310 315 320
 Gly Arg Val Asp Thr Ile Val Phe Thr Ala Gly Val Gly Glu Asn Ala
 325 330 335
 Gln Phe Val Arg Glu Asp Ala Leu Ala Gly Leu Glu Met Tyr Gly Ile
 340 345 350
 Glu Ile Asp Pro Glu Arg Asn Ala Leu Pro Asn Asp Gly Pro Arg Leu
 355 360 365
 Ile Ser Thr Asp Ala Ser Lys Val Lys Val Phe Val Ile Pro Thr Asn
 370 375 380
 Glu Glu Leu Ala Ile Ala Arg Tyr Ala Val Lys Phe Ala
 385 390 395

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<211> 927

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(904)

<223> RXA00686

<400> 207

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ttcacgag tgccagggga acttagagga gcattaaata atg gcg gga gga aat 115
 Met Ala Gly Gly Asn
 1 5

cgc gaa cct gga cgt aca gtc acc tcc aag gtg atc gcc gta ctg gga 163
 Arg Glu Pro Gly Arg Thr Val Thr Ser Lys Val Ile Ala Val Leu Gly
 10 15 20

gct ttt gaa cac acc atg cgt cca ctt ggt gtc act gaa atc gct gag 211
 Ala Phe Glu His Thr Met Arg Pro Leu Gly Val Thr Glu Ile Ala Glu
 25 30 35

ctg gca gac ctc cca cca agt acc acc cac cgt ctc gtt tct gaa tta 259
 Leu Ala Asp Leu Pro Pro Ser Thr Thr His Arg Leu Val Ser Glu Leu
 40 45 50

acc gaa ggc gga cta ctc agc aag aaa tct gat ggg cgc tac caa ttg 307
 Thr Glu Gly Gly Leu Leu Ser Lys Lys Ser Asp Gly Arg Tyr Gln Leu
 55 60 65

ggc tta cgt atc tgg gaa ctc gcc caa aat aca gga cgg cag tta cgc 355
 Gly Leu Arg Ile Trp Glu Leu Ala Gln Asn Thr Gly Arg Gln Leu Arg
 70 75 80 85

gac act gca cgc ccg ttc atc caa gag ctc tac tca ctt act tcc gag 403
 Asp Thr Ala Arg Pro Phe Ile Gln Glu Leu Tyr Ser Leu Thr Ser Glu
 90 95 100

act gcg cag cta gtg gtc cgc gat aaa gat gaa gca ctt ttg att gac 451
 Thr Ala Gln Leu Val Val Arg Asp Lys Asp Glu Ala Leu Leu Ile Asp
 105 110 115

cga gcc tac ggc acg aag aaa att cca cgc tcg gct cga gtc ggt ggt 499
 Arg Ala Tyr Gly Thr Lys Lys Ile Pro Arg Ser Ala Arg Val Gly Gly
 120 125 130

cga cta cct ctg aac tcc act gcg gtt ggc aag att ctc ctt gcg ttt 547
 Arg Leu Pro Leu Asn Ser Thr Ala Val Gly Lys Ile Leu Leu Ala Phe
 135 140 145

gat gag cca tgg gta aaa cag tcc tat ctc aag ctg cca ctc aac gcc 595
 Asp Glu Pro Trp Val Lys Gln Ser Tyr Leu Lys Leu Pro Leu Asn Ala
 150 155 160 165

tcc acc cca aag aca att gtg aat ccc gac gtc ttg gct gcg cag ctg 643
 Ser Thr Pro Lys Thr Ile Val Asn Pro Asp Val Leu Ala Ala Gln Leu
 170 175 180

aaa caa att cac tcg caa ggc ttt gcc atc aca cat gac gag caa cga 691
 Lys Gln Ile His Ser Gln Gly Phe Ala Ile Thr His Asp Glu Gln Arg
 185 190 195

atc ggc ggc gca tcg atc gcc gta ccg gtc tgg cat aca gga aaa ctg 739
 Ile Gly Gly Ala Ser Ile Ala Val Pro Val Trp His Thr Gly Lys Leu
 200 205 210

gga gca gca ctg ggg ttg gtg gtt ccc acc gca cag gct gca aat ctt 787
 Gly Ala Ala Leu Gly Leu Val Val Pro Thr Ala Gln Ala Ala Asn Leu
 215 220 225

gag cgc tat ctc ccg atc ctt cag gcg aca agt cag aga att aca aaa 835
 Glu Arg Tyr Leu Pro Ile Leu Gln Ala Thr Ser Gln Arg Ile Thr Lys
 230 235 240 245

gca acc gcg ctc att cct ttg gac aca ctt ttg gct tca cac aaa aat 883
 Ala Thr Ala Leu Ile Pro Leu Asp Thr Leu Leu Ala Ser His Lys Asn
 250 255 260

gca gaa cga aaa ggc gat acc taaaccgcc ctccatctgc ata 927
 Ala Glu Arg Lys Gly Asp Thr
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<210> 208

<211> 268

<212> PRT

<213> Corynebacterium glutamicum

<400> 208

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Ile Ala Val Leu Gly Ala Phe Glu His Thr Met Arg Pro Leu Gly Val
      20           25           30

Thr Glu Ile Ala Glu Leu Ala Asp Leu Pro Pro Ser Thr Thr His Arg
      35           40           45

Leu Val Ser Glu Leu Thr Glu Gly Gly Leu Leu Ser Lys Lys Ser Asp
      50           55           60

Gly Arg Tyr Gln Leu Gly Leu Arg Ile Trp Glu Leu Ala Gln Asn Thr
      65           70           75           80

Gly Arg Gln Leu Arg Asp Thr Ala Arg Pro Phe Ile Gln Glu Leu Tyr
      85           90           95

Ser Leu Thr Ser Glu Thr Ala Gln Leu Val Val Arg Asp Lys Asp Glu
      100          105          110

Ala Leu Leu Ile Asp Arg Ala Tyr Gly Thr Lys Lys Ile Pro Arg Ser
      115          120          125

Ala Arg Val Gly Gly Arg Leu Pro Leu Asn Ser Thr Ala Val Gly Lys
      130          135          140

Ile Leu Leu Ala Phe Asp Glu Pro Trp Val Lys Gln Ser Tyr Leu Lys
      145          150          155          160

Leu Pro Leu Asn Ala Ser Thr Pro Lys Thr Ile Val Asn Pro Asp Val
      165          170          175

Leu Ala Ala Gln Leu Lys Gln Ile His Ser Gln Gly Phe Ala Ile Thr
      180          185          190

His Asp Glu Gln Arg Ile Gly Gly Ala Ser Ile Ala Val Pro Val Trp
      195          200          205

His Thr Gly Lys Leu Gly Ala Ala Leu Gly Leu Val Val Pro Thr Ala
      210          215          220

Gln Ala Ala Asn Leu Glu Arg Tyr Leu Pro Ile Leu Gln Ala Thr Ser
      225          230          235          240

Gln Arg Ile Thr Lys Ala Thr Ala Leu Ile Pro Leu Asp Thr Leu Leu
      245          250          255

Ala Ser His Lys Asn Ala Glu Arg Lys Gly Asp Thr
      260          265

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<211> 1158

<212> DNA

<213> *Corynebacterium glutamicum*

<220>

<221> CDS

<222> (101)..(1135)

<223> RXA00246

<400> 209

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 Met Thr Thr Ala Ala
 1 5

ccc caa gaa ttt acc gct gct gtt gtt gaa aaa ttc ggt cat gac gtg 163
 Pro Gln Glu Phe Thr Ala Ala Val Val Glu Lys Phe Gly His Asp Val
 10 15 20

acc gtg aag gat att gac ctt cca aag cca ggg cca cac cag gca ttg 211
 Thr Val Lys Asp Ile Asp Leu Pro Lys Pro Gly Pro His Gln Ala Leu
 25 30 35

gtg aag gta ctc acc tcc ggc atc tgc cac acc gac ctc cac gcc ttg 259
 Val Lys Val Leu Thr Ser Gly Ile Cys His Thr Asp Leu His Ala Leu
 40 45 50

gag ggc gat tgg cca gta aag ccg gaa cca cca ttc gta cca gga cac 307
 Glu Gly Asp Trp Pro Val Lys Pro Glu Pro Pro Phe Val Pro Gly His
 55 60 65

gaa ggt gta ggt gaa gtt gtt gag ctc gga cca ggt gaa cac gat gtg 355
 Glu Gly Val Gly Glu Val Val Glu Leu Gly Pro Gly Glu His Asp Val
 70 75 80 85

aag gtc ggc gat att gtc ggc aat gcg tgg ctc tgg tca gcg tgt ggc 403
 Lys Val Gly Asp Ile Val Gly Asn Ala Trp Leu Trp Ser Ala Cys Gly
 90 95 100

acc tgc gaa tac tgc atc acc ggc agg gaa act cag tgc aac gaa gct 451
 Thr Cys Glu Tyr Cys Ile Thr Gly Arg Glu Thr Gln Cys Asn Glu Ala
 105 110 115

gag tat ggt ggc tac acc caa aat gga tcc ttc ggc cag tac atg ctg 499
 Glu Tyr Gly Gly Tyr Thr Gln Asn Gly Ser Phe Gly Gln Tyr Met Leu
 120 125 130

gtg gat acc cgt tac gcc gct cgc atc cca gac ggc gtg gac tac ctc 547
 Val Asp Thr Arg Tyr Ala Ala Arg Ile Pro Asp Gly Val Asp Tyr Leu
 135 140 145

gaa gca gca cca att ctg tgt gca ggc gtg act gtc tac aag gca ctc 595
 Glu Ala Ala Pro Ile Leu Cys Ala Gly Val Thr Val Tyr Lys Ala Leu
 150 155 160 165

aaa gtc tct gaa acc cgc ccg ggc caa ttc atg gtg atc tcc ggt gtc 643
 Lys Val Ser Glu Thr Arg Pro Gly Gln Phe Met Val Ile Ser Gly Val
 170 175 180

ggc gga ctt ggc cac atc gca gtc caa tac gca gcg gcg atg ggc atg 691
 Gly Gly Leu Gly His Ile Ala Val Gln Tyr Ala Ala Ala Met Gly Met
 185 190 195

cgt gtc att gcg gta gat att gcc gat gac aag ctg gaa ctt gcc cgt 739
 Arg Val Ile Ala Val Asp Ile Ala Asp Asp Lys Leu Glu Leu Ala Arg
 200 205 210

aag cac ggt gcg gaa ttt acc gtg aat gcg cgt aat gaa gat tca ggc 787
 Lys His Gly Ala Glu Phe Thr Val Asn Ala Arg Asn Glu Asp Ser Gly
 215 220 225

 gaa gct gta cag aag tac acc aac ggt ggc gca cac ggc gtg ctt gtg 835
 Glu Ala Val Gln Lys Tyr Thr Asn Gly Gly Ala His Gly Val Leu Val
 230 235 240 245

 act gca gtt cac gag gca gca ttc ggc cag gca ctg gat atg gct cga 883
 Thr Ala Val His Glu Ala Ala Phe Gly Gln Ala Leu Asp Met Ala Arg
 250 255 260

 cgt gca gga aca att gtg ttc aac ggt ctg cca ccg gga gag ttc cca 931
 Arg Ala Gly Thr Ile Val Phe Asn Gly Leu Pro Pro Gly Glu Phe Pro
 265 270 275

 gca tcc gtg ttc aac atc gta ttc aag ggc ctg acc atc cgt gga tcc 979
 Ala Ser Val Phe Asn Ile Val Phe Lys Gly Leu Thr Ile Arg Gly Ser
 280 285 290

 ctc gtg gga acc cgc caa gac ttg gcc gaa gcg ctc gat ttc ttt gca 1027
 Leu Val Gly Thr Arg Gln Asp Leu Ala Glu Ala Leu Asp Phe Phe Ala
 295 300 305

 cgc gga cta atc aag cca acc gtg agt gag tgc tcc ctc gat gag gtc 1075
 Arg Gly Leu Ile Lys Pro Thr Val Ser Glu Cys Ser Leu Asp Glu Val
 310 315 320 325

 aat ggt gtg ctt gac cgc atg cga aac ggc aag atc gat ggt cgt gtg 1123
 Asn Gly Val Leu Asp Arg Met Arg Asn Gly Lys Ile Asp Gly Arg Val
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 Ala Ile Arg Phe
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 <213> Corynebacterium glutamicum

<400> 210
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 Pro His Gln Ala Leu Val Lys Val Leu Thr Ser Gly Ile Cys His Thr
 35 40 45

 Asp Leu His Ala Leu Glu Gly Asp Trp Pro Val Lys Pro Glu Pro Pro
 50 55 60

 Phe Val Pro Gly His Glu Gly Val Gly Glu Val Val Glu Leu Gly Pro
 65 70 75 80

 Gly Glu His Asp Val Lys Val Gly Asp Ile Val Gly Asn Ala Trp Leu
 85 90 95

Trp Ser Ala Cys Gly Thr Cys Glu Tyr Cys Ile Thr Gly Arg Glu Thr
 100 105 110
 Gln Cys Asn Glu Ala Glu Tyr Gly Gly Tyr Thr Gln Asn Gly Ser Phe
 115 120 125
 Gly Gln Tyr Met Leu Val Asp Thr Arg Tyr Ala Ala Arg Ile Pro Asp
 130 135 140
 Gly Val Asp Tyr Leu Glu Ala Ala Pro Ile Leu Cys Ala Gly Val Thr
 145 150 155 160
 Val Tyr Lys Ala Leu Lys Val Ser Glu Thr Arg Pro Gly Gln Phe Met
 165 170 175
 Val Ile Ser Gly Val Gly Gly Leu Gly His Ile Ala Val Gln Tyr Ala
 180 185 190
 Ala Ala Met Gly Met Arg Val Ile Ala Val Asp Ile Ala Asp Asp Lys
 195 200 205
 Leu Glu Leu Ala Arg Lys His Gly Ala Glu Phe Thr Val Asn Ala Arg
 210 215 220
 Asn Glu Asp Ser Gly Glu Ala Val Gln Lys Tyr Thr Asn Gly Gly Ala
 225 230 235 240
 His Gly Val Leu Val Thr Ala Val His Glu Ala Ala Phe Gly Gln Ala
 245 250 255
 Leu Asp Met Ala Arg Arg Ala Gly Thr Ile Val Phe Asn Gly Leu Pro
 260 265 270
 Pro Gly Glu Phe Pro Ala Ser Val Phe Asn Ile Val Phe Lys Gly Leu
 275 280 285
 Thr Ile Arg Gly Ser Leu Val Gly Thr Arg Gln Asp Leu Ala Glu Ala
 290 295 300
 Leu Asp Phe Phe Ala Arg Gly Leu Ile Lys Pro Thr Val Ser Glu Cys
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 Ser Leu Asp Glu Val Asn Gly Val Leu Asp Arg Met Arg Asn Gly Lys
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 Ile Asp Gly Arg Val Ala Ile Arg Phe
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 <213> Corynebacterium glutamicum

<220>
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 <222> (101)..(700)
 <223> RXA01571

<400> 211

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				Val	Ser	Ile	Ser	Val	5							
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aaa	gca	cta	caa	aag	tcc	ggc	cca	gaa	gca	cct	ttc	gag	gtc	aag	atc	163
Lys	Ala	Leu	Gln	Lys	Ser	Gly	Pro	Glu	Ala	Pro	Phe	Glu	Val	Lys	Ile	20
				10					15							
att	gaa	cgc	cgt	gac	cca	cgc	gca	gat	gat	gtg	gtt	att	gat	atc	aaa	211
Ile	Glu	Arg	Arg	Asp	Pro	Arg	Ala	Asp	Asp	Val	Val	Ile	Asp	Ile	Lys	35
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gct	gcg	ggc	atc	tgc	cac	agc	gat	atc	cac	acc	atc	cgc	aac	gaa	tgg	259
Ala	Ala	Gly	Ile	Cys	His	Ser	Asp	Ile	His	Thr	Ile	Arg	Asn	Glu	Trp	40
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Gly	Glu	Ala	His	Phe	Pro	Leu	Thr	Val	Gly	His	Glu	Ile	Ala	Gly	Val	55
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gtc	tct	gcg	gtt	gga	tcc	gat	gta	acc	aaa	tgg	aaa	gtc	ggc	gac	cgc	355
Val	Ser	Ala	Val	Gly	Ser	Asp	Val	Thr	Lys	Trp	Lys	Val	Gly	Asp	Arg	70
					75					80					85	
gtg	ggc	gtc	ggc	tgc	ctc	gtt	aac	tcc	tgc	ggc	gaa	tgc	gaa	cag	tgc	403
Val	Gly	Val	Gly	Cys	Leu	Val	Asn	Ser	Cys	Gly	Glu	Cys	Glu	Gln	Cys	90
				90					95					100		
gtc	gca	gga	ttt	gaa	aac	aac	tgc	ctt	cgc	gga	aac	gtc	gga	acc	tac	451
Val	Ala	Gly	Phe	Glu	Asn	Asn	Cys	Leu	Arg	Gly	Asn	Val	Gly	Thr	Tyr	105
							110						115			
aac	tct	aac	gac	gtc	gac	ggc	acc	atc	acc	caa	ggc	ggc	tac	gct	gaa	499
Asn	Ser	Asn	Asp	Val	Asp	Gly	Thr	Ile	Thr	Gln	Gly	Gly	Tyr	Ala	Glu	120
							125					130				
aag	gta	gtg	gtc	aac	gaa	cgt	ttc	ctg	tgc	agc	atc	cca	gag	gaa	ctt	547
Lys	Val	Val	Val	Asn	Glu	Arg	Phe	Leu	Cys	Ser	Ile	Pro	Glu	Glu	Leu	135
						140					145					
aac	ttc	gat	gtc	gca	gca	cca	ctg	ctg	tgc	gca	ggc	atc	acc	acc	tac	595
Asn	Phe	Asp	Val	Ala	Ala	Pro	Leu	Leu	Cys	Ala	Gly	Ile	Thr	Thr	Tyr	150
					155					160					165	
tcc	cca	atc	gct	cgc	tgg	aac	gtt	aaa	gaa	ggc	gac	aaa	gta	gca	gtc	643
Ser	Pro	Ile	Ala	Arg	Trp	Asn	Val	Lys	Glu	Gly	Asp	Lys	Val	Ala	Val	170
									175					180		
atg	ggc	ctc	ggc	ggg	act	cgg	aca	cat	ggg	tgt	cca	gat	cgc	tgc	agc	691
Met	Gly	Leu	Gly	Gly	Thr	Arg	Thr	His	Gly	Cys	Pro	Asp	Arg	Cys	Ser	185
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Gln	Gly	Cys					</									

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<211> 200

<212> PRT

<213> Corynebacterium glutamicum

<400> 212

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 20 25 30

Val Ile Asp Ile Lys Ala Ala Gly Ile Cys His Ser Asp Ile His Thr
 35 40 45

Ile Arg Asn Glu Trp Gly Glu Ala His Phe Pro Leu Thr Val Gly His
 50 55 60

Glu Ile Ala Gly Val Val Ser Ala Val Gly Ser Asp Val Thr Lys Trp
 65 70 75 80

Lys Val Gly Asp Arg Val Gly Val Gly Cys Leu Val Asn Ser Cys Gly
 85 90 95

Glu Cys Glu Gln Cys Val Ala Gly Phe Glu Asn Asn Cys Leu Arg Gly
 100 105 110

Asn Val Gly Thr Tyr Asn Ser Asn Asp Val Asp Gly Thr Ile Thr Gln
 115 120 125

Gly Gly Tyr Ala Glu Lys Val Val Val Asn Glu Arg Phe Leu Cys Ser
 130 135 140

Ile Pro Glu Glu Leu Asn Phe Asp Val Ala Ala Pro Leu Leu Cys Ala
 145 150 155 160

Gly Ile Thr Thr Tyr Ser Pro Ile Ala Arg Trp Asn Val Lys Glu Gly
 165 170 175

Asp Lys Val Ala Val Met Gly Leu Gly Gly Thr Arg Thr His Gly Cys
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Pro Asp Arg Cys Ser Gln Gly Cys
 195 200

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<212> DNA

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<220>

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<222> (101)..(592)

<223> RXA01572

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gacaaagtag cagtcattggg cctcggcggg actcggacac atg ggt gtc cag atc 115
 Met Gly Val Gln Ile
 1 5

gct gca gcc aag ggt gct gag gtt acc gtt ctg tcc cgt tcc ctg cgc 163
 Ala Ala Ala Lys Gly Ala Glu Val Thr Val Leu Ser Arg Ser Leu Arg
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 aag gca gaa ctt gcc aag gaa ctc ggc gca gct cgc acg ctt gcg act 211
 Lys Ala Glu Leu Ala Lys Glu Leu Gly Ala Ala Arg Thr Leu Ala Thr
 25 30 35

 tct gat gag gat ttc ttc acc gaa cac gcc ggt gaa ttc gac ttc atc 259
 Ser Asp Glu Asp Phe Phe Thr Glu His Ala Gly Glu Phe Asp Phe Ile
 40 45 50

 ctc aac acc att agc gca tcc atc cca gtc gac aag tac ctg agc ctt 307
 Leu Asn Thr Ile Ser Ala Ser Ile Pro Val Asp Lys Tyr Leu Ser Leu
 55 60 65

 ctc aag cca cac ggt gtc atg gct gtt gtc ggt ctg cca cca gag aag 355
 Leu Lys Pro His Gly Val Met Ala Val Val Gly Leu Pro Pro Glu Lys
 70 75 80 85

 cag cca ctg agc ttc ggt gcg ctc atc ggc ggc gga aaa gtc ctc acc 403
 Gln Pro Leu Ser Phe Gly Ala Leu Ile Gly Gly Gly Lys Val Leu Thr
 90 95 100

 gga tcc aac att ggc ggc atc cct gaa acc cag gaa atg ctc gac ttc 451
 Gly Ser Asn Ile Gly Gly Ile Pro Glu Thr Gln Glu Met Leu Asp Phe
 105 110 115

 tgt gca aaa cac ggc ctc ggt gcg atg atc gaa act gtc ggc gtc aac 499
 Cys Ala Lys His Gly Leu Gly Ala Met Ile Glu Thr Val Gly Val Asn
 120 125 130

 gat gtt gat gca gcc tac gac cgt gtt gtt gcc ggc gac gtt cag ttc 547
 Asp Val Asp Ala Ala Tyr Asp Arg Val Val Ala Gly Asp Val Gln Phe
 135 140 145

 cgc gtt gtc att gat act gct tcg ttt gct gag gtt gag gcg gtt 592
 Arg Val Val Ile Asp Thr Ala Ser Phe Ala Glu Val Glu Ala Val
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 taggtttact gaagttcaga ctt 615

<210> 214

<211> 164

<212> PRT

<213> Corynebacterium glutamicum

<400> 214

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 20 25 30

Arg Thr Leu Ala Thr Ser Asp Glu Asp Phe Phe Thr Glu His Ala Gly
 35 40 45

Glu Phe Asp Phe Ile Leu Asn Thr Ile Ser Ala Ser Ile Pro Val Asp
 50 55 60

Lys Tyr Leu Ser Leu Leu Lys Pro His Gly Val Met Ala Val Val Gly
 65 70 75 80
 Leu Pro Pro Glu Lys Gln Pro Leu Ser Phe Gly Ala Leu Ile Gly Gly
 85 90 95
 Gly Lys Val Leu Thr Gly Ser Asn Ile Gly Gly Ile Pro Glu Thr Gln
 100 105 110
 Glu Met Leu Asp Phe Cys Ala Lys His Gly Leu Gly Ala Met Ile Glu
 115 120 125
 Thr Val Gly Val Asn Asp Val Asp Ala Ala Tyr Asp Arg Val Val Ala
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 Gly Asp Val Gln Phe Arg Val Val Ile Asp Thr Ala Ser Phe Ala Glu
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 Val Glu Ala Val

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 <212> DNA
 <213> Corynebacterium glutamicum

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 <222> (101)..(1117)
 <223> RXA01758

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 Met Pro Lys Tyr Ile
 1 5
 gcc atg cag gta tcc gaa tcc ggt gca ccg tta gcc gcg aat ctc gtg 163
 Ala Met Gln Val Ser Glu Ser Gly Ala Pro Leu Ala Ala Asn Leu Val
 10 15 20
 caa cct gct ccg ttg aaa tcg agg gaa gtc cgc gtg gaa atc gct gct 211
 Gln Pro Ala Pro Leu Lys Ser Arg Glu Val Arg Val Glu Ile Ala Ala
 25 30 35
 agt ggt gtg tgc cat gca gat att ggc acg gca gca gca tcg ggg aag 259
 Ser Gly Val Cys His Ala Asp Ile Gly Thr Ala Ala Ala Ser Gly Lys
 40 45 50
 cac act gtt ttt cct gtt acc cct ggt cat gag att gca gga acc atc 307
 His Thr Val Phe Pro Val Thr Pro Gly His Glu Ile Ala Gly Thr Ile
 55 60 65
 gcg gaa att ggt gaa aac gta tct cgg tgg acg gtt ggt gat cgc gtt 355
 Ala Glu Ile Gly Glu Asn Val Ser Arg Trp Thr Val Gly Asp Arg Val
 70 75 80 85
 gca atc ggt tgg ttt ggt ggc aat tgc ggt gac tgc gct ttt tgt cgt 403
 Ala Ile Gly Trp Phe Gly Gly Asn Cys Gly Asp Cys Ala Phe Cys Arg

90										95										100										
gca ggt gat cct gtg cat tgc aga gag cgg aag att cct ggc gtt tct	451																													
Ala Gly Asp Pro Val His Cys Arg Glu Arg Lys Ile Pro Gly Val Ser																														
105 110 115																														
tat gcg ggt ggt tgg gca cag aat att gtt gtt cca gcg gag gct ctt	499																													
Tyr Ala Gly Gly Trp Ala Gln Asn Ile Val Val Pro Ala Glu Ala Leu																														
120 125 130																														
gct gcg att cca gat ggc atg gac ttt tac gag ccc gcc ccg atg ggc	547																													
Ala Ala Ile Pro Asp Gly Met Asp Phe Tyr Glu Pro Ala Pro Met Gly																														
135 140 145																														
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Cys Ala Gly Val Thr Thr Phe Asn Ala Leu Arg Asn Leu Lys Leu Asp																														
150 155 160 165																														
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Pro Gly Ala Ala Val Ala Val Phe Gly Ile Gly Gly Leu Val Arg Leu																														
170 175 180																														
gct att cag ttt gct gcg aaa atg ggt tat cga acc atc acc atc gcc	691																													
Ala Ile Gln Phe Ala Ala Lys Met Gly Tyr Arg Thr Ile Thr Ile Ala																														
185 190 195																														
cgc ggt tta gag cgt gag gag cta gct agg caa ctt ggc gcc aac cac	739																													
Arg Gly Leu Glu Arg Glu Glu Leu Ala Arg Gln Leu Gly Ala Asn His																														
200 205 210																														
tac atc gat agc aat gat ctg cac cct ggc cag gcg tta ttt gaa ctt	787																													
Tyr Ile Asp Ser Asn Asp Leu His Pro Gly Gln Ala Leu Phe Glu Leu																														
215 220 225																														
ggc ggg gct gac ttg atc ttg tct act gcg tcc acc acg gag cct ctt	835																													
Gly Gly Ala Asp Leu Ile Leu Ser Thr Ala Ser Thr Thr Glu Pro Leu																														
230 235 240 245																														
tcg gag ttg tct acc ggt ctt tct att ggc ggg cag cta acc att atc	883																													
Ser Glu Leu Ser Thr Gly Leu Ser Ile Gly Gly Gln Leu Thr Ile Ile																														
250 255 260																														
gga gtt gat ggg gga gat atc acc gtt tcg gca gcc caa ttg atg atg	931																													
Gly Val Asp Gly Gly Asp Ile Thr Val Ser Ala Ala Gln Leu Met Met																														
265 270 275																														
aac cgt cag atc atc aca ggt cac ctc act gga agt gcg aat gac acg	979																													
Asn Arg Gln Ile Ile Thr Gly His Leu Thr Gly Ser Ala Asn Asp Thr																														
280 285 290																														
gaa cag act atg aaa ttt gct cat ctc cat ggc gtg aaa ccg ctt att	1027																													
Glu Gln Thr Met Lys Phe Ala His Leu His Gly Val Lys Pro Leu Ile																														
295 300 305																														
gaa cgg atg cct ctc gat caa gcc aac gag gct att gca cgt att tca	1075																													
Glu Arg Met Pro Leu Asp Gln Ala Asn Glu Ala Ile Ala Arg Ile Ser																														
310 315 320 325																														
gct ggt aaa cca cgt ttc cgt att gtc ttg gag ccg aat tca	1117																													
Ala Gly Lys Pro Arg Phe Arg Ile Val Leu Glu Pro Asn Ser																														
330 335																														

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1140

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<211> 339

<212> PRT

<213> Corynebacterium glutamicum

<400> 216

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Ala	Ala	Asn	Leu	Val	Gln	Pro	Ala	Pro	Leu	Lys	Ser	Arg	Glu	Val	Arg
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Val	Glu	Ile	Ala	Ala	Ser	Gly	Val	Cys	His	Ala	Asp	Ile	Gly	Thr	Ala
	35						40					45			

Ala	Ala	Ser	Gly	Lys	His	Thr	Val	Phe	Pro	Val	Thr	Pro	Gly	His	Glu
	50					55					60				

Ile	Ala	Gly	Thr	Ile	Ala	Glu	Ile	Gly	Glu	Asn	Val	Ser	Arg	Trp	Thr
65				70						75					80

Val	Gly	Asp	Arg	Val	Ala	Ile	Gly	Trp	Phe	Gly	Gly	Asn	Cys	Gly	Asp
				85					90					95	

Cys	Ala	Phe	Cys	Arg	Ala	Gly	Asp	Pro	Val	His	Cys	Arg	Glu	Arg	Lys
		100						105					110		

Ile	Pro	Gly	Val	Ser	Tyr	Ala	Gly	Gly	Trp	Ala	Gln	Asn	Ile	Val	Val
	115						120					125			

Pro	Ala	Glu	Ala	Leu	Ala	Ala	Ile	Pro	Asp	Gly	Met	Asp	Phe	Tyr	Glu
	130					135					140				

Pro	Ala	Pro	Met	Gly	Cys	Ala	Gly	Val	Thr	Thr	Phe	Asn	Ala	Leu	Arg
145					150					155					160

Asn	Leu	Lys	Leu	Asp	Pro	Gly	Ala	Ala	Val	Ala	Val	Phe	Gly	Ile	Gly
			165						170					175	

Gly	Leu	Val	Arg	Leu	Ala	Ile	Gln	Phe	Ala	Ala	Lys	Met	Gly	Tyr	Arg
		180						185					190		

Thr	Ile	Thr	Ile	Ala	Arg	Gly	Leu	Glu	Arg	Glu	Glu	Leu	Ala	Arg	Gln
	195						200					205			

Leu	Gly	Ala	Asn	His	Tyr	Ile	Asp	Ser	Asn	Asp	Leu	His	Pro	Gly	Gln
	210					215					220				

Ala	Leu	Phe	Glu	Leu	Gly	Gly	Ala	Asp	Leu	Ile	Leu	Ser	Thr	Ala	Ser
225					230					235					240

Thr	Thr	Glu	Pro	Leu	Ser	Glu	Leu	Ser	Thr	Gly	Leu	Ser	Ile	Gly	Gly
				245					250					255	

Gln	Leu	Thr	Ile	Ile	Gly	Val	Asp	Gly	Gly	Asp	Ile	Thr	Val	Ser	Ala
			260					265					270		

Ala Gln Leu Met Met Asn Arg Gln Ile Ile Thr Gly His Leu Thr Gly
 275 280 285

Ser Ala Asn Asp Thr Glu Gln Thr Met Lys Phe Ala His Leu His Gly
 290 295 300

Val Lys Pro Leu Ile Glu Arg Met Pro Leu Asp Gln Ala Asn Glu Ala
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Ile Ala Arg Ile Ser Ala Gly Lys Pro Arg Phe Arg Ile Val Leu Glu
 325 330 335

Pro Asn Ser

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 <212> DNA
 <213> Corynebacterium glutamicum

<220>
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 <222> (101)..(1618)
 <223> RXA02539

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 Met Thr Val Tyr Ala
 1 5

aat cca gga acc gaa ggc tcg atc gtt aac tat gaa aag cgc tac gag 163
 Asn Pro Gly Thr Glu Gly Ser Ile Val Asn Tyr Glu Lys Arg Tyr Glu
 10 15 20

aac tac att ggt ggc aag tgg gtt cca ccg gta gag ggc cag tac ctt 211
 Asn Tyr Ile Gly Gly Lys Trp Val Pro Pro Val Glu Gly Gln Tyr Leu
 25 30 35

gag aac att tca cct gtc act ggt gaa gtt ttc tgt gag gtc gca cgt 259
 Glu Asn Ile Ser Pro Val Thr Gly Glu Val Phe Cys Glu Val Ala Arg
 40 45 50

ggc acc gca gcg gac gtg gag ctt gca ctg gat gct gca cat gca gcc 307
 Gly Thr Ala Ala Asp Val Glu Leu Ala Leu Asp Ala Ala His Ala Ala
 55 60 65

gct gat gcg tgg ggc aag act tct gtc gct gaa cgt gct ctg atc ctg 355
 Ala Asp Ala Trp Gly Lys Thr Ser Val Ala Glu Arg Ala Leu Ile Leu
 70 75 80 85

cac cgc att gcg gac cgc atg gaa gag cac ctg gaa gaa atc gca gtt 403
 His Arg Ile Ala Asp Arg Met Glu Glu His Leu Glu Glu Ile Ala Val
 90 95 100

gca gaa acc tgg gag aac ggc aag gca gtc cgt gag act ctt gct gca 451
 Ala Glu Thr Trp Glu Asn Gly Lys Ala Val Arg Glu Thr Leu Ala Ala
 105 110 115

gat atc cca ctg gca atc gac cac ttc cgc tac ttt gct ggc gcg atc	499
Asp Ile Pro Leu Ala Ile Asp His Phe Arg Tyr Phe Ala Gly Ala Ile	
120 125 130	
cgt gct cag gaa gat cgt tcc tca cag atc gac cac aac act gtt gct	547
Arg Ala Gln Glu Asp Arg Ser Ser Gln Ile Asp His Asn Thr Val Ala	
135 140 145	
tac cac ttc aac gag cca atc ggt gtt gtt ggt cag atc att cct tgg	595
Tyr His Phe Asn Glu Pro Ile Gly Val Val Gly Gln Ile Ile Pro Trp	
150 155 160 165	
aac ttc cca atc ctc atg gct acc tgg aag ctc gca ccg gca ctt gct	643
Asn Phe Pro Ile Leu Met Ala Thr Trp Lys Leu Ala Pro Ala Leu Ala	
170 175 180	
gca ggt aac gcg atc gtc atg aag cca gct gag cag acc cca gca tcc	691
Ala Gly Asn Ala Ile Val Met Lys Pro Ala Glu Gln Thr Pro Ala Ser	
185 190 195	
att ttg tat ctg att aac atc atc ggc gat ctc atc cca gag ggc gtc	739
Ile Leu Tyr Leu Ile Asn Ile Ile Gly Asp Leu Ile Pro Glu Gly Val	
200 205 210	
ctc aac atc gtc aac gga ctc ggc ggt gaa gca ggc gct gca ctg tcc	787
Leu Asn Ile Val Asn Gly Leu Gly Gly Glu Ala Gly Ala Ala Leu Ser	
215 220 225	
ggc tct aat cgg att ggc aag att gct ttc acc ggt tcc acc gag gtc	835
Gly Ser Asn Arg Ile Gly Lys Ile Ala Phe Thr Gly Ser Thr Glu Val	
230 235 240 245	
ggc aag ctg atc aac cgc gct gca tcc gac aag atc att cct gtc acc	883
Gly Lys Leu Ile Asn Arg Ala Ala Ser Asp Lys Ile Ile Pro Val Thr	
250 255 260	
ctg gag ctc ggc ggt aag tcc cca tcc atc ttc ttc tcc gat gtt ctg	931
Leu Glu Leu Gly Gly Lys Ser Pro Ser Ile Phe Phe Ser Asp Val Leu	
265 270 275	
tca cag gat gac gcc ttc gca gag aag gca gtt gaa ggc ttc gcg atg	979
Ser Gln Asp Asp Ala Phe Ala Glu Lys Ala Val Glu Gly Phe Ala Met	
280 285 290	
ttc gcc ctc aat cag ggt gaa gtt tgt acc tgt cct tcc cgt gca ctt	1027
Phe Ala Leu Asn Gln Gly Glu Val Cys Thr Cys Pro Ser Arg Ala Leu	
295 300 305	
gtt cat gag tcc atc gct gat gaa ttc ctc gag ctt ggc gtg aag cga	1075
Val His Glu Ser Ile Ala Asp Glu Phe Leu Glu Leu Gly Val Lys Arg	
310 315 320 325	
gtt cag aac atc aag ctg ggt aac cca ctt gat act gaa acc atg atg	1123
Val Gln Asn Ile Lys Leu Gly Asn Pro Leu Asp Thr Glu Thr Met Met	
330 335 340	
ggc gct cag gcg tcc cag gag cag atg gac aag atc tcc tcc tac ctg	1171
Gly Ala Gln Ala Ser Gln Glu Gln Met Asp Lys Ile Ser Ser Tyr Leu	
345 350 355	
aag atc ggc cca gaa gaa ggc gct caa acc ctc act ggt ggc aag gtc	1219

Lys Ile Gly Pro Glu Glu Gly Ala Gln Thr Leu Thr Gly Gly Lys Val
 360 365 370
 aac aag gtt gat ggc atg gag aac ggt tac tac att gag cca acc gtt 1267
 Asn Lys Val Asp Gly Met Glu Asn Gly Tyr Tyr Ile Glu Pro Thr Val
 375 380 385
 ttc cgc ggc acc aac gac atg agg atc ttc cgc gag gaa atc ttc gga 1315
 Phe Arg Gly Thr Asn Asp Met Arg Ile Phe Arg Glu Glu Ile Phe Gly
 390 395 400 405
 cca gtc ctt tct gtt gct acc ttc agc gac ttc gat gag gcc atc cgt 1363
 Pro Val Leu Ser Val Ala Thr Phe Ser Asp Phe Asp Glu Ala Ile Arg
 410 415 420
 att gca aac gac acc aac tac ggc ctc ggc gct ggt gtc tgg agc cgt 1411
 Ile Ala Asn Asp Thr Asn Tyr Gly Leu Gly Ala Gly Val Trp Ser Arg
 425 430 435
 gac caa aac acc att tat cgt gca ggt cgc gca atc cag gct ggt cga 1459
 Asp Gln Asn Thr Ile Tyr Arg Ala Gly Arg Ala Ile Gln Ala Gly Arg
 440 445 450
 gtt tgg gtc aac cag tac cac aac tac cca gcg cac tcc gct ttc ggt 1507
 Val Trp Val Asn Gln Tyr His Asn Tyr Pro Ala His Ser Ala Phe Gly
 455 460 465
 gga tac aag gag tcc ggc atc ggc cgt gag aac cac ctc atg atg ctg 1555
 Gly Tyr Lys Glu Ser Gly Ile Gly Arg Glu Asn His Leu Met Met Leu
 470 475 480 485
 aac cac tac cag cag acc aag aac ctg ttg gtc tcc tac gat cca aac 1603
 Asn His Tyr Gln Gln Thr Lys Asn Leu Leu Val Ser Tyr Asp Pro Asn
 490 495 500
 cca acc gga ctg ttc tgatctaagc gttaagtcct aga 1641
 Pro Thr Gly Leu Phe
 505

<210> 218

<211> 506

<212> PRT

<213> Corynebacterium glutamicum

<400> 218

Met Thr Val Tyr Ala Asn Pro Gly Thr Glu Gly Ser Ile Val Asn Tyr
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 Glu Lys Arg Tyr Glu Asn Tyr Ile Gly Gly Lys Trp Val Pro Pro Val
 20 25 30
 Glu Gly Gln Tyr Leu Glu Asn Ile Ser Pro Val Thr Gly Glu Val Phe
 35 40 45
 Cys Glu Val Ala Arg Gly Thr Ala Ala Asp Val Glu Leu Ala Leu Asp
 50 55 60
 Ala Ala His Ala Ala Ala Asp Ala Trp Gly Lys Thr Ser Val Ala Glu
 65 70 75 80

Arg Ala Leu Ile Leu His Arg Ile Ala Asp Arg Met Glu Glu His Leu
 85 90 95
 Glu Glu Ile Ala Val Ala Glu Thr Trp Glu Asn Gly Lys Ala Val Arg
 100 105 110
 Glu Thr Leu Ala Ala Asp Ile Pro Leu Ala Ile Asp His Phe Arg Tyr
 115 120 125
 Phe Ala Gly Ala Ile Arg Ala Gln Glu Asp Arg Ser Ser Gln Ile Asp
 130 135 140
 His Asn Thr Val Ala Tyr His Phe Asn Glu Pro Ile Gly Val Val Gly
 145 150 155 160
 Gln Ile Ile Pro Trp Asn Phe Pro Ile Leu Met Ala Thr Trp Lys Leu
 165 170 175
 Ala Pro Ala Leu Ala Ala Gly Asn Ala Ile Val Met Lys Pro Ala Glu
 180 185 190
 Gln Thr Pro Ala Ser Ile Leu Tyr Leu Ile Asn Ile Ile Gly Asp Leu
 195 200 205
 Ile Pro Glu Gly Val Leu Asn Ile Val Asn Gly Leu Gly Gly Glu Ala
 210 215 220
 Gly Ala Ala Leu Ser Gly Ser Asn Arg Ile Gly Lys Ile Ala Phe Thr
 225 230 235 240
 Gly Ser Thr Glu Val Gly Lys Leu Ile Asn Arg Ala Ala Ser Asp Lys
 245 250 255
 Ile Ile Pro Val Thr Leu Glu Leu Gly Gly Lys Ser Pro Ser Ile Phe
 260 265 270
 Phe Ser Asp Val Leu Ser Gln Asp Asp Ala Phe Ala Glu Lys Ala Val
 275 280 285
 Glu Gly Phe Ala Met Phe Ala Leu Asn Gln Gly Glu Val Cys Thr Cys
 290 295 300
 Pro Ser Arg Ala Leu Val His Glu Ser Ile Ala Asp Glu Phe Leu Glu
 305 310 315 320
 Leu Gly Val Lys Arg Val Gln Asn Ile Lys Leu Gly Asn Pro Leu Asp
 325 330 335
 Thr Glu Thr Met Met Gly Ala Gln Ala Ser Gln Glu Gln Met Asp Lys
 340 345 350
 Ile Ser Ser Tyr Leu Lys Ile Gly Pro Glu Glu Gly Ala Gln Thr Leu
 355 360 365
 Thr Gly Gly Lys Val Asn Lys Val Asp Gly Met Glu Asn Gly Tyr Tyr
 370 375 380
 Ile Glu Pro Thr Val Phe Arg Gly Thr Asn Asp Met Arg Ile Phe Arg
 385 390 395 400
 Glu Glu Ile Phe Gly Pro Val Leu Ser Val Ala Thr Phe Ser Asp Phe

<400> 219																
ctgccaccac	tggtcattgc	agaggacact	ctccgtgatg	gtcttcaggt	gtagtcgca	60										
gccctagagc	gcgaaaccgc	gcaccagaag	gtgggctaaa	gtg	tct	ttg	acc	ttc	115							
				Val	Ser	Leu	Thr	Phe								
				1				5								
cca gta atc aac ccc agc gat ggc tcc acc atc acc gag cta gaa aac	163															
Pro Val Ile Asn Pro Ser Asp Gly Ser Thr Ile Thr Glu Leu Glu Asn																
	10								15					20		
cac gat tcc acc cag tgg atg tcc gcg ctc tct gat gca gtt gca gct	211															
His Asp Ser Thr Gln Trp Met Ser Ala Leu Ser Asp Ala Val Ala Ala																
	25								30					35		
ggt cct tca tgg gct gcg aaa act ccc cgc gaa aga tcc gtg gta ctc	259															
Gly Pro Ser Trp Ala Ala Lys Thr Pro Arg Glu Arg Ser Val Val Leu																
	40								45					50		
acc gca atc ttc gaa gca ctg acc gaa cgc gcc caa gaa ctt gca gag	307															
Thr Ala Ile Phe Glu Ala Leu Thr Glu Arg Ala Gln Glu Leu Ala Glu																
	55								60					65		
atc atc cac ctg gaa gct gga aaa tcc gat gca gaa gct ctt ggt gaa	355															
Ile Ile His Leu Glu Ala Gly Lys Ser Asp Ala Glu Ala Leu Gly Glu																
	70								75					80		
gtc gct tat ggt gca gaa tac ttc cgt tgg ttt gcg gaa gaa gca gtg	403															
Val Ala Tyr Gly Ala Glu Tyr Phe Arg Trp Phe Ala Glu Glu Ala Val																
	90								95					100		

cgc ctg ccc ggc cgc tac gga cag tca
 Arg Leu Pro Gly Arg Tyr Gly Gln Ser
 105 110

430

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<210> 220
<211> 110
<212> PRT
<213> Corynebacterium glutamicum
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<400> 220
Val Ser Leu Thr Phe Pro Val Ile Asn Pro Ser Asp Gly Ser Thr Ile
  1                      5                      10                      15

Thr Glu Leu Glu Asn His Asp Ser Thr Gln Trp Met Ser Ala Leu Ser
          20                      25                      30

Asp Ala Val Ala Ala Gly Pro Ser Trp Ala Ala Lys Thr Pro Arg Glu
          35                      40                      45

Arg Ser Val Val Leu Thr Ala Ile Phe Glu Ala Leu Thr Glu Arg Ala
  50                      55                      60

Gln Glu Leu Ala Glu Ile Ile His Leu Glu Ala Gly Lys Ser Asp Ala
  65                      70                      75                      80

Glu Ala Leu Gly Glu Val Ala Tyr Gly Ala Glu Tyr Phe Arg Trp Phe
          85                      90                      95

Ala Glu Glu Ala Val Arg Leu Pro Gly Arg Tyr Gly Gln Ser
          100                      105                      110

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<210> 221
<211> 747
<212> DNA
<213> Corynebacterium glutamicum
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<220>
<221> CDS
<222> (101)..(724)
<223> RXN03150
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<400> 221
tttaacagag tgcgtttcaa tgcctgtagt gttccggcaa ttttgaatgt cgttacggtt 60
      10      20      30      40      50
acccaaggct gaattcctga gtcacacctg tacaagatca gtg gaa gcc cag ttc 115
      60      70      80      90     100
      Val Glu Ala Gln Phe
              1              5
acc tct ccc ctg ctc aac aat ggg caa acc tgt ttc ctt ggt acc cga 163
Thr Ser Pro Leu Leu Asn Asn Gly Gln Thr Cys Phe Leu Gly Thr Arg
      10      20      30      40      50
atc ctt gct cca aaa tca cgt tac gcg gaa gta gtc gat gca ttc acc 211
Ile Leu Ala Pro Lys Ser Arg Tyr Ala Glu Val Val Asp Ala Phe Thr
      10      20      30      40      50
gct ttc gct ggc agc ctg cag gtt gga gtc acg tcc tcc cct gac act 259
Ala Phe Ala Gly Ser Leu Gln Val Gly Val Thr Ser Ser Pro Asp Thr
      10      20      30      40      50

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40	45	50	
cag atc gga ccg atg gcg act gcc cgg cag cgt gag cgc gtg gaa tcc			307
Gln Ile Gly Pro Met Ala Thr Ala Arg Gln Arg Glu Arg Val Glu Ser			
55	60	65	
tac att tcc caa ggc aaa aat gct gga gcc cgc atc act gtc ggt ggc			355
Tyr Ile Ser Gln Gly Lys Asn Ala Gly Ala Arg Ile Thr Val Gly Gly			
70	75	80	85
agc cgt cca cga gat ctt gac gcc gga ttc ttc gtt gag cca aca gtg			403
Ser Arg Pro Arg Asp Leu Asp Ala Gly Phe Phe Val Glu Pro Thr Val			
90	95	100	
ttc gcc gat gta gac aat cgc gca gcc att gcc caa gat gaa atc ttc			451
Phe Ala Asp Val Asp Asn Arg Ala Ala Ile Ala Gln Asp Glu Ile Phe			
105	110	115	
gga ccg gtg ccc tct gtt gtt tcc tac caa gac gat gaa cac gcc atc			499
Gly Pro Val Pro Ser Val Val Ser Tyr Gln Asp Asp Glu His Ala Ile			
120	125	130	
caa cta gcc aac gat tcc gaa ttc ggt ctc ggc gga act gtc tgg acg			547
Gln Leu Ala Asn Asp Ser Glu Phe Gly Leu Gly Gly Thr Val Trp Thr			
135	140	145	
agc gat ccc gag cgc ggc gct gca ttg gcc cgc cga gtt cac aca gga			595
Ser Asp Pro Glu Arg Gly Ala Ala Leu Ala Arg Arg Val His Thr Gly			
150	155	160	165
acc att ggc atc aac cgc tat atc cct gat ccc gcc gca cca ttt gga			643
Thr Ile Gly Ile Asn Arg Tyr Ile Pro Asp Pro Ala Ala Pro Phe Gly			
170	175	180	
ggg gtg aaa aac agt ggc ctt ggc aga gaa ctc ggc ccc gaa ggt ctt			691
Gly Val Lys Asn Ser Gly Leu Gly Arg Glu Leu Gly Pro Glu Gly Leu			
185	190	195	
gct tcc tac caa gaa acc caa acc att tat ctc taatccaaac tgcacctata			744
Ala Ser Tyr Gln Glu Thr Gln Thr Ile Tyr Leu			
200	205		
tat			747

<210> 222

<211> 208

<212> PRT

<213> Corynebacterium glutamicum

<400> 222

Val	Glu	Ala	Gln	Phe	Thr	Ser	Pro	Leu	Leu	Asn	Asn	Gly	Gln	Thr	Cys
1				5					10					15	

Phe	Leu	Gly	Thr	Arg	Ile	Leu	Ala	Pro	Lys	Ser	Arg	Tyr	Ala	Glu	Val
			20					25					30		

Val	Asp	Ala	Phe	Thr	Ala	Phe	Ala	Gly	Ser	Leu	Gln	Val	Gly	Val	Thr
	35						40					45			

Ser	Ser	Pro	Asp	Thr	Gln	Ile	Gly	Pro	Met	Ala	Thr	Ala	Arg	Gln	Arg
-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----

50 55 60
 Glu Arg Val Glu Ser Tyr Ile Ser Gln Gly Lys Asn Ala Gly Ala Arg
 65 70 75 80
 Ile Thr Val Gly Gly Ser Arg Pro Arg Asp Leu Asp Ala Gly Phe Phe
 85 90 95
 Val Glu Pro Thr Val Phe Ala Asp Val Asp Asn Arg Ala Ala Ile Ala
 100 105 110
 Gln Asp Glu Ile Phe Gly Pro Val Pro Ser Val Val Ser Tyr Gln Asp
 115 120 125
 Asp Glu His Ala Ile Gln Leu Ala Asn Asp Ser Glu Phe Gly Leu Gly
 130 135 140
 Gly Thr Val Trp Thr Ser Asp Pro Glu Arg Gly Ala Ala Leu Ala Arg
 145 150 155 160
 Arg Val His Thr Gly Thr Ile Gly Ile Asn Arg Tyr Ile Pro Asp Pro
 165 170 175
 Ala Ala Pro Phe Gly Gly Val Lys Asn Ser Gly Leu Gly Arg Glu Leu
 180 185 190
 Gly Pro Glu Gly Leu Ala Ser Tyr Gln Glu Thr Gln Thr Ile Tyr Leu
 195 200 205

<210> 223

<211> 881

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (1)..(858)

<223> RXN01340

<400> 223

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 Lys Val Gly Glu Ile Ile Ala Ser Val Phe Asp Thr Phe Asn Ile Pro
 1 5 10 15
 cag ggc ttg gtc tca atc atc acc acc act cga gat gca gag cta tcg 96
 Gln Gly Leu Val Ser Ile Ile Thr Thr Thr Arg Asp Ala Glu Leu Ser
 20 25 30
 gca gaa ctc atg gct gat cct cgc ttg gct aaa gtc acc ttc act gga 144
 Ala Glu Leu Met Ala Asp Pro Arg Leu Ala Lys Val Thr Phe Thr Gly
 35 40 45
 tca acc aac gtg gga cgc atc ctg gtc cgc caa tcc gcg gac cga ctg 192
 Ser Thr Asn Val Gly Arg Ile Leu Val Arg Gln Ser Ala Asp Arg Leu
 50 55 60
 ctg cgc acc tcc atg gaa ctc ggc gga aat gca gct ttt gtt atc gac 240

Leu Arg Thr Ser Met Glu Leu Gly Gly Asn Ala Ala Phe Val Ile Asp
 65 70 75 80
 gaa gcc gca gac ctc gac gaa gcc gta tcc ggt gcc atc gcc gca aaa 288
 Glu Ala Ala Asp Leu Asp Glu Ala Val Ser Gly Ala Ile Ala Ala Lys
 85 90 95
 ctc cgc aac gcc ggc caa gta tgc atc gca gct aac cgt ttc ttg gtt 336
 Leu Arg Asn Ala Gly Gln Val Cys Ile Ala Ala Asn Arg Phe Leu Val
 100 105 110
 cat gaa tcc cgc gct gcc gaa ttc acc tca aag ctg gcg aca gcc atg 384
 His Glu Ser Arg Ala Ala Glu Phe Thr Ser Lys Leu Ala Thr Ala Met
 115 120 125
 cag aac act ccc att ggg ccg gtg att tct gcc cgc caa cgc gac cgg 432
 Gln Asn Thr Pro Ile Gly Pro Val Ile Ser Ala Arg Gln Arg Asp Arg
 130 135 140
 atc gca gca cta gtg gat gaa gcc atc acc gac ggc gcc cgc ctc atc 480
 Ile Ala Ala Leu Val Asp Glu Ala Ile Thr Asp Gly Ala Arg Leu Ile
 145 150 155 160
 atc ggt ggg gag gtc ccc gac ggc tcc ggc ttc ttc tat cca gcc acc 528
 Ile Gly Gly Glu Val Pro Asp Gly Ser Gly Phe Phe Tyr Pro Ala Thr
 165 170 175
 atc ttg gcc gat gtc cct gca cag tca cgg att gtg cat gag gaa atc 576
 Ile Leu Ala Asp Val Pro Ala Gln Ser Arg Ile Val His Glu Glu Ile
 180 185 190
 ttc gga cct gtg gcc acc att gcc act ttc acc gac ttg gcc gaa ggc 624
 Phe Gly Pro Val Ala Thr Ile Ala Thr Phe Thr Asp Leu Ala Glu Gly
 195 200 205
 gtt gca caa gca aat tcc acc gaa ttc ggc ctc gca gcc tac gga ttc 672
 Val Ala Gln Ala Asn Ser Thr Glu Phe Gly Leu Ala Ala Tyr Gly Phe
 210 215 220
 agc aac aat gtg aaa gca aca cag tac atg gcg gaa cac ttg gaa gcc 720
 Ser Asn Asn Val Lys Ala Thr Gln Tyr Met Ala Glu His Leu Glu Ala
 225 230 235 240
 gga atg gtc gga atc aac aga ggc gcc atc tct gac cca gca gca cct 768
 Gly Met Val Gly Ile Asn Arg Gly Ala Ile Ser Asp Pro Ala Ala Pro
 245 250 255
 ttt ggc ggc atc gga caa tcc ggc ttc ggc aga gaa ggc gga acc gaa 816
 Phe Gly Gly Ile Gly Gln Ser Gly Phe Gly Arg Glu Gly Gly Thr Glu
 260 265 270
 gga atc gaa gaa tat ctc tcc gtg cgt tac ctc gct ttg ccg 858
 Gly Ile Glu Glu Tyr Leu Ser Val Arg Tyr Leu Ala Leu Pro
 275 280 285
 tgacacatga gctgtccggt gaa 881

<210> 224

<211> 286

<212> PRT

<213> Corynebacterium glutamicum

<400> 224

Lys Val Gly Glu Ile Ile Ala Ser Val Phe Asp Thr Phe Asn Ile Pro
 1 5 10 15
 Gln Gly Leu Val Ser Ile Ile Thr Thr Thr Arg Asp Ala Glu Leu Ser
 20 25 30
 Ala Glu Leu Met Ala Asp Pro Arg Leu Ala Lys Val Thr Phe Thr Gly
 35 40 45
 Ser Thr Asn Val Gly Arg Ile Leu Val Arg Gln Ser Ala Asp Arg Leu
 50 55 60
 Leu Arg Thr Ser Met Glu Leu Gly Gly Asn Ala Ala Phe Val Ile Asp
 65 70 75 80
 Glu Ala Ala Asp Leu Asp Glu Ala Val Ser Gly Ala Ile Ala Ala Lys
 85 90 95
 Leu Arg Asn Ala Gly Gln Val Cys Ile Ala Ala Asn Arg Phe Leu Val
 100 105 110
 His Glu Ser Arg Ala Ala Glu Phe Thr Ser Lys Leu Ala Thr Ala Met
 115 120 125
 Gln Asn Thr Pro Ile Gly Pro Val Ile Ser Ala Arg Gln Arg Asp Arg
 130 135 140
 Ile Ala Ala Leu Val Asp Glu Ala Ile Thr Asp Gly Ala Arg Leu Ile
 145 150 155 160
 Ile Gly Gly Glu Val Pro Asp Gly Ser Gly Phe Phe Tyr Pro Ala Thr
 165 170 175
 Ile Leu Ala Asp Val Pro Ala Gln Ser Arg Ile Val His Glu Glu Ile
 180 185 190
 Phe Gly Pro Val Ala Thr Ile Ala Thr Phe Thr Asp Leu Ala Glu Gly
 195 200 205
 Val Ala Gln Ala Asn Ser Thr Glu Phe Gly Leu Ala Ala Tyr Gly Phe
 210 215 220
 Ser Asn Asn Val Lys Ala Thr Gln Tyr Met Ala Glu His Leu Glu Ala
 225 230 235 240
 Gly Met Val Gly Ile Asn Arg Gly Ala Ile Ser Asp Pro Ala Ala Pro
 245 250 255
 Phe Gly Gly Ile Gly Gln Ser Gly Phe Gly Arg Glu Gly Gly Thr Glu
 260 265 270
 Gly Ile Glu Glu Tyr Leu Ser Val Arg Tyr Leu Ala Leu Pro
 275 280 285

<210> 225

<211> 1686

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(1663)

<223> RXN01498

<400> 225

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accacacgag	catcagaacg	cgaacgaag	gtaaaagccc	atg	atc	aaa	cgt	ctt	115
				Met	Ile	Lys	Arg	Leu	
				1				5	

cct	tta	ggt	ccg	ctg	cct	aaa	gaa	ctt	cat	cag	act	ctg	ctt	gat	ctg	163
Pro	Leu	Gly	Pro	Leu	Pro	Lys	Glu	Leu	His	Gln	Thr	Leu	Leu	Asp	Leu	
			10						15					20		

acc	gca	aat	gcc	caa	gat	gcg	gcg	aaa	gtg	gag	gtt	ata	gcg	cca	ttt	211
Thr	Ala	Asn	Ala	Gln	Asp	Ala	Ala	Lys	Val	Glu	Val	Ile	Ala	Pro	Phe	
			25					30					35			

act	ggc	gag	acc	ctc	gga	ttt	ggt	ttt	gat	ggt	gat	gag	caa	gac	gtc	259
Thr	Gly	Glu	Thr	Leu	Gly	Phe	Gly	Phe	Asp	Gly	Asp	Glu	Gln	Asp	Val	
		40					45					50				

gag	cat	gct	ttt	gca	ctt	tca	agg	gca	gcc	cag	aaa	aag	tgg	gtg	cac	307
Glu	His	Ala	Phe	Ala	Leu	Ser	Arg	Ala	Ala	Gln	Lys	Lys	Trp	Val	His	
	55					60					65					

acc	acg	gca	gtg	gaa	cgg	aag	aag	atc	ttc	ctg	aag	gtt	cat	gat	ctg	355
Thr	Thr	Ala	Val	Glu	Arg	Lys	Lys	Ile	Phe	Leu	Lys	Val	His	Asp	Leu	
	70				75					80				85		

gta	ttg	aaa	aac	cgt	gag	ctg	ctc	atg	gac	atc	gtg	cag	ttg	gaa	aca	403
Val	Leu	Lys	Asn	Arg	Glu	Leu	Leu	Met	Asp	Ile	Val	Gln	Leu	Glu	Thr	
			90						95					100		

ggc	aaa	aat	cga	gca	tcg	gct	gcc	gat	gag	gtg	ttg	gac	gtt	gcg	atc	451
Gly	Lys	Asn	Arg	Ala	Ser	Ala	Ala	Asp	Glu	Val	Leu	Asp	Val	Ala	Ile	
			105					110					115			

acc	acc	cgc	ttc	tac	gca	aac	aat	gca	gga	aag	ttt	tta	aat	gac	aag	499
Thr	Thr	Arg	Phe	Tyr	Ala	Asn	Asn	Ala	Gly	Lys	Phe	Leu	Asn	Asp	Lys	
		120					125					130				

aaa	cgc	ccc	ggc	gcg	ctt	ccg	atc	atc	acg	aaa	aac	aca	caa	cag	tat	547
Lys	Arg	Pro	Gly	Ala	Leu	Pro	Ile	Ile	Thr	Lys	Asn	Thr	Gln	Gln	Tyr	
	135					140					145					

gtg	ccc	aag	gga	gtg	gtc	ggg	cag	atc	acg	ccg	tgg	aat	tac	cct	tta	595
Val	Pro	Lys	Gly	Val	Val	Gly	Gln	Ile	Thr	Pro	Trp	Asn	Tyr	Pro	Leu	
	150					155				160					165	

act	ttg	gga	gta	tct	gat	gct	gtt	ccg	gcg	ctg	ctg	gca	gga	aac	gca	643
Thr	Leu	Gly	Val	Ser	Asp	Ala	Val	Pro	Ala	Leu	Leu	Ala	Gly	Asn	Ala	
			170						175					180		

gtg	gtg	gct	aaa	cct	gac	ctc	gcg	aca	cct	ttc	tcc	tgc	ttg	atc	atg	691
Val	Val	Ala	Lys	Pro	Asp	Leu	Ala	Thr	Pro	Phe	Ser	Cys	Leu	Ile	Met	
			185					190							195	

gtg cac ctg ctc att gaa gcc ggt ctg ccg cgt gat ttg atg cag gtt	739
Val His Leu Leu Ile Glu Ala Gly Leu Pro Arg Asp Leu Met Gln Val	
200 205 210	
gtc acc ggc cct ggc gat att gtt ggc ggt gcg att gca gct cag tgt	787
Val Thr Gly Pro Gly Asp Ile Val Gly Gly Ala Ile Ala Ala Gln Cys	
215 220 225	
gat ttc ctc atg ttc act gga tcc acg gcc acg ggc cgg atc ttg ggt	835
Asp Phe Leu Met Phe Thr Gly Ser Thr Ala Thr Gly Arg Ile Leu Gly	
230 235 240 245	
cgg aca atg ggt gag cgt ttg gtg ggt ttc tct gcg gaa tta ggc gga	883
Arg Thr Met Gly Glu Arg Leu Val Gly Phe Ser Ala Glu Leu Gly Gly	
250 255 260	
aag aac cct ctt att gtg gcc aag gat gca gat ctg gac aag gtg gaa	931
Lys Asn Pro Leu Ile Val Ala Lys Asp Ala Asp Leu Asp Lys Val Glu	
265 270 275	
gct gag ctt ccg cag gcg tgt ttt tcc aac tcg ggg caa ttg tgt gtc	979
Ala Glu Leu Pro Gln Ala Cys Phe Ser Asn Ser Gly Gln Leu Cys Val	
280 285 290	
tcc act gaa cgt att tat gtg gag gaa gac gtg tac gag gag gtg att	1027
Ser Thr Glu Arg Ile Tyr Val Glu Glu Asp Val Tyr Glu Glu Val Ile	
295 300 305	
gca cgg ttt agc aag gcg gcg aaa gcc atg tcc att ggt gcc gga ttt	1075
Ala Arg Phe Ser Lys Ala Ala Lys Ala Met Ser Ile Gly Ala Gly Phe	
310 315 320 325	
gag tgg aaa tat gag atg ggt tcg ttg atc aat cac gcg cag ctg gat	1123
Glu Trp Lys Tyr Glu Met Gly Ser Leu Ile Asn His Ala Gln Leu Asp	
330 335 340	
cgg gtg agc acc ttt gtt gat cag gct aaa gct gcg ggc gcc acg gtg	1171
Arg Val Ser Thr Phe Val Asp Gln Ala Lys Ala Ala Gly Ala Thr Val	
345 350 355	
ctg tgc ggt ggc aag tca cgc cct gat att ggt ccc ttc ttc tat gag	1219
Leu Cys Gly Gly Lys Ser Arg Pro Asp Ile Gly Pro Phe Phe Tyr Glu	
360 365 370	
ccc acg gta ttg gcg gat gtc cca gag ggc acc cca ctg ctc acg gag	1267
Pro Thr Val Leu Ala Asp Val Pro Glu Gly Thr Pro Leu Leu Thr Glu	
375 380 385	
gaa gtc ttc ggg ccg gtg gtg ttc atc gaa aag gta gcc aca ctg gaa	1315
Glu Val Phe Gly Pro Val Val Phe Ile Glu Lys Val Ala Thr Leu Glu	
390 395 400 405	
gaa gcc gtc gat aag gca aat ggc acg ccc tac ggc ctg aat gcg tcc	1363
Glu Ala Val Asp Lys Ala Asn Gly Thr Pro Tyr Gly Leu Asn Ala Ser	
410 415 420	
gtc ttt ggg tcg tcg gaa acc ggc aat ctt gtt gca ggc cag ctg gaa	1411
Val Phe Gly Ser Ser Glu Thr Gly Asn Leu Val Ala Gly Gln Leu Glu	
425 430 435	

gct ggc ggt atc ggt att aat gat ggc tac gcc gcg acg tgg gcg agc 1459
 Ala Gly Gly Ile Gly Ile Asn Asp Gly Tyr Ala Ala Thr Trp Ala Ser
 440 445 450

gtg tcc acg cct ctg ggt ggc atg aag cag tgc ggg ctg ggg cac cgc 1507
 Val Ser Thr Pro Leu Gly Gly Met Lys Gln Ser Gly Leu Gly His Arg
 455 460 465

cat ggt gcg gag gga att aca aaa tat gcg gag atc cga aac atc gcg 1555
 His Gly Ala Glu Gly Ile Thr Lys Tyr Ala Glu Ile Arg Asn Ile Ala
 470 475 480 485

gag cag cgc tgg atg tct atg cgt ggg ccg gcc aaa atg ccg cga aag 1603
 Glu Gln Arg Trp Met Ser Met Arg Gly Pro Ala Lys Met Pro Arg Lys
 490 495 500

gtg tac tca gac acc gtg gcc aca gcg cta aag ctg ggc aaa atc ttt 1651
 Val Tyr Ser Asp Thr Val Ala Thr Ala Leu Lys Leu Gly Lys Ile Phe
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aaa gtt ttg ccg tagcaaaaaag ccggaccctt gct 1686
 Lys Val Leu Pro
 520

<210> 226

<211> 521

<212> PRT

<213> Corynebacterium glutamicum

<400> 226

Met Ile Lys Arg Leu Pro Leu Gly Pro Leu Pro Lys Glu Leu His Gln
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Thr Leu Leu Asp Leu Thr Ala Asn Ala Gln Asp Ala Ala Lys Val Glu
 20 25 30

Val Ile Ala Pro Phe Thr Gly Glu Thr Leu Gly Phe Gly Phe Asp Gly
 35 40 45

Asp Glu Gln Asp Val Glu His Ala Phe Ala Leu Ser Arg Ala Ala Gln
 50 55 60

Lys Lys Trp Val His Thr Thr Ala Val Glu Arg Lys Lys Ile Phe Leu
 65 70 75 80

Lys Val His Asp Leu Val Leu Lys Asn Arg Glu Leu Leu Met Asp Ile
 85 90 95

Val Gln Leu Glu Thr Gly Lys Asn Arg Ala Ser Ala Ala Asp Glu Val
 100 105 110

Leu Asp Val Ala Ile Thr Thr Arg Phe Tyr Ala Asn Asn Ala Gly Lys
 115 120 125

Phe Leu Asn Asp Lys Lys Arg Pro Gly Ala Leu Pro Ile Ile Thr Lys
 130 135 140

Asn Thr Gln Gln Tyr Val Pro Lys Gly Val Val Gly Gln Ile Thr Pro
 145 150 155 160

Trp Asn Tyr Pro Leu Thr Leu Gly Val Ser Asp Ala Val Pro Ala Leu
 165 170 175
 Leu Ala Gly Asn Ala Val Val Ala Lys Pro Asp Leu Ala Thr Pro Phe
 180 185 190
 Ser Cys Leu Ile Met Val His Leu Leu Ile Glu Ala Gly Leu Pro Arg
 195 200 205
 Asp Leu Met Gln Val Val Thr Gly Pro Gly Asp Ile Val Gly Gly Ala
 210 215 220
 Ile Ala Ala Gln Cys Asp Phe Leu Met Phe Thr Gly Ser Thr Ala Thr
 225 230 235 240
 Gly Arg Ile Leu Gly Arg Thr Met Gly Glu Arg Leu Val Gly Phe Ser
 245 250 255
 Ala Glu Leu Gly Gly Lys Asn Pro Leu Ile Val Ala Lys Asp Ala Asp
 260 265 270
 Leu Asp Lys Val Glu Ala Glu Leu Pro Gln Ala Cys Phe Ser Asn Ser
 275 280 285
 Gly Gln Leu Cys Val Ser Thr Glu Arg Ile Tyr Val Glu Glu Asp Val
 290 295 300
 Tyr Glu Glu Val Ile Ala Arg Phe Ser Lys Ala Ala Lys Ala Met Ser
 305 310 315 320
 Ile Gly Ala Gly Phe Glu Trp Lys Tyr Glu Met Gly Ser Leu Ile Asn
 325 330 335
 His Ala Gln Leu Asp Arg Val Ser Thr Phe Val Asp Gln Ala Lys Ala
 340 345 350
 Ala Gly Ala Thr Val Leu Cys Gly Gly Lys Ser Arg Pro Asp Ile Gly
 355 360 365
 Pro Phe Phe Tyr Glu Pro Thr Val Leu Ala Asp Val Pro Glu Gly Thr
 370 375 380
 Pro Leu Leu Thr Glu Glu Val Phe Gly Pro Val Val Phe Ile Glu Lys
 385 390 395 400
 Val Ala Thr Leu Glu Glu Ala Val Asp Lys Ala Asn Gly Thr Pro Tyr
 405 410 415
 Gly Leu Asn Ala Ser Val Phe Gly Ser Ser Glu Thr Gly Asn Leu Val
 420 425 430
 Ala Gly Gln Leu Glu Ala Gly Gly Ile Gly Ile Asn Asp Gly Tyr Ala
 435 440 445
 Ala Thr Trp Ala Ser Val Ser Thr Pro Leu Gly Gly Met Lys Gln Ser
 450 455 460
 Gly Leu Gly His Arg His Gly Ala Glu Gly Ile Thr Lys Tyr Ala Glu
 465 470 475 480
 Ile Arg Asn Ile Ala Glu Gln Arg Trp Met Ser Met Arg Gly Pro Ala

322

gtc gga gtg att agt cca tgg aat ttc cca ctg aac ctc tcg atc cgc	595
Val Gly Val Ile Ser Pro Trp Asn Phe Pro Leu Asn Leu Ser Ile Arg	
150 155 160 165	
tcg gtt gct ccg gca cta gcc gtg ggc aac gcc gta gtg att aag cct	643
Ser Val Ala Pro Ala Leu Ala Val Gly Asn Ala Val Val Ile Lys Pro	
170 175 180	
gcg agt gat acc cca gtt act ggt ggt gta att cct gca cga atc ttt	691
Ala Ser Asp Thr Pro Val Thr Gly Gly Val Ile Pro Ala Arg Ile Phe	
185 190 195	
gag gag gcc gga gtt cct gca ggc gtg atc agc acg gtt gcg ggc gca	739
Glu Glu Ala Gly Val Pro Ala Gly Val Ile Ser Thr Val Ala Gly Ala	
200 205 210	
gga tct gaa atc ggt gat cac ttt gtc acc cac gcc gtg cca aag ctg	787
Gly Ser Glu Ile Gly Asp His Phe Val Thr His Ala Val Pro Lys Leu	
215 220 225	
att tct ttc acc ggt tca acc cca gtc ggt cgt cgt gtc ggt gag ctg	835
Ile Ser Phe Thr Gly Ser Thr Pro Val Gly Arg Arg Val Gly Glu Leu	
230 235 240 245	
gca att aat ggt gga cca atg aaa act gtt gca cta gag ctc ggt ggc	883
Ala Ile Asn Gly Gly Pro Met Lys Thr Val Ala Leu Glu Leu Gly Gly	
250 255 260	
aac gcg ccg ttc gtt gtg ctt gcc gac gcc gac atc gac gcc gct gcc	931
Asn Ala Pro Phe Val Val Leu Ala Asp Ala Asp Ile Asp Ala Ala Ala	
265 270 275	
cag gct gcc gca gtt ggc gct ttc cta cac cag gga cag att tgt atg	979
Gln Ala Ala Val Gly Ala Phe Leu His Gln Gly Gln Ile Cys Met	
280 285 290	
tca atc aac cga gtc att gtt gat gct gca gtt cat gat gaa ttc cta	1027
Ser Ile Asn Arg Val Ile Val Asp Ala Ala Val His Asp Glu Phe Leu	
295 300 305	
gag aag ttc gtt gaa gca gtg aag aac att cca acc ggc gat cca agc	1075
Glu Lys Phe Val Glu Ala Val Lys Asn Ile Pro Thr Gly Asp Pro Ser	
310 315 320 325	
gca gaa gga acc ctt gtt gga cct gtc att aat gac agt cag ctc agt	1123
Ala Glu Gly Thr Leu Val Gly Pro Val Ile Asn Asp Ser Gln Leu Ser	
330 335 340	
ggt ttg aag gaa aag atc gag ttg gcc aaa aag gaa ggc gca acc gtc	1171
Gly Leu Lys Glu Lys Ile Glu Leu Ala Lys Lys Glu Gly Ala Thr Val	
345 350 355	
cag gtt gaa ggg cca att gaa ggc cga ctg gtt cat ccg cat gtg ttc	1219
Gln Val Glu Gly Pro Ile Glu Gly Arg Leu Val His Pro His Val Phe	
360 365 370	
tct gat gtc acc tct gac atg gaa atc gct cgt gag gaa atc ttc gga	1267
Ser Asp Val Thr Ser Asp Met Glu Ile Ala Arg Glu Glu Ile Phe Gly	
375 380 385	

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cct ctc atc agc gtg ctg aag gcc gat gat gag gca cac gca gca gag 1315
Pro Leu Ile Ser Val Leu Lys Ala Asp Asp Glu Ala His Ala Ala Glu
390 395 400 405

ctg gcc aat gct tcc gac ttt ggt ttg agc gcg gca gtg tgg tcg aag 1363
Leu Ala Asn Ala Ser Asp Phe Gly Leu Ser Ala Ala Val Trp Ser Lys
410 415 420

gat att gat cgt gca gcc cag ttt gct ctg cag att gat tcc ggc atg 1411
Asp Ile Asp Arg Ala Ala Gln Phe Ala Leu Gln Ile Asp Ser Gly Met
425 430 435

gtt cac atc aat gac ctc acc gtc aac gat gaa cca cac gtg atg ttc 1459
Val His Ile Asn Asp Leu Thr Val Asn Asp Glu Pro His Val Met Phe
440 445 450

ggg ggt tca aag aac tct ggc ctc ggc cgc ttc aac ggc gat tgg gcg 1507
Gly Gly Ser Lys Asn Ser Gly Leu Gly Arg Phe Asn Gly Asp Trp Ala
455 460 465

atc gag gag ttc acc aca gat cga tgg atc ggc atc aag cgc agc 1552
Ile Glu Glu Phe Thr Thr Asp Arg Trp Ile Gly Ile Lys Arg Ser
470 475 480

taattgtttt tcgacgtaac ccc 1575

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<210> 228

<211> 484

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 228

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Gly Gln Trp Val Glu Gly Asn Ser Asp Arg Ile Ser Thr Asn Ile Asn
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Pro Tyr Asp Asp Ser Val Ile Ala Glu Ser Lys Gln Ala Ser Ile Ala
35 40 45

Asp Val Asp Ala Ala Tyr Glu Ala Ala Lys Lys Ala Gln Ala Glu Trp
50 55 60

Ala Ala Thr Pro Ala Ala Glu Arg Ser Ala Ile Ile Tyr Arg Ala Ala
65 70 75 80

Glu Leu Leu Glu Glu His Arg Glu Glu Ile Val Glu Trp Leu Ile Lys
85 90 95

Glu Ser Gly Ser Thr Arg Ser Lys Ala Asn Leu Glu Ile Thr Leu Ala
100 105 110

Gly Asn Ile Thr Lys Glu Ser Ala Ser Phe Pro Gly Arg Val His Gly
115 120 125

Arg Ile Ser Pro Ser Asn Thr Pro Gly Lys Glu Asn Arg Val Tyr Arg
130 135 140

Val Ala Lys Gly Val Val Gly Val Ile Ser Pro Trp Asn Phe Pro Leu

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145	150	155	160
Asn Leu Ser Ile Arg Ser Val Ala Pro Ala Leu Ala Val Gly Asn Ala	165	170	175
Val Val Ile Lys Pro Ala Ser Asp Thr Pro Val Thr Gly Gly Val Ile	180	185	190
Pro Ala Arg Ile Phe Glu Glu Ala Gly Val Pro Ala Gly Val Ile Ser	195	200	205
Thr Val Ala Gly Ala Gly Ser Glu Ile Gly Asp His Phe Val Thr His	210	215	220
Ala Val Pro Lys Leu Ile Ser Phe Thr Gly Ser Thr Pro Val Gly Arg	225	230	240
Arg Val Gly Glu Leu Ala Ile Asn Gly Gly Pro Met Lys Thr Val Ala	245	250	255
Leu Glu Leu Gly Gly Asn Ala Pro Phe Val Val Leu Ala Asp Ala Asp	260	265	270
Ile Asp Ala Ala Ala Gln Ala Ala Ala Val Gly Ala Phe Leu His Gln	275	280	285
Gly Gln Ile Cys Met Ser Ile Asn Arg Val Ile Val Asp Ala Ala Val	290	295	300
His Asp Glu Phe Leu Glu Lys Phe Val Glu Ala Val Lys Asn Ile Pro	305	310	315
Thr Gly Asp Pro Ser Ala Glu Gly Thr Leu Val Gly Pro Val Ile Asn	325	330	335
Asp Ser Gln Leu Ser Gly Leu Lys Glu Lys Ile Glu Leu Ala Lys Lys	340	345	350
Glu Gly Ala Thr Val Gln Val Glu Gly Pro Ile Glu Gly Arg Leu Val	355	360	365
His Pro His Val Phe Ser Asp Val Thr Ser Asp Met Glu Ile Ala Arg	370	375	380
Glu Glu Ile Phe Gly Pro Leu Ile Ser Val Leu Lys Ala Asp Asp Glu	385	390	395
Ala His Ala Ala Glu Leu Ala Asn Ala Ser Asp Phe Gly Leu Ser Ala	405	410	415
Ala Val Trp Ser Lys Asp Ile Asp Arg Ala Ala Gln Phe Ala Leu Gln	420	425	430
Ile Asp Ser Gly Met Val His Ile Asn Asp Leu Thr Val Asn Asp Glu	435	440	445
Pro His Val Met Phe Gly Gly Ser Lys Asn Ser Gly Leu Gly Arg Phe	450	455	460
Asn Gly Asp Trp Ala Ile Glu Glu Phe Thr Thr Asp Arg Trp Ile Gly	465	470	480

cag ttg ttc tct att gcg ttg gct gcg atg cgt gtg ttg act gat ccc	643
Gln Leu Phe Ser Ile Ala Leu Ala Ala Met Arg Val Leu Thr Asp Pro	
170 175 180	
gca gaa acc ggt gcg gtc acc att gcg ctt cca gaa gat gtg cag gct	691
Ala Glu Thr Gly Ala Val Thr Ile Ala Leu Pro Glu Asp Val Gln Ala	
185 190 195	
gaa atg ctc gat gtg ccg gtg gag ttc ttg cag gat cgt gag tgg cac	739
Glu Met Leu Asp Val Pro Val Glu Phe Leu Gln Asp Arg Glu Trp His	
200 205 210	
att agg cgc cca cgt cca gag cgt gct gcg ttg gct cgt gcg att gaa	787
Ile Arg Arg Pro Arg Pro Glu Arg Ala Ala Leu Ala Arg Ala Ile Glu	
215 220 225	
gtc atc aaa aac gct aag aat ccg atg atc att gct ggt ggc gga gtg	835
Val Ile Lys Asn Ala Lys Asn Pro Met Ile Ile Ala Gly Gly Gly Val	
230 235 240 245	
ttg tac tcc gat gcg gaa acg cag ctg cag gca ctt gtg gag cag act	883
Leu Tyr Ser Asp Ala Glu Thr Gln Leu Gln Ala Leu Val Glu Gln Thr	
250 255 260	
ggc att cca gtg ggt acc tcc caa gct ggt ggt ggc gtg ttg gcg tgg	931
Gly Ile Pro Val Gly Thr Ser Gln Ala Gly Gly Gly Val Leu Ala Trp	
265 270 275	
gat cat gca caa aac tta ggt ggt gtg ggt gcc acc gga acg ttg gct	979
Asp His Ala Gln Asn Leu Gly Gly Val Gly Ala Thr Gly Thr Leu Ala	
280 285 290	
gcc aac cgc att gcg ggt gat gct gat gtg atc atc ggt atc ggt act	1027
Ala Asn Arg Ile Ala Gly Asp Ala Asp Val Ile Ile Gly Ile Gly Thr	
295 300 305	
cgt tac agc gat ttc acc acc gca tct cgc act gcg ttc caa aac cct	1075
Arg Tyr Ser Asp Phe Thr Thr Ala Ser Arg Thr Ala Phe Gln Asn Pro	
310 315 320 325	
gat gtc acc ttc atc aac atc aat gtt gct tcc ttc gat gct tac aag	1123
Asp Val Thr Phe Ile Asn Ile Asn Val Ala Ser Phe Asp Ala Tyr Lys	
330 335 340	
cat ggc act cag ttg cct gtg att gca gat gca cgc gag gca att gtg	1171
His Gly Thr Gln Leu Pro Val Ile Ala Asp Ala Arg Glu Ala Ile Val	
345 350 355	
gag ctt gct gaa gcc ctg cag gga ttc acc gtg gca gag gat tac gcg	1219
Glu Leu Ala Glu Ala Leu Gln Gly Phe Thr Val Ala Glu Asp Tyr Ala	
360 365 370	
cag cgc atc gcg aag gaa aag gct gcg tgg gac gca gaa gta gat aag	1267
Gln Arg Ile Ala Lys Glu Lys Ala Ala Trp Asp Ala Glu Val Asp Lys	
375 380 385	
tct ttt gcc ccc tcc ggt ctt gcg ctg cct gga cag ccg gag atc atc	1315
Ser Phe Ala Pro Ser Gly Leu Ala Leu Pro Gly Gln Pro Glu Ile Ile	
390 395 400 405	

ggc gcg gtg cag gcg tcg aca agc gaa aaa gac gtc att gtg cag gcc	1363
Gly Ala Val Gln Ala Ser Thr Ser Glu Lys Asp Val Ile Val Gln Ala	
410 415 420	
gct gga tcc ttg cct ggt gac ctg cac aag ctg tgg cgt gtg cgc gat	1411
Ala Gly Ser Leu Pro Gly Asp Leu His Lys Leu Trp Arg Val Arg Asp	
425 430 435	
gcg ctg ggc tac cac gtg gaa tat gcg ttc tcg tgc atg ggc tat gaa	1459
Ala Leu Gly Tyr His Val Glu Tyr Ala Phe Ser Cys Met Gly Tyr Glu	
440 445 450	
atc gcg ggc ggt atc ggc gcg aag cgt gga ctt gat gcc gca ggc gat	1507
Ile Ala Gly Gly Ile Gly Ala Lys Arg Gly Leu Asp Ala Ala Gly Asp	
455 460 465	
gac cgc gac gtg gtg atc atg gtt ggt gat ggg tcc tac ctc atg ctc	1555
Asp Arg Asp Val Val Ile Met Val Gly Asp Gly Ser Tyr Leu Met Leu	
470 475 480 485	
aac act gag ctg gtc acg gcc gtg gca gaa ggt atc aag gtg att gtg	1603
Asn Thr Glu Leu Val Thr Ala Val Ala Glu Gly Ile Lys Val Ile Val	
490 495 500	
gtg ctc atc caa aac cac ggt tat gcc tcc atc ggc cac ctg tct gaa	1651
Val Leu Ile Gln Asn His Gly Tyr Ala Ser Ile Gly His Leu Ser Glu	
505 510 515	
act gtc ggt tcg cag cgt ttt ggt act tgg tac cgc gaa tat gac gct	1699
Thr Val Gly Ser Gln Arg Phe Gly Thr Trp Tyr Arg Glu Tyr Asp Ala	
520 525 530	
gag gcg aaa aac ttc cag ggc gag cag att ctg cct gtt gac ctg gcg	1747
Glu Ala Lys Asn Phe Gln Gly Glu Gln Ile Leu Pro Val Asp Leu Ala	
535 540 545	
atg aat gca cgc agc tac ggc atg gat gtc att gaa gtg gaa cca agc	1795
Met Asn Ala Arg Ser Tyr Gly Met Asp Val Ile Glu Val Glu Pro Ser	
550 555 560 565	
gcg aat gcg atc gag gat ctc aaa gca gcg atg gca acc gcg aag gct	1843
Ala Asn Ala Ile Glu Asp Leu Lys Ala Ala Met Ala Thr Ala Lys Ala	
570 575 580	
tcg gag aaa tcc acc ttc atc cac atc aac agc gat ccg ttg atc tac	1891
Ser Glu Lys Ser Thr Phe Ile His Ile Asn Ser Asp Pro Leu Ile Tyr	
585 590 595	
gca cca gac ggt gct ggt tgg tgg gac gtg ccg gtg tcg gag acg tcc	1939
Ala Pro Asp Gly Ala Gly Trp Trp Asp Val Pro Val Ser Glu Thr Ser	
600 605 610	
act ctg gat agc acc aac gcg gct cgt gaa gat tac ctg aaa aac caa	1987
Thr Leu Asp Ser Thr Asn Ala Ala Arg Glu Asp Tyr Leu Lys Asn Gln	
615 620 625	
gcc ctc cag cgt ccg ctg ctc ggc taaaccagtt ggctaaacca aaa	2034
Ala Leu Gln Arg Pro Leu Leu Gly	
630 635	

<210> 230
 <211> 637
 <212> PRT
 <213> Corynebacterium glutamicum

<400> 230

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Leu Gly His Gln Trp Thr Val Asp Gly Asp Ile Arg Glu Arg Thr Ile
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Pro Gly Met Phe Gly Ile Phe Gly His Gly Asn Val Ala Gly Ile Gly
      35           40           45

Gln Ala Leu Lys Gln Tyr Asn Val Glu Gln Pro Glu Leu Met Pro Tyr
      50           55           60

Tyr Gln Ala Arg Asn Glu Gln Ala Met Val His Gln Ser Val Gly Tyr
      65           70           75           80

Ala Arg Met His Arg Arg Arg Gly Thr Tyr Ala Ser Ala Ala Ser Val
          85           90           95

Gly Pro Gly Ala Thr Asn Leu Leu Thr Gly Ala Ala Leu Ala Thr Thr
      100           105           110

Asn Arg Leu Pro Ala Leu Leu Leu Pro Ser Asp Thr Phe Ala Thr Arg
      115           120           125

Val Ala Asp Pro Val Leu Gln Gln Leu Glu Gln Pro Trp Asp Ile Gly
      130           135           140

Leu Thr Val Asn Asp Ala Phe Arg Pro Val Ser Lys Phe Phe Asp Arg
      145           150           155           160

Val Gln Arg Pro Glu Gln Leu Phe Ser Ile Ala Leu Ala Ala Met Arg
          165           170           175

Val Leu Thr Asp Pro Ala Glu Thr Gly Ala Val Thr Ile Ala Leu Pro
      180           185           190

Glu Asp Val Gln Ala Glu Met Leu Asp Val Pro Val Glu Phe Leu Gln
      195           200           205

Asp Arg Glu Trp His Ile Arg Arg Pro Arg Pro Glu Arg Ala Ala Leu
      210           215           220

Ala Arg Ala Ile Glu Val Ile Lys Asn Ala Lys Asn Pro Met Ile Ile
      225           230           235           240

Ala Gly Gly Gly Val Leu Tyr Ser Asp Ala Glu Thr Gln Leu Gln Ala
          245           250           255

Leu Val Glu Gln Thr Gly Ile Pro Val Gly Thr Ser Gln Ala Gly Gly
      260           265           270

Gly Val Leu Ala Trp Asp His Ala Gln Asn Leu Gly Gly Val Gly Ala
      275           280           285

Thr Gly Thr Leu Ala Ala Asn Arg Ile Ala Gly Asp Ala Asp Val Ile

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290					295					300				
Ile Gly Ile Gly Thr	Arg Tyr Ser Asp Phe Thr Thr Ala Ser Arg Thr													
305	310	315	320											
Ala Phe Gln Asn Pro Asp Val Thr Phe Ile Asn Ile Asn Val Ala Ser														
	325	330	335											
Phe Asp Ala Tyr Lys His Gly Thr Gln Leu Pro Val Ile Ala Asp Ala														
	340	345	350											
Arg Glu Ala Ile Val Glu Leu Ala Glu Ala Leu Gln Gly Phe Thr Val														
	355	360	365											
Ala Glu Asp Tyr Ala Gln Arg Ile Ala Lys Glu Lys Ala Ala Trp Asp														
	370	375	380											
Ala Glu Val Asp Lys Ser Phe Ala Pro Ser Gly Leu Ala Leu Pro Gly														
	385	390	395	400										
Gln Pro Glu Ile Ile Gly Ala Val Gln Ala Ser Thr Ser Glu Lys Asp														
	405	410	415											
Val Ile Val Gln Ala Ala Gly Ser Leu Pro Gly Asp Leu His Lys Leu														
	420	425	430											
Trp Arg Val Arg Asp Ala Leu Gly Tyr His Val Glu Tyr Ala Phe Ser														
	435	440	445											
Cys Met Gly Tyr Glu Ile Ala Gly Gly Ile Gly Ala Lys Arg Gly Leu														
	450	455	460											
Asp Ala Ala Gly Asp Asp Arg Asp Val Val Ile Met Val Gly Asp Gly														
	465	470	475	480										
Ser Tyr Leu Met Leu Asn Thr Glu Leu Val Thr Ala Val Ala Glu Gly														
	485	490	495											
Ile Lys Val Ile Val Val Leu Ile Gln Asn His Gly Tyr Ala Ser Ile														
	500	505	510											
Gly His Leu Ser Glu Thr Val Gly Ser Gln Arg Phe Gly Thr Trp Tyr														
	515	520	525											
Arg Glu Tyr Asp Ala Glu Ala Lys Asn Phe Gln Gly Glu Gln Ile Leu														
	530	535	540											
Pro Val Asp Leu Ala Met Asn Ala Arg Ser Tyr Gly Met Asp Val Ile														
	545	550	555	560										
Glu Val Glu Pro Ser Ala Asn Ala Ile Glu Asp Leu Lys Ala Ala Met														
	565	570	575											
Ala Thr Ala Lys Ala Ser Glu Lys Ser Thr Phe Ile His Ile Asn Ser														
	580	585	590											
Asp Pro Leu Ile Tyr Ala Pro Asp Gly Ala Gly Trp Trp Asp Val Pro														
	595	600	605											
Val Ser Glu Thr Ser Thr Leu Asp Ser Thr Asn Ala Ala Arg Glu Asp														
	610	615	620											

Tyr Leu Lys Asn Gln Ala Leu Gln Arg Pro Leu Leu Gly
 625 630 635

<210> 231
 <211> 1142
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (1)..(1119)
 <223> RXN01143

<400> 231
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 Ile Pro Val Val Thr Thr Leu Met Ala Leu Gly Thr Phe Pro Glu Ser
 1 5 10 15
 cac gag ctg cac atg ggt atg cca ggc atg cat ggc act gtg tcc gct 96
 His Glu Leu His Met Gly Met Pro Gly Met His Gly Thr Val Ser Ala
 20 25 30
 gtt ggt gca ctg cag cgc agc gac ctg ctg att gct atc ggc tcc cgc 144
 Val Gly Ala Leu Gln Arg Ser Asp Leu Leu Ile Ala Ile Gly Ser Arg
 35 40 45
 ttt gat gac cgc gtc acc ggt gac gtt gac acc ttc gcg cct gac gcc 192
 Phe Asp Asp Arg Val Thr Gly Asp Val Asp Thr Phe Ala Pro Asp Ala
 50 55 60
 aag atc att cac gcc gac att gat cct gcc gaa atc ggc aag atc aag 240
 Lys Ile Ile His Ala Asp Ile Asp Pro Ala Glu Ile Gly Lys Ile Lys
 65 70 75 80
 cag gtt gag gtt cca atc gtg ggc gat gcc cgc gaa gtt ctt gct cgt 288
 Gln Val Glu Val Pro Ile Val Gly Asp Ala Arg Glu Val Leu Ala Arg
 85 90 95
 ctg ctg gaa acc acc aag gca agc aag gca gag acc gag gac atc tcc 336
 Leu Leu Glu Thr Thr Lys Ala Ser Lys Ala Glu Thr Glu Asp Ile Ser
 100 105 110
 gag tgg gtt gac tac ctc aag ggc ctc aag gca cgt ttc ccg cgt ggc 384
 Glu Trp Val Asp Tyr Leu Lys Gly Leu Lys Ala Arg Phe Pro Arg Gly
 115 120 125
 tac gac gag cag cca ggc gat ctg ctg gca cca cag ttt gtc att gaa 432
 Tyr Asp Glu Gln Pro Gly Asp Leu Leu Ala Pro Gln Phe Val Ile Glu
 130 135 140
 acc ctg tcc aag gaa gtt ggc ccc gac gca att tac tgc gcc ggc gtt 480
 Thr Leu Ser Lys Glu Val Gly Pro Asp Ala Ile Tyr Cys Ala Gly Val
 145 150 155 160
 ggc cag cac caa atg tgg gca gct cag ttc gtt gac ttt gaa aag cca 528
 Gly Gln His Gln Met Trp Ala Ala Gln Phe Val Asp Phe Glu Lys Pro
 165 170 175
 cgc acc tgg ctc aac tcc ggt gga ctg ggc acc atg ggc tac gca gtt 576

Arg Thr Trp Leu Asn Ser Gly Gly Leu Gly Thr Met Gly Tyr Ala Val
 180 185 190
 cct gcg gcc ctt gga gca aag gct ggc gca cct gac aag gaa gtc tgg 624
 Pro Ala Ala Leu Gly Ala Lys Ala Gly Ala Pro Asp Lys Glu Val Trp
 195 200 205
 gct atc gac ggc gac ggc tgt ttc cag atg acc aac cag gaa ctc acc 672
 Ala Ile Asp Gly Asp Gly Cys Phe Gln Met Thr Asn Gln Glu Leu Thr
 210 215 220
 acc gcc gca gtt gaa ggt ttc ccc att aag atc gca cta atc aac aac 720
 Thr Ala Ala Val Glu Gly Phe Pro Ile Lys Ile Ala Leu Ile Asn Asn
 225 230 235 240
 gga aaa cct ggg gca tgg gtt cgc caa tgg cag acc cta ttc tat gaa 768
 Gly Lys Pro Gly Ala Trp Val Arg Gln Trp Gln Thr Leu Phe Tyr Glu
 245 250 255
 gga cgg tac tca aat act aaa ctt cgt aac cag ggc gag tac atg ccc 816
 Gly Arg Tyr Ser Asn Thr Lys Leu Arg Asn Gln Gly Glu Tyr Met Pro
 260 265 270
 gac ttt gtt acc ctt tct gag gga ctt ggc tgt gtt gcc atc cgc gtc 864
 Asp Phe Val Thr Leu Ser Glu Gly Leu Gly Cys Val Ala Ile Arg Val
 275 280 285
 acc aaa gcg gag gaa gta ctg cca gcc atc caa aag gct cga gag atc 912
 Thr Lys Ala Glu Glu Val Leu Pro Ala Ile Gln Lys Ala Arg Glu Ile
 290 295 300
 aac gac cgc cca gta gtc atc gac ttc atc gtc ggt gaa gac gca cag 960
 Asn Asp Arg Pro Val Val Ile Asp Phe Ile Val Gly Glu Asp Ala Gln
 305 310 315 320
 gta tgg cca atg gtg tct gct gga tca tcc aac tcc gat atc cag tac 1008
 Val Trp Pro Met Val Ser Ala Gly Ser Ser Asn Ser Asp Ile Gln Tyr
 325 330 335
 gca ctc gga ttg cgc cca ttc ttt gat ggt gat gaa tct gca gca gaa 1056
 Ala Leu Gly Leu Arg Pro Phe Phe Asp Gly Asp Glu Ser Ala Ala Glu
 340 345 350
 gat cct gcc gac att cac gaa gcc gtc agc gac att gat gcc gcc gtt 1104
 Asp Pro Ala Asp Ile His Glu Ala Val Ser Asp Ile Asp Ala Ala Val
 355 360 365
 gaa tcg acc gag gca taaggagaga cccaagatgg cta 1142
 Glu Ser Thr Glu Ala
 370

<210> 232

<211> 373

<212> PRT

<213> Corynebacterium glutamicum

<400> 232

Ile Pro Val Val Thr Thr Leu Met Ala Leu Gly Thr Phe Pro Glu Ser
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His Glu Leu His Met Gly Met Pro Gly Met His Gly Thr Val Ser Ala
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 Val Gly Ala Leu Gln Arg Ser Asp Leu Leu Ile Ala Ile Gly Ser Arg
 35 40 45
 Phe Asp Asp Arg Val Thr Gly Asp Val Asp Thr Phe Ala Pro Asp Ala
 50 55 60
 Lys Ile Ile His Ala Asp Ile Asp Pro Ala Glu Ile Gly Lys Ile Lys
 65 70 75 80
 Gln Val Glu Val Pro Ile Val Gly Asp Ala Arg Glu Val Leu Ala Arg
 85 90 95
 Leu Leu Glu Thr Thr Lys Ala Ser Lys Ala Glu Thr Glu Asp Ile Ser
 100 105 110
 Glu Trp Val Asp Tyr Leu Lys Gly Leu Lys Ala Arg Phe Pro Arg Gly
 115 120 125
 Tyr Asp Glu Gln Pro Gly Asp Leu Leu Ala Pro Gln Phe Val Ile Glu
 130 135 140
 Thr Leu Ser Lys Glu Val Gly Pro Asp Ala Ile Tyr Cys Ala Gly Val
 145 150 155 160
 Gly Gln His Gln Met Trp Ala Ala Gln Phe Val Asp Phe Glu Lys Pro
 165 170 175
 Arg Thr Trp Leu Asn Ser Gly Gly Leu Gly Thr Met Gly Tyr Ala Val
 180 185 190
 Pro Ala Ala Leu Gly Ala Lys Ala Gly Ala Pro Asp Lys Glu Val Trp
 195 200 205
 Ala Ile Asp Gly Asp Gly Cys Phe Gln Met Thr Asn Gln Glu Leu Thr
 210 215 220
 Thr Ala Ala Val Glu Gly Phe Pro Ile Lys Ile Ala Leu Ile Asn Asn
 225 230 235 240
 Gly Lys Pro Gly Ala Trp Val Arg Gln Trp Gln Thr Leu Phe Tyr Glu
 245 250 255
 Gly Arg Tyr Ser Asn Thr Lys Leu Arg Asn Gln Gly Glu Tyr Met Pro
 260 265 270
 Asp Phe Val Thr Leu Ser Glu Gly Leu Gly Cys Val Ala Ile Arg Val
 275 280 285
 Thr Lys Ala Glu Glu Val Leu Pro Ala Ile Gln Lys Ala Arg Glu Ile
 290 295 300
 Asn Asp Arg Pro Val Val Ile Asp Phe Ile Val Gly Glu Asp Ala Gln
 305 310 315 320
 Val Trp Pro Met Val Ser Ala Gly Ser Ser Asn Ser Asp Ile Gln Tyr
 325 330 335
 Ala Leu Gly Leu Arg Pro Phe Phe Asp Gly Asp Glu Ser Ala Ala Glu

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340          345          350
Asp Pro Ala Asp Ile His Glu Ala Val Ser Asp Ile Asp Ala Ala Val
355          360          365

Glu Ser Thr Glu Ala
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<210> 233
<211> 793
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(793)
<223> RXN01146

<400> 233
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cacggttgca agccgtggtc gatccgccgc ccctgagcgg atg aca ggt gca aag 115
Met Thr Gly Ala Lys
1 5

gca att gtt cga tcg ctc gag gag ctt aac gcc gac atc gtg ttc ggt 163
Ala Ile Val Arg Ser Leu Glu Glu Leu Asn Ala Asp Ile Val Phe Gly
10 15 20

att cct ggt ggt gcg gtg cta ccg gtg tat gac ccg ctc tat tcc tcc 211
Ile Pro Gly Gly Ala Val Leu Pro Val Tyr Asp Pro Leu Tyr Ser Ser
25 30 35

aca aag gtg cgc cac gtc ttg gtg cgc cac gag cag ggc gca ggc cac 259
Thr Lys Val Arg His Val Leu Val Arg His Glu Gln Gly Ala Gly His
40 45 50

gca gca acc ggc tac gcg cag gtt act gga cgc gtt ggc gtc tgc att 307
Ala Ala Thr Gly Tyr Ala Gln Val Thr Gly Arg Val Gly Val Cys Ile
55 60 65

gca acc tct ggc cca gga gca acc aac ttg gtt acc cca atc gct gat 355
Ala Thr Ser Gly Pro Gly Ala Thr Asn Leu Val Thr Pro Ile Ala Asp
70 75 80 85

gca aac ttg gac tcc gtt ccc atg gtt gcc atc acc ggc cag gtc gga 403
Ala Asn Leu Asp Ser Val Pro Met Val Ala Ile Thr Gly Gln Val Gly
90 95 100

agt ggc ctg ctg ggt acc gac gct ttc cag gaa gcc gat atc cgc ggc 451
Ser Gly Leu Leu Gly Thr Asp Ala Phe Gln Glu Ala Asp Ile Arg Gly
105 110 115

atc acc atg cca gtg acc aag cac aac ttc atg gtc acc aac cct aac 499
Ile Thr Met Pro Val Thr Lys His Asn Phe Met Val Thr Asn Pro Asn
120 125 130

gac att cca cag gca ttg gct gag gca ttc cac ctc gcg att act ggt 547
Asp Ile Pro Gln Ala Leu Ala Glu Ala Phe His Leu Ala Ile Thr Gly
135 140 145

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cgc cct ggc cct gtt ctg gtg gat att cct aag gat gtc cag aac gct 595
 Arg Pro Gly Pro Val Leu Val Asp Ile Pro Lys Asp Val Gln Asn Ala
 150 155 160 165

 gaa ttg gat ttc gtc tgg cca cca aag atc gac ctg cca ggc tac cgc 643
 Glu Leu Asp Phe Val Trp Pro Pro Lys Ile Asp Leu Pro Gly Tyr Arg
 170 175 180

 cca gtt tca aca cca cat gct cgc cag atc gag cag gca gtc aag ctg 691
 Pro Val Ser Thr Pro His Ala Arg Gln Ile Glu Gln Ala Val Lys Leu
 185 190 195

 atc ggt gag gcc aag aag ccc gtc ctt tac gtt ggt ggt ggc gta atc 739
 Ile Gly Glu Ala Lys Lys Pro Val Leu Tyr Val Gly Gly Gly Val Ile
 200 205 210

 aag gct gac gca cac gaa gag ctt cgt gcg ttc gct gag tac acc ggc 787
 Lys Ala Asp Ala His Glu Glu Leu Arg Ala Phe Ala Glu Tyr Thr Gly
 215 220 225

 atc cca 793
 Ile Pro
 230

<210> 234
 <211> 231
 <212> PRT
 <213> *Corynebacterium glutamicum*

<400> 234
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 20 25 30

 Pro Leu Tyr Ser Ser Thr Lys Val Arg His Val Leu Val Arg His Glu
 35 40 45

 Gln Gly Ala Gly His Ala Ala Thr Gly Tyr Ala Gln Val Thr Gly Arg
 50 55 60

 Val Gly Val Cys Ile Ala Thr Ser Gly Pro Gly Ala Thr Asn Leu Val
 65 70 75 80

 Thr Pro Ile Ala Asp Ala Asn Leu Asp Ser Val Pro Met Val Ala Ile
 85 90 95

 Thr Gly Gln Val Gly Ser Gly Leu Leu Gly Thr Asp Ala Phe Gln Glu
 100 105 110

 Ala Asp Ile Arg Gly Ile Thr Met Pro Val Thr Lys His Asn Phe Met
 115 120 125

 Val Thr Asn Pro Asn Asp Ile Pro Gln Ala Leu Ala Glu Ala Phe His
 130 135 140

 Leu Ala Ile Thr Gly Arg Pro Gly Pro Val Leu Val Asp Ile Pro Lys
 145 150 155 160

Asp Val Gln Asn Ala Glu Leu Asp Phe Val Trp Pro Pro Lys Ile Asp
 165 170 175
 Leu Pro Gly Tyr Arg Pro Val Ser Thr Pro His Ala Arg Gln Ile Glu
 180 185 190
 Gln Ala Val Lys Leu Ile Gly Glu Ala Lys Lys Pro Val Leu Tyr Val
 195 200 205
 Gly Gly Gly Val Ile Lys Ala Asp Ala His Glu Glu Leu Arg Ala Phe
 210 215 220
 Ala Glu Tyr Thr Gly Ile Pro
 225 230

<210> 235

<211> 639

<212> DNA

<213> *Corynebacterium glutamicum*

<220>

<221> CDS

<222> (101)..(616)

<223> RXN01144

<400> 235

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 Met Ala Asn Ser Asp
 1 5
 gtc acc cgc cac atc ctg tcc gta ctc gtt cag gac gta gac gga atc 163
 Val Thr Arg His Ile Leu Ser Val Leu Val Gln Asp Val Asp Gly Ile
 10 15 20
 att tcc cgc gta tca ggt atg ttc acc cga cgc gca ttc aac ctc gtg 211
 Ile Ser Arg Val Ser Gly Met Phe Thr Arg Arg Ala Phe Asn Leu Val
 25 30 35
 ttc ctc gtg tct gca aag acc gaa aca cac ggc atc aac cgc atc acg 259
 Phe Leu Val Ser Ala Lys Thr Glu Thr His Gly Ile Asn Arg Ile Thr
 40 45 50
 gtt gtt gtc gac gcc gac gag ctc aac att gag cag atc acc aag cag 307
 Val Val Val Asp Ala Asp Glu Leu Asn Ile Glu Gln Ile Thr Lys Gln
 55 60 65
 ctc aac aag ctg atc ccc gtg ctc aaa gtc gtg cga ctt gat gaa gag 355
 Leu Asn Lys Leu Ile Pro Val Leu Lys Val Val Arg Leu Asp Glu Glu
 70 75 80 85
 acc act atc gcc cgc gca atc atg ctg gtt aag gtc tct gcg gac agc 403
 Thr Thr Ile Ala Arg Ala Ile Met Leu Val Lys Val Ser Ala Asp Ser
 90 95 100
 acc aac cgt ccg cag atc gtc gac gcc gcg aac atc ttc cgc gcc cga 451
 Thr Asn Arg Pro Gln Ile Val Asp Ala Ala Asn Ile Phe Arg Ala Arg
 105 110 115

gtc gtc gac gtg gct cca gac tct gtg gtt att gaa tcc aca ggc acc 499
 Val Val Asp Val Ala Pro Asp Ser Val Val Ile Glu Ser Thr Gly Thr
 120 125 130

cca ggc aag ctc cgc gca ctg ctt gac gtg atg gaa cca ttc gga atc 547
 Pro Gly Lys Leu Arg Ala Leu Leu Asp Val Met Glu Pro Phe Gly Ile
 135 140 145

cgc gaa ctg atc caa tcc gga cag att gca ctc aac cgc ggt ccg aag 595
 Arg Glu Leu Ile Gln Ser Gly Gln Ile Ala Leu Asn Arg Gly Pro Lys
 150 155 160 165

acc atg gct ccg gcc aag atc taaacagcaa ttaatctgat tgc 639
 Thr Met Ala Pro Ala Lys Ile
 170

<210> 236

<211> 172

<212> PRT

<213> Corynebacterium glutamicum

<400> 236

Met Ala Asn Ser Asp Val Thr Arg His Ile Leu Ser Val Leu Val Gln
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Asp Val Asp Gly Ile Ile Ser Arg Val Ser Gly Met Phe Thr Arg Arg
 20 25 30

Ala Phe Asn Leu Val Phe Leu Val Ser Ala Lys Thr Glu Thr His Gly
 35 40 45

Ile Asn Arg Ile Thr Val Val Val Asp Ala Asp Glu Leu Asn Ile Glu
 50 55 60

Gln Ile Thr Lys Gln Leu Asn Lys Leu Ile Pro Val Leu Lys Val Val
 65 70 75 80

Arg Leu Asp Glu Glu Thr Thr Ile Ala Arg Ala Ile Met Leu Val Lys
 85 90 95

Val Ser Ala Asp Ser Thr Asn Arg Pro Gln Ile Val Asp Ala Ala Asn
 100 105 110

Ile Phe Arg Ala Arg Val Val Asp Val Ala Pro Asp Ser Val Val Ile
 115 120 125

Glu Ser Thr Gly Thr Pro Gly Lys Leu Arg Ala Leu Leu Asp Val Met
 130 135 140

Glu Pro Phe Gly Ile Arg Glu Leu Ile Gln Ser Gly Gln Ile Ala Leu
 145 150 155 160

Asn Arg Gly Pro Lys Thr Met Ala Pro Ala Lys Ile
 165 170

<210> 237

<211> 897

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(874)

<223> RXA02474

<400> 237

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aatcttgaga atttattttg aggaagcaag aggaagtgtc atg agc aaa gtt gca 115
                               Met Ser Lys Val Ala
                               1 5

atg gtt acc ggt ggt gca caa ggc atc ggt cgt gga att tca gag aag 163
Met Val Thr Gly Gly Ala Gln Gly Ile Gly Arg Gly Ile Ser Glu Lys
                               10 15 20

ctg gca gca gat ggt ttc gat att gcc gta gcc gac ctg cca caa cag 211
Leu Ala Ala Asp Gly Phe Asp Ile Ala Val Ala Asp Leu Pro Gln Gln
                               25 30 35

gaa gaa caa gct gca gag acc atc aag ttg att gaa gct gca ggt caa 259
Glu Glu Gln Ala Ala Glu Thr Ile Lys Leu Ile Glu Ala Ala Gly Gln
                               40 45 50

aag gct gta ttc gtt gga tta gat gtc acc gat aag gct aat ttc gac 307
Lys Ala Val Phe Val Gly Leu Asp Val Thr Asp Lys Ala Asn Phe Asp
                               55 60 65

agt gca att gat gag gca gca gag aaa ctt ggc ggc ttc gat gtg cta 355
Ser Ala Ile Asp Glu Ala Ala Glu Lys Leu Gly Gly Phe Asp Val Leu
                               70 75 80 85

gta aac aac gcc ggc atc gca caa att aag cca ctt ctg gaa gtc acc 403
Val Asn Asn Ala Gly Ile Ala Gln Ile Lys Pro Leu Leu Glu Val Thr
                               90 95 100

gaa gaa gac cta aag cag atc tac tcc gtg aac gtt ttt agc gta ttt 451
Glu Glu Asp Leu Lys Gln Ile Tyr Ser Val Asn Val Phe Ser Val Phe
                               105 110 115

ttt ggt att caa gca gca tcc cga aag ttc gat gag ctt ggc gta aaa 499
Phe Gly Ile Gln Ala Ala Ser Arg Lys Phe Asp Glu Leu Gly Val Lys
                               120 125 130

ggc aag atc atc aac gct gca tca atc gct gct atc caa ggt ttc cca 547
Gly Lys Ile Ile Asn Ala Ala Ser Ile Ala Ala Ile Gln Gly Phe Pro
                               135 140 145

atc ttg agc gcc tac tcc acc acc aaa ttc gcg gtt cgt ggc ctc acc 595
Ile Leu Ser Ala Tyr Ser Thr Thr Lys Phe Ala Val Arg Gly Leu Thr
                               150 155 160 165

cag gct gct gcg caa gaa ctc gca ccc aag ggt cac acc gtg aat gcc 643
Gln Ala Ala Ala Gln Glu Leu Ala Pro Lys Gly His Thr Val Asn Ala
                               170 175 180

tac gca cct ggc atc gtg ggc acc gga atg tgg gag caa atc gat gcc 691
Tyr Ala Pro Gly Ile Val Gly Thr Gly Met Trp Glu Gln Ile Asp Ala
                               185 190 195

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gag ctt tcc aag atc aac ggc aag cca atc ggt gag aac ttc aag gag 739
 Glu Leu Ser Lys Ile Asn Gly Lys Pro Ile Gly Glu Asn Phe Lys Glu
 200 205 210

tac tcc tcc tca atc gca ttg ggc cga cca tca gta cct gag gat gta 787
 Tyr Ser Ser Ser Ile Ala Leu Gly Arg Pro Ser Val Pro Glu Asp Val
 215 220 225

gcc ggt ctg gtt tcc ttc ctg gct tct gaa aac tcc aac tac atc acc 835
 Ala Gly Leu Val Ser Phe Leu Ala Ser Glu Asn Ser Asn Tyr Ile Thr
 230 235 240 245

gga cag gtc atg ctt gtc gac ggc ggc atg ctc tac aac taggggttgc 884
 Gly Gln Val Met Leu Val Asp Gly Gly Met Leu Tyr Asn
 250 255

tttcccgcac tca 897

<210> 238
 <211> 258
 <212> PRT
 <213> Corynebacterium glutamicum

<400> 238
 Met Ser Lys Val Ala Met Val Thr Gly Gly Ala Gln Gly Ile Gly Arg
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Gly Ile Ser Glu Lys Leu Ala Ala Asp Gly Phe Asp Ile Ala Val Ala
 20 25 30

Asp Leu Pro Gln Gln Glu Glu Gln Ala Ala Glu Thr Ile Lys Leu Ile
 35 40 45

Glu Ala Ala Gly Gln Lys Ala Val Phe Val Gly Leu Asp Val Thr Asp
 50 55 60

Lys Ala Asn Phe Asp Ser Ala Ile Asp Glu Ala Ala Glu Lys Leu Gly
 65 70 75 80

Gly Phe Asp Val Leu Val Asn Asn Ala Gly Ile Ala Gln Ile Lys Pro
 85 90 95

Leu Leu Glu Val Thr Glu Glu Asp Leu Lys Gln Ile Tyr Ser Val Asn
 100 105 110

Val Phe Ser Val Phe Phe Gly Ile Gln Ala Ala Ser Arg Lys Phe Asp
 115 120 125

Glu Leu Gly Val Lys Gly Lys Ile Ile Asn Ala Ala Ser Ile Ala Ala
 130 135 140

Ile Gln Gly Phe Pro Ile Leu Ser Ala Tyr Ser Thr Thr Lys Phe Ala
 145 150 155 160

Val Arg Gly Leu Thr Gln Ala Ala Ala Gln Glu Leu Ala Pro Lys Gly
 165 170 175

His Thr Val Asn Ala Tyr Ala Pro Gly Ile Val Gly Thr Gly Met Trp
 180 185 190

Glu Gln Ile Asp Ala Glu Leu Ser Lys Ile Asn Gly Lys Pro Ile Gly
 195 200 205

Glu Asn Phe Lys Glu Tyr Ser Ser Ser Ile Ala Leu Gly Arg Pro Ser
 210 215 220

Val Pro Glu Asp Val Ala Gly Leu Val Ser Phe Leu Ala Ser Glu Asn
 225 230 235 240

Ser Asn Tyr Ile Thr Gly Gln Val Met Leu Val Asp Gly Gly Met Leu
 245 250 255

Tyr Asn

<210> 239
 <211> 876
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
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 <222> (101)..(853)
 <223> RXA02453

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tcgtgccagc tcagggcata tctcacctaa agtaaacacc atg aaa tca atc ttc 115
 Met Lys Ser Ile Phe
 1 5

att tcc ggt gcg gcg aac gga att ggc aaa gct gtg gcg ttg aaa ttt 163
 Ile Ser Gly Ala Ala Asn Gly Ile Gly Lys Ala Val Ala Leu Lys Phe
 10 15 20

ctt cac gaa ggt tgg ctc gtt gga gcc tac gac ctc gcg gaa atc acc 211
 Leu His Glu Gly Trp Leu Val Gly Ala Tyr Asp Leu Ala Glu Ile Thr
 25 30 35

tac tca cac ccc aat ctt cgc tgg ggc tac ctc aat gtt cga cag tcc 259
 Tyr Ser His Pro Asn Leu Arg Trp Gly Tyr Leu Asn Val Arg Gln Ser
 40 45 50

gag tcg tgg gac aaa gcc cta gaa gac ttt gcg acg cac acc gga ggc 307
 Glu Ser Trp Asp Lys Ala Leu Glu Asp Phe Ala Thr His Thr Gly Gly
 55 60 65

acc atc gat gtg gtg gac aat aat gcc ggc gta att att gag gga ccg 355
 Thr Ile Asp Val Val Asp Asn Asn Ala Gly Val Ile Ile Glu Gly Pro
 70 75 80 85

ctg cag gac gca gag gag ggg agc gtc gac aag ctt ctt gca atc aac 403
 Leu Gln Asp Ala Glu Gly Ser Val Asp Lys Leu Leu Ala Ile Asn
 90 95 100

gtc aat ggc gtg act ctt ggt gcc cgc gcc gct cat cct tat ttg gcg 451
 Val Asn Gly Val Thr Leu Gly Ala Arg Ala Ala His Pro Tyr Leu Ala
 105 110 115

cgc acg ccg ggc gcc cag ttg tta aac atg tcc tcg gcg tcg gcg gtg 499
 Arg Thr Pro Gly Ala Gln Leu Leu Asn Met Ser Ser Ala Ser Ala Val
 120 125 130

tac ggg cag ccc cag atc gcg gtg tat tcg gct tcg aag ttt tac gtc 547
 Tyr Gly Gln Pro Gln Ile Ala Val Tyr Ser Ala Ser Lys Phe Tyr Val
 135 140 145

gca ggt ctt act gag gcg ctg aat ttg gag tgg cgg aaa gac gat att 595
 Ala Gly Leu Thr Glu Ala Leu Asn Leu Glu Trp Arg Lys Asp Asp Ile
 150 155 160 165

cgc gtg gtc gat gtt tgg cct ttg tgg gcg aaa acc gat ttg gtg aac 643
 Arg Val Val Asp Val Trp Pro Leu Trp Ala Lys Thr Asp Leu Val Asn
 170 175 180

ggc gtg aag gct aag tca ctg aag cgt ttg ggt gtc cgg atc act ccg 691
 Gly Val Lys Ala Lys Ser Leu Lys Arg Leu Gly Val Arg Ile Thr Pro
 185 190 195

gaa cag gtg gca cag gcg gta tgg gat gcg gtg cat ccg aaa tct cgg 739
 Glu Gln Val Ala Gln Ala Val Trp Asp Ala Val His Pro Lys Ser Arg
 200 205 210

tgg gcg aag gga aag gtg cat cac ggg gtg tca aag ttg gat aag gcg 787
 Trp Ala Lys Gly Lys Val His His Gly Val Ser Lys Leu Asp Lys Ala
 215 220 225

ctg tat ctc atg aaa tct ctg tcg cct gat cgg gta gcg atg tgt ttt 835
 Leu Tyr Leu Met Lys Ser Leu Ser Pro Asp Arg Val Ala Met Cys Phe
 230 235 240 245

gcg cga cta atc gcc gga taaatgaatt gattatttta ggc 876
 Ala Arg Leu Ile Ala Gly
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<210> 240

<211> 251

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 240

Met Lys Ser Ile Phe Ile Ser Gly Ala Ala Asn Gly Ile Gly Lys Ala
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Val Ala Leu Lys Phe Leu His Glu Gly Trp Leu Val Gly Ala Tyr Asp
 20 25 30

Leu Ala Glu Ile Thr Tyr Ser His Pro Asn Leu Arg Trp Gly Tyr Leu
 35 40 45

Asn Val Arg Gln Ser Glu Ser Trp Asp Lys Ala Leu Glu Asp Phe Ala
 50 55 60

Thr His Thr Gly Gly Thr Ile Asp Val Val Asp Asn Asn Ala Gly Val
 65 70 75 80

Ile Ile Glu Gly Pro Leu Gln Asp Ala Glu Glu Gly Ser Val Asp Lys
 85 90 95

Leu Leu Ala Ile Asn Val Asn Gly Val Thr Leu Gly Ala Arg Ala Ala
 100 105 110
 His Pro Tyr Leu Ala Arg Thr Pro Gly Ala Gln Leu Leu Asn Met Ser
 115 120 125
 Ser Ala Ser Ala Val Tyr Gly Gln Pro Gln Ile Ala Val Tyr Ser Ala
 130 135 140
 Ser Lys Phe Tyr Val Ala Gly Leu Thr Glu Ala Leu Asn Leu Glu Trp
 145 150 155 160
 Arg Lys Asp Asp Ile Arg Val Val Asp Val Trp Pro Leu Trp Ala Lys
 165 170 175
 Thr Asp Leu Val Asn Gly Val Lys Ala Lys Ser Leu Lys Arg Leu Gly
 180 185 190
 Val Arg Ile Thr Pro Glu Gln Val Ala Gln Ala Val Trp Asp Ala Val
 195 200 205
 His Pro Lys Ser Arg Trp Ala Lys Gly Lys Val His His Gly Val Ser
 210 215 220
 Lys Leu Asp Lys Ala Leu Tyr Leu Met Lys Ser Leu Ser Pro Asp Arg
 225 230 235 240
 Val Ala Met Cys Phe Ala Arg Leu Ile Ala Gly
 245 250

<210> 241
 <211> 1140
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(1117)
 <223> RXS01758

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 Met Pro Lys Tyr Ile
 1 5
 gcc atg cag gta tcc gaa tcc ggt gca ccg tta gcc gcg aat ctc gtg 163
 Ala Met Gln Val Ser Glu Ser Gly Ala Pro Leu Ala Ala Asn Leu Val
 10 15 20
 caa cct gct ccg ttg aaa tcg agg gaa gtc cgc gtg gaa atc gct gct 211
 Gln Pro Ala Pro Leu Lys Ser Arg Glu Val Arg Val Glu Ile Ala Ala
 25 30 35
 agt ggt gtg tgc cat gca gat att ggc acg gca gca gca tcg ggg aag 259
 Ser Gly Val Cys His Ala Asp Ile Gly Thr Ala Ala Ala Ser Gly Lys
 40 45 50

cac act gtt ttt cct gtt acc cct ggt cat gag att gca gga acc atc	307
His Thr Val Phe Pro Val Thr Pro Gly His Glu Ile Ala Gly Thr Ile	
55 60 65	
gcg gaa att ggt gaa aac gta tct cgg tgg acg gtt ggt gat cgc gtt	355
Ala Glu Ile Gly Glu Asn Val Ser Arg Trp Thr Val Gly Asp Arg Val	
70 75 80 85	
gca atc ggt tgg ttt ggt ggc aat tgc ggt gac tgc gct ttt tgt cgt	403
Ala Ile Gly Trp Phe Gly Gly Asn Cys Gly Asp Cys Ala Phe Cys Arg	
90 95 100	
gca ggt gat cct gtg cat tgc aga gag cgg aag att cct ggc gtt tct	451
Ala Gly Asp Pro Val His Cys Arg Glu Arg Lys Ile Pro Gly Val Ser	
105 110 115	
tat gcg ggt ggt tgg gca cag aat att gtt gtt cca gcg gag gct ctt	499
Tyr Ala Gly Gly Trp Ala Gln Asn Ile Val Val Pro Ala Glu Ala Leu	
120 125 130	
gct gcg att cca gat ggc atg gac ttt tac gag ccc gcc ccg atg ggc	547
Ala Ala Ile Pro Asp Gly Met Asp Phe Tyr Glu Pro Ala Pro Met Gly	
135 140 145	
tgc gca ggt gtg aca aca ttc aat gcg ttg cga aac ctg aag ctg gat	595
Cys Ala Gly Val Thr Phe Asn Ala Leu Arg Asn Leu Lys Leu Asp	
150 155 160 165	
ccc ggt gcg gct gtc gcg gtc ttt gga atc ggc ggt tta gtg cgc cta	643
Pro Gly Ala Ala Val Ala Val Phe Gly Ile Gly Gly Leu Val Arg Leu	
170 175 180	
gct att cag ttt gct gcg aaa atg ggt tat cga acc atc acc atc gcc	691
Ala Ile Gln Phe Ala Ala Lys Met Gly Tyr Arg Thr Ile Thr Ile Ala	
185 190 195	
cgc ggt tta gag cgt gag gag cta gct agg caa ctt ggc gcc aac cac	739
Arg Gly Leu Glu Arg Glu Glu Leu Ala Arg Gln Leu Gly Ala Asn His	
200 205 210	
tac atc gat agc aat gat ctg cac cct ggc cag gcg tta ttt gaa ctt	787
Tyr Ile Asp Ser Asn Asp Leu His Pro Gly Gln Ala Leu Phe Glu Leu	
215 220 225	
ggc ggg gct gac ttg atc ttg tct act gcg tcc acc acg gag cct ctt	835
Gly Gly Ala Asp Leu Ile Leu Ser Thr Ala Ser Thr Thr Glu Pro Leu	
230 235 240 245	
tcg gag ttg tct acc ggt ctt tct att ggc ggg cag cta acc att atc	883
Ser Glu Leu Ser Thr Gly Leu Ser Ile Gly Gly Gln Leu Thr Ile Ile	
250 255 260	
gga gtt gat ggg gga gat atc acc gtt tcg gca gcc caa ttg atg atg	931
Gly Val Asp Gly Gly Asp Ile Thr Val Ser Ala Ala Gln Leu Met Met	
265 270 275	
aac cgt cag atc atc aca ggt cac ctc act gga agt gcg aat gac acg	979
Asn Arg Gln Ile Ile Thr Gly His Leu Thr Gly Ser Ala Asn Asp Thr	
280 285 290	
gaa cag act atg aaa ttt gct cat ctc cat ggc gtg aaa ccg ctt att	1027

Glu Gln Thr Met Lys Phe Ala His Leu His Gly Val Lys Pro Leu Ile
 295 300 305

gaa cgg atg cct ctc gat caa gcc aac gag gct att gca cgt att tca 1075
 Glu Arg Met Pro Leu Asp Gln Ala Asn Glu Ala Ile Ala Arg Ile Ser
 310 315 320 325

gct ggt aaa cca cgt ttc cgt att gtc ttg gag ccg aat tca 1117
 Ala Gly Lys Pro Arg Phe Arg Ile Val Leu Glu Pro Asn Ser
 330 335

taatgccaac agcaagccca att 1140

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 <213> Corynebacterium glutamicum

<400> 242
 Met Pro Lys Tyr Ile Ala Met Gln Val Ser Glu Ser Gly Ala Pro Leu
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Ala Ala Asn Leu Val Gln Pro Ala Pro Leu Lys Ser Arg Glu Val Arg
 20 25 30

Val Glu Ile Ala Ala Ser Gly Val Cys His Ala Asp Ile Gly Thr Ala
 35 40 45

Ala Ala Ser Gly Lys His Thr Val Phe Pro Val Thr Pro Gly His Glu
 50 55 60

Ile Ala Gly Thr Ile Ala Glu Ile Gly Glu Asn Val Ser Arg Trp Thr
 65 70 75 80

Val Gly Asp Arg Val Ala Ile Gly Trp Phe Gly Gly Asn Cys Gly Asp
 85 90 95

Cys Ala Phe Cys Arg Ala Gly Asp Pro Val His Cys Arg Glu Arg Lys
 100 105 110

Ile Pro Gly Val Ser Tyr Ala Gly Gly Trp Ala Gln Asn Ile Val Val
 115 120 125

Pro Ala Glu Ala Leu Ala Ala Ile Pro Asp Gly Met Asp Phe Tyr Glu
 130 135 140

Pro Ala Pro Met Gly Cys Ala Gly Val Thr Thr Phe Asn Ala Leu Arg
 145 150 155 160

Asn Leu Lys Leu Asp Pro Gly Ala Ala Val Ala Val Phe Gly Ile Gly
 165 170 175

Gly Leu Val Arg Leu Ala Ile Gln Phe Ala Ala Lys Met Gly Tyr Arg
 180 185 190

Thr Ile Thr Ile Ala Arg Gly Leu Glu Arg Glu Glu Leu Ala Arg Gln
 195 200 205

Leu Gly Ala Asn His Tyr Ile Asp Ser Asn Asp Leu His Pro Gly Gln
 210 215 220

Ala Leu Phe Glu Leu Gly Gly Ala Asp Leu Ile Leu Ser Thr Ala Ser
 225 230 235 240

Thr Thr Glu Pro Leu Ser Glu Leu Ser Thr Gly Leu Ser Ile Gly Gly
 245 250 255

Gln Leu Thr Ile Ile Gly Val Asp Gly Gly Asp Ile Thr Val Ser Ala
 260 265 270

Ala Gln Leu Met Met Asn Arg Gln Ile Ile Thr Gly His Leu Thr Gly
 275 280 285

Ser Ala Asn Asp Thr Glu Gln Thr Met Lys Phe Ala His Leu His Gly
 290 295 300

Val Lys Pro Leu Ile Glu Arg Met Pro Leu Asp Gln Ala Asn Glu Ala
 305 310 315 320

Ile Ala Arg Ile Ser Ala Gly Lys Pro Arg Phe Arg Ile Val Leu Glu
 325 330 335

Pro Asn Ser

<210> 243
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 <223> RXA02737

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acacatcttt cattaaagaa aggatcgtga cactaccatc gtg agc aca aac acg 115
 Val Ser Thr Asn Thr
 1 5

acc ccc tcc agc tgg aca aac cca ctg cgc gac ccg cag gat aaa cga 163
 Thr Pro Ser Ser Trp Thr Asn Pro Leu Arg Asp Pro Gln Asp Lys Arg
 10 15 20

ctc ccc cgc atc gct ggc cct tcc ggc atg gtg atc ttc ggt gtc act 211
 Leu Pro Arg Ile Ala Gly Pro Ser Gly Met Val Ile Phe Gly Val Thr
 25 30 35

ggc gac ttg gct cga aag aag ctg ctc ccc gcc att tat gat cta gca 259
 Gly Asp Leu Ala Arg Lys Lys Leu Leu Pro Ala Ile Tyr Asp Leu Ala
 40 45 50

aac cgc gga ttg ctg ccc cca gga ttc tcg ttg gta ggt tac ggc cgc 307
 Asn Arg Gly Leu Leu Pro Pro Gly Phe Ser Leu Val Gly Tyr Gly Arg
 55 60 65

cgc gaa tgg tcc aaa gaa gac ttt gaa aaa tac gta cgc gat gcc gca 355
 Arg Glu Trp Ser Lys Glu Asp Phe Glu Lys Tyr Val Arg Asp Ala Ala

70	75	80	85	
agt gct ggt gct cgt acg gaa ttc cgt gaa aat gtt tgg gag cgc ctc				403
Ser Ala Gly Ala Arg Thr Glu Phe Arg Glu Asn Val Trp Glu Arg Leu	90	95	100	
gcc gag ggt atg gaa ttt gtt cgc ggc aac ttt gat gat gat gca gct				451
Ala Glu Gly Met Glu Phe Val Arg Gly Asn Phe Asp Asp Ala Ala	105	110	115	
ttc gac aac ctc gct gca aca ctc aag cgc atc gac aaa acc cgc ggc				499
Phe Asp Asn Leu Ala Ala Thr Leu Lys Arg Ile Asp Lys Thr Arg Gly	120	125	130	
acc gcc ggc aac tgg gct tac tac ctg tcc att cca cca gat tcc ttc				547
Thr Ala Gly Asn Trp Ala Tyr Leu Ser Ile Pro Pro Asp Ser Phe	135	140	145	
aca gcg gtc tgc cac cag ctg gag cgt tcc ggc atg gct gaa tcc acc				595
Thr Ala Val Cys His Gln Leu Glu Arg Ser Gly Met Ala Glu Ser Thr	150	155	160	165
gaa gaa gca tgg cgc cgc gtg atc atc gag aag cct ttc ggc cac aac				643
Glu Glu Ala Trp Arg Val Ile Ile Glu Lys Pro Phe Gly His Asn	170	175	180	
ctc gaa tcc gca cac gag ctc aac cag ctg gtc aac gca gtc ttc cca				691
Leu Glu Ser Ala His Glu Leu Asn Gln Leu Val Asn Ala Val Phe Pro	185	190	195	
gaa tct tct gtg ttc cgc atc gac cac tat ttg ggc aag gaa aca gtt				739
Glu Ser Ser Val Phe Arg Ile Asp His Tyr Leu Gly Lys Glu Thr Val	200	205	210	
caa aac atc ctg gct ctg cgt ttt gct aac cag ctg ttt gag cca ctg				787
Gln Asn Ile Leu Ala Leu Arg Phe Ala Asn Gln Leu Phe Glu Pro Leu	215	220	225	
tgg aac tcc aac tac gtt gac cac gtc cag atc acc atg gct gaa gat				835
Trp Asn Ser Asn Tyr Val Asp His Val Gln Ile Thr Met Ala Glu Asp	230	235	240	245
att ggc ttg ggt gga cgt gct ggt tac tac gac ggc atc ggc gca gcc				883
Ile Gly Leu Gly Gly Arg Ala Gly Tyr Tyr Asp Gly Ile Gly Ala Ala	250	255	260	
cgc gac gtc atc cag aac cac ctg atc cag ctc ttg gct ctg gtt gcc				931
Arg Asp Val Ile Gln Asn His Leu Ile Gln Leu Leu Ala Leu Val Ala	265	270	275	
atg gaa gaa cca att tct ttc gtg cca gcg cag ctg cag gca gaa aag				979
Met Glu Glu Pro Ile Ser Phe Val Pro Ala Gln Leu Gln Ala Glu Lys	280	285	290	
atc aag gtg ctc tct gcg aca aag ccg tgc tac cca ttg gat aaa acc				1027
Ile Lys Val Leu Ser Ala Thr Lys Pro Cys Tyr Pro Leu Asp Lys Thr	295	300	305	
tcc gct cgt ggt cag tac gct gcc ggt tgg cag ggc tct gag tta gtc				1075
Ser Ala Arg Gly Gln Tyr Ala Ala Gly Trp Gln Gly Ser Glu Leu Val	310	315	320	325

aag gga ctt cgc gaa gaa gat ggc ttc aac cct gag tcc acc act gag 1123
Lys Gly Leu Arg Glu Glu Asp Gly Phe Asn Pro Glu Ser Thr Thr Glu
330 335 340

act ttt gcg gct tgt acc tta gag atc acg tct cgt cgc tgg gct ggt 1171
Thr Phe Ala Ala Cys Thr Leu Glu Ile Thr Ser Arg Arg Trp Ala Gly
345 350 355

gtg ccg ttc tac ctg cgc acc ggt aag cgt ctt ggt cgc cgt gtt act 1219
Val Pro Phe Tyr Leu Arg Thr Gly Lys Arg Leu Gly Arg Arg Val Thr
360 365 370

gag att gcc gtg gtg ttt aaa gac gca cca cac cag cct ttc gac ggc 1267
Glu Ile Ala Val Val Phe Lys Asp Ala Pro His Gln Pro Phe Asp Gly
375 380 385

gac atg act gta tcc ctt ggc caa aac gcc atc gtg att cgc gtg cag 1315
Asp Met Thr Val Ser Leu Gly Gln Asn Ala Ile Val Ile Arg Val Gln
390 395 400 405

cct gat gaa ggt gtg ctc atc cgc ttc ggt tcc aag gtt cca ggt tct 1363
Pro Asp Glu Gly Val Leu Ile Arg Phe Gly Ser Lys Val Pro Gly Ser
410 415 420

gcc atg gaa gtc cgt gac gtc aac atg gac ttc tcc tac tca gaa tcc 1411
Ala Met Glu Val Arg Asp Val Asn Met Asp Phe Ser Tyr Ser Glu Ser
425 430 435

ttc act gaa gaa tca cct gaa gca tac gag cgc ctc att ttg gat gcg 1459
Phe Thr Glu Glu Ser Pro Glu Ala Tyr Glu Arg Leu Ile Leu Asp Ala
440 445 450

ctg tta gat gaa tcc agc ctc ttc cct acc aac gag gaa gtg gaa ctg 1507
Leu Leu Asp Glu Ser Ser Leu Phe Pro Thr Asn Glu Glu Val Glu Leu
455 460 465

agc tgg aag att ctg gat cca att ctt gaa gca tgg gat gcc gat gga 1555
Ser Trp Lys Ile Leu Asp Pro Ile Leu Glu Ala Trp Asp Ala Asp Gly
470 475 480 485

gaa cca gag gat tac cca gcg ggt acg tgg ggt cca aag agc gct gat 1603
Glu Pro Glu Asp Tyr Pro Ala Gly Thr Trp Gly Pro Lys Ser Ala Asp
490 495 500

gaa atg ctt tcc cgc aac ggt cac acc tgg cgc agg cca taatttaggg 1652
Glu Met Leu Ser Arg Asn Gly His Thr Trp Arg Arg Pro
505 510

gcaaaaaatg atc 1665

<210> 244

<211> 514

<212> PRT

<213> Corynebacterium glutamicum

<400> 244

Val Ser Thr Asn Thr Thr Pro Ser Ser Trp Thr Asn Pro Leu Arg Asp
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Pro Gln Asp Lys Arg Leu Pro Arg Ile Ala Gly Pro Ser Gly Met Val
 20 25 30
 Ile Phe Gly Val Thr Gly Asp Leu Ala Arg Lys Lys Leu Leu Pro Ala
 35 40 45
 Ile Tyr Asp Leu Ala Asn Arg Gly Leu Leu Pro Pro Gly Phe Ser Leu
 50 55 60
 Val Gly Tyr Gly Arg Arg Glu Trp Ser Lys Glu Asp Phe Glu Lys Tyr
 65 70 75 80
 Val Arg Asp Ala Ala Ser Ala Gly Ala Arg Thr Glu Phe Arg Glu Asn
 85 90 95
 Val Trp Glu Arg Leu Ala Glu Gly Met Glu Phe Val Arg Gly Asn Phe
 100 105 110
 Asp Asp Asp Ala Ala Phe Asp Asn Leu Ala Ala Thr Leu Lys Arg Ile
 115 120 125
 Asp Lys Thr Arg Gly Thr Ala Gly Asn Trp Ala Tyr Tyr Leu Ser Ile
 130 135 140
 Pro Pro Asp Ser Phe Thr Ala Val Cys His Gln Leu Glu Arg Ser Gly
 145 150 155 160
 Met Ala Glu Ser Thr Glu Glu Ala Trp Arg Arg Val Ile Ile Glu Lys
 165 170 175
 Pro Phe Gly His Asn Leu Glu Ser Ala His Glu Leu Asn Gln Leu Val
 180 185 190
 Asn Ala Val Phe Pro Glu Ser Ser Val Phe Arg Ile Asp His Tyr Leu
 195 200 205
 Gly Lys Glu Thr Val Gln Asn Ile Leu Ala Leu Arg Phe Ala Asn Gln
 210 215 220
 Leu Phe Glu Pro Leu Trp Asn Ser Asn Tyr Val Asp His Val Gln Ile
 225 230 235 240
 Thr Met Ala Glu Asp Ile Gly Leu Gly Gly Arg Ala Gly Tyr Tyr Asp
 245 250 255
 Gly Ile Gly Ala Ala Arg Asp Val Ile Gln Asn His Leu Ile Gln Leu
 260 265 270
 Leu Ala Leu Val Ala Met Glu Glu Pro Ile Ser Phe Val Pro Ala Gln
 275 280 285
 Leu Gln Ala Glu Lys Ile Lys Val Leu Ser Ala Thr Lys Pro Cys Tyr
 290 295 300
 Pro Leu Asp Lys Thr Ser Ala Arg Gly Gln Tyr Ala Ala Gly Trp Gln
 305 310 315 320
 Gly Ser Glu Leu Val Lys Gly Leu Arg Glu Glu Asp Gly Phe Asn Pro
 325 330 335
 Glu Ser Thr Thr Glu Thr Phe Ala Ala Cys Thr Leu Glu Ile Thr Ser

340 345 350
 Arg Arg Trp Ala Gly Val Pro Phe Tyr Leu Arg Thr Gly Lys Arg Leu
 355 360 365
 Gly Arg Arg Val Thr Glu Ile Ala Val Val Phe Lys Asp Ala Pro His
 370 375 380
 Gln Pro Phe Asp Gly Asp Met Thr Val Ser Leu Gly Gln Asn Ala Ile
 385 390 395 400
 Val Ile Arg Val Gln Pro Asp Glu Gly Val Leu Ile Arg Phe Gly Ser
 405 410 415
 Lys Val Pro Gly Ser Ala Met Glu Val Arg Asp Val Asn Met Asp Phe
 420 425 430
 Ser Tyr Ser Glu Ser Phe Thr Glu Glu Ser Pro Glu Ala Tyr Glu Arg
 435 440 445
 Leu Ile Leu Asp Ala Leu Leu Asp Glu Ser Ser Leu Phe Pro Thr Asn
 450 455 460
 Glu Glu Val Glu Leu Ser Trp Lys Ile Leu Asp Pro Ile Leu Glu Ala
 465 470 475 480
 Trp Asp Ala Asp Gly Glu Pro Glu Asp Tyr Pro Ala Gly Thr Trp Gly
 485 490 495
 Pro Lys Ser Ala Asp Glu Met Leu Ser Arg Asn Gly His Thr Trp Arg
 500 505 510

Arg Pro

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 <211> 1203
 <212> DNA
 <213> Corynebacterium glutamicum

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 <222> (101)..(1180)
 <223> RXA02738

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 cacagttcaa gaacaattct ttaaggaaa atttagtttc atg tct cac att gat 115
 Met Ser His Ile Asp
 1 5
 gat ctt gca cag ctg ggc act tcc act tgg ctg gac gac ctg tcc cgc 163
 Asp Leu Ala Gln Leu Gly Thr Ser Thr Trp Leu Asp Asp Leu Ser Arg
 10 15 20
 gag cgc att act tcc ggc aat ctg agc cag gtt att gag gaa aag tct 211
 Glu Arg Ile Thr Ser Gly Asn Leu Ser Gln Val Ile Glu Glu Lys Ser
 25 30 35

gta gtc ggt gtc acc acc aac cca gct att ttc gca gca gca atg tcc	259
Val Val Gly Val Thr Thr Asn Pro Ala Ile Phe Ala Ala Ala Met Ser	
40 45 50	
aag ggc gat tcc tac gac gct cag atc gca gag ctc aag gcc gct ggc	307
Lys Gly Asp Ser Tyr Asp Ala Gln Ile Ala Glu Leu Lys Ala Ala Gly	
55 60 65	
gca tct gtt gac cag gct gtt tac gcc atg agc atc gac gac gtt cgc	355
Ala Ser Val Asp Gln Ala Val Tyr Ala Met Ser Ile Asp Asp Val Arg	
70 75 80 85	
aat gct tgt gat ctg ttc acc ggc atc ttc gag tcc tcc aac ggc tac	403
Asn Ala Cys Asp Leu Phe Thr Gly Ile Phe Glu Ser Ser Asn Gly Tyr	
90 95 100	
gac ggc cgc gtg tcc atc gag gtt gac cca cgt atc tct gct gac cgc	451
Asp Gly Arg Val Ser Ile Glu Val Asp Pro Arg Ile Ser Ala Asp Arg	
105 110 115	
gac gca acc ctg gct cag gcc aag gag ctg tgg gca aag gtt gat cgt	499
Asp Ala Thr Leu Ala Gln Ala Lys Glu Leu Trp Ala Lys Val Asp Arg	
120 125 130	
cca aac gtc atg atc aag atc cct gca acc cca ggt tct ttg cca gca	547
Pro Asn Val Met Ile Lys Ile Pro Ala Thr Pro Gly Ser Leu Pro Ala	
135 140 145	
atc acc gac gct ttg gct gag ggc atc agc gtt aac gtc acc ttg atc	595
Ile Thr Asp Ala Leu Ala Glu Gly Ile Ser Val Asn Val Thr Leu Ile	
150 155 160 165	
ttc tcc gtt gct cgc tac cgc gag gtc atc gct gcg ttc atc gag ggc	643
Phe Ser Val Ala Arg Tyr Arg Glu Val Ile Ala Ala Phe Ile Glu Gly	
170 175 180	
atc aag cag gct gct gca aac ggc cac gac gtc tcc aag atc cac tct	691
Ile Lys Gln Ala Ala Asn Gly His Asp Val Ser Lys Ile His Ser	
185 190 195	
gtg gct tcc ttc ttc gtc tcc cgc gtc gac gtt gag atc gac aag cgc	739
Val Ala Ser Phe Phe Val Ser Arg Val Asp Val Glu Ile Asp Lys Arg	
200 205 210	
ctc gag gca atc gga tcc gat gag gct ttg gct ctg cgc ggc aag gca	787
Leu Glu Ala Ile Gly Ser Asp Glu Ala Leu Ala Arg Gly Lys Ala	
215 220 225	
ggc gtt gcc aac gct cag cgc gct tac gct gtg tac aag gag ctt ttc	835
Gly Val Ala Asn Ala Gln Arg Ala Tyr Ala Val Tyr Lys Glu Leu Phe	
230 235 240 245	
gac gcc gcc gag ctg cct gaa ggt gcc aac act cag cgc cca ctg tgg	883
Asp Ala Ala Glu Leu Pro Glu Gly Ala Asn Thr Gln Arg Pro Leu Trp	
250 255 260	
gca tcc acc ggc gtg aag aac cct gcg tac gct gca act ctt tac gtt	931
Ala Ser Thr Gly Val Lys Asn Pro Ala Tyr Ala Ala Thr Leu Tyr Val	
265 270 275	
tcc gag ctg gct ggt cca aac acc gtc aac acc atg cca gaa ggc acc	979

Ser Glu Leu Ala Gly Pro Asn Thr Val Asn Thr Met Pro Glu Gly Thr
 280 285 290

atc gac gcg gtt ctg gag cag ggc aac ctg cac ggt gac acc ctg tcc 1027
 Ile Asp Ala Val Leu Glu Gln Gly Asn Leu His Gly Asp Thr Leu Ser
 295 300 305

aac tcc gcg gca gaa gct gac gct gtg ttc tcc cag ctt gag gct ctg 1075
 Asn Ser Ala Ala Glu Ala Asp Ala Val Phe Ser Gln Leu Glu Ala Leu
 310 315 320 325

ggc gtt gac ttg gca gat gtc ttc cag gtc ctg gag acc gag ggt gtg 1123
 Gly Val Asp Leu Ala Asp Val Phe Gln Val Leu Glu Thr Glu Gly Val
 330 335 340

gac aag ttc gtt gct tct tgg agc gaa ctg ctt gag tcc atg gaa gct 1171
 Asp Lys Phe Val Ala Ser Trp Ser Glu Leu Leu Glu Ser Met Glu Ala
 345 350 355

cgc ctg aag tagaatcagc acgctgcac agt 1203
 Arg Leu Lys
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<210> 246

<211> 360

<212> PRT

<213> Corynebacterium glutamicum

<400> 246

Met Ser His Ile Asp Asp Leu Ala Gln Leu Gly Thr Ser Thr Trp Leu
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Asp Asp Leu Ser Arg Glu Arg Ile Thr Ser Gly Asn Leu Ser Gln Val
 20 25 30

Ile Glu Glu Lys Ser Val Val Gly Val Thr Thr Asn Pro Ala Ile Phe
 35 40 45

Ala Ala Ala Met Ser Lys Gly Asp Ser Tyr Asp Ala Gln Ile Ala Glu
 50 55 60

Leu Lys Ala Ala Gly Ala Ser Val Asp Gln Ala Val Tyr Ala Met Ser
 65 70 75 80

Ile Asp Asp Val Arg Asn Ala Cys Asp Leu Phe Thr Gly Ile Phe Glu
 85 90 95

Ser Ser Asn Gly Tyr Asp Gly Arg Val Ser Ile Glu Val Asp Pro Arg
 100 105 110

Ile Ser Ala Asp Arg Asp Ala Thr Leu Ala Gln Ala Lys Glu Leu Trp
 115 120 125

Ala Lys Val Asp Arg Pro Asn Val Met Ile Lys Ile Pro Ala Thr Pro
 130 135 140

Gly Ser Leu Pro Ala Ile Thr Asp Ala Leu Ala Glu Gly Ile Ser Val
 145 150 155 160

Asn Val Thr Leu Ile Phe Ser Val Ala Arg Tyr Arg Glu Val Ile Ala

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<212> DNA
<213> Corynebacterium glutamicum
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<222> (101) .. (2200)  
<223> RXA02739
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aacgaaccaa aactttggtc ccggtttaac ccaggaagga ttg acc acc ttg acg 115
Leu Thr Thr Leu Thr
1 5

ctg tca cct gaa ctt cag gcg ctc act gta cgc aat tac ccc tct gat 163
Leu Ser Pro Glu Leu Gln Ala Leu Thr Val Arg Asn Tyr Pro Ser Asp
10 15 20

tgg tcc gat gtg gac acc aag gct gta gac act gtt cgt gtc ctc gct 211

Trp	Ser	Asp	Val	Asp	Thr	Lys	Ala	Val	Asp	Thr	Val	Arg	Val	Leu	Ala	
			25					30					35			
gca	gac	gct	gta	gaa	aac	tgt	ggc	tcc	ggc	cac	cca	ggc	acc	gca	atg	259
Ala	Asp	Ala	Val	Glu	Asn	Cys	Gly	Ser	Gly	His	Pro	Gly	Thr	Ala	Met	
		40					45					50				
agc	ctg	gct	ccc	ctt	gca	tac	acc	ttg	tac	cag	cgg	gtt	atg	aac	gta	307
Ser	Leu	Ala	Pro	Leu	Ala	Tyr	Thr	Leu	Tyr	Gln	Arg	Val	Met	Asn	Val	
	55					60					65					
gat	cca	cag	gac	acc	aac	tgg	gca	ggc	cgt	gac	cgc	ttc	gtt	ctt	tct	355
Asp	Pro	Gln	Asp	Thr	Asn	Trp	Ala	Gly	Arg	Asp	Arg	Phe	Val	Leu	Ser	
70					75					80					85	
tgt	ggc	cac	tcc	tct	ttg	acc	cag	tac	atc	cag	ctt	tac	ttg	ggt	gga	403
Cys	Gly	His	Ser	Ser	Leu	Thr	Gln	Tyr	Ile	Gln	Leu	Tyr	Leu	Gly	Gly	
				90					95					100		
ttc	ggc	ctt	gag	atg	gat	gac	ctg	aag	gct	ctg	cgc	acc	tgg	gat	tcc	451
Phe	Gly	Leu	Glu	Met	Asp	Asp	Leu	Lys	Ala	Leu	Arg	Thr	Trp	Asp	Ser	
			105					110					115			
ttg	acc	cca	gga	cac	cct	gag	tac	cgc	cac	acc	aag	ggc	gtt	gag	atc	499
Leu	Thr	Pro	Gly	His	Pro	Glu	Tyr	Arg	His	Thr	Lys	Gly	Val	Glu	Ile	
		120					125					130				
acc	act	ggc	cct	ctt	ggc	cag	ggt	ctt	gca	tct	gca	gtt	ggt	atg	gcc	547
Thr	Thr	Gly	Pro	Leu	Gly	Gln	Gly	Leu	Ala	Ser	Ala	Val	Gly	Met	Ala	
		135				140					145					
atg	gct	gct	cgt	cgt	gag	cgt	ggc	cta	ttc	gac	cca	acc	gct	gct	gag	595
Met	Ala	Ala	Arg	Arg	Glu	Arg	Gly	Leu	Phe	Asp	Pro	Thr	Ala	Ala	Glu	
150					155					160					165	
ggc	gaa	tcc	cca	ttc	gac	cac	cac	atc	tac	gtc	att	gct	tct	gat	ggt	643
Gly	Glu	Ser	Pro	Phe	Asp	His	His	Ile	Tyr	Val	Ile	Ala	Ser	Asp	Gly	
				170					175					180		
gac	ctg	cag	gaa	ggt	gtc	acc	tct	gag	gca	tcc	tcc	atc	gct	ggc	acc	691
Asp	Leu	Gln	Glu	Gly	Val	Thr	Ser	Glu	Ala	Ser	Ser	Ile	Ala	Gly	Thr	
			185					190					195			
cag	cag	ctg	ggc	aac	ctc	atc	gtg	ttc	tgg	gat	gac	aac	cgc	atc	tcc	739
Gln	Gln	Leu	Gly	Asn	Leu	Ile	Val	Phe	Trp	Asp	Asp	Asn	Arg	Ile	Ser	
		200					205					210				
atc	gaa	gac	aac	act	gag	atc	gct	ttc	aac	gag	gac	gtt	gtt	gct	cgt	787
Ile	Glu	Asp	Asn	Thr	Glu	Ile	Ala	Phe	Asn	Glu	Asp	Val	Val	Ala	Arg	
	215					220					225					
tac	aag	gct	tac	ggc	tgg	cag	acc	att	gag	gtt	gag	gct	ggc	gag	gac	835
Tyr	Lys	Ala	Tyr	Gly	Trp	Gln	Thr	Ile	Glu	Val	Glu	Ala	Gly	Glu	Asp	
230					235					240				245		
gtt	gca	gca	atc	gaa	gct	gca	gtg	gct	gag	gct	aag	aag	gac	acc	aag	883
Val	Ala	Ala	Ile	Glu	Ala	Ala	Val	Ala	Glu	Ala	Lys	Lys	Asp	Thr	Lys	
				250					255					260		
cga	cct	acc	ttc	atc	cgc	gtt	cgc	acc	atc	atc	ggc	ttc	cca	gct	cca	931
Arg	Pro	Thr	Phe	Ile	Arg	Val	Arg	Thr	Ile	Ile	Gly	Phe	Pro	Ala	Pro	

			265						270						275						
act	atg	atg	aac	acc	ggc	gct	gtg	cac	ggc	gct	gct	ctt	ggc	gca	gct	979					
Thr	Met	Met	Asn	Thr	Gly	Ala	Val	His	Gly	Ala	Ala	Leu	Gly	Ala	Ala						
		280					285					290									
gag	gtt	gca	gca	acc	aag	act	gag	ctt	gga	ttc	gat	cct	gag	gct	cac	1027					
Glu	Val	Ala	Ala	Thr	Lys	Thr	Glu	Leu	Gly	Phe	Asp	Pro	Glu	Ala	His						
	295					300					305										
ttc	gcg	atc	gac	gat	gag	gtt	atc	gct	cac	acc	cgc	tcc	ctc	gca	gag	1075					
Phe	Ala	Ile	Asp	Asp	Glu	Val	Ile	Ala	His	Thr	Arg	Ser	Leu	Ala	Glu						
310					315					320					325						
cgc	gct	gca	cag	aag	aag	gct	gca	tgg	cag	gtc	aag	ttc	gat	gag	tgg	1123					
Arg	Ala	Ala	Gln	Lys	Lys	Ala	Ala	Trp	Gln	Val	Lys	Phe	Asp	Glu	Trp						
				330					335					340							
gca	gct	gcc	aac	cct	gag	aac	aag	gct	ctg	ttc	gat	cgc	ctg	aac	tcc	1171					
Ala	Ala	Ala	Asn	Pro	Glu	Asn	Lys	Ala	Leu	Phe	Asp	Arg	Leu	Asn	Ser						
			345					350					355								
cgt	gag	ctt	cca	gcg	ggc	tac	gct	gac	gag	ctc	cca	aca	tgg	gat	gca	1219					
Arg	Glu	Leu	Pro	Ala	Gly	Tyr	Ala	Asp	Glu	Leu	Pro	Thr	Trp	Asp	Ala						
		360					365					370									
gat	gag	aag	ggc	gtc	gca	act	cgt	aag	gct	tcc	gag	gct	gca	ctt	cag	1267					
Asp	Glu	Lys	Gly	Val	Ala	Thr	Arg	Lys	Ala	Ser	Glu	Ala	Ala	Leu	Gln						
	375					380					385										
gca	ctg	ggc	aag	acc	ctt	cct	gag	ctg	tgg	ggc	ggt	tcc	gct	gac	ctc	1315					
Ala	Leu	Gly	Lys	Thr	Leu	Pro	Glu	Leu	Trp	Gly	Gly	Ser	Ala	Asp	Leu						
390					395					400					405						
gca	ggt	tcc	aac	aac	acc	gtg	atc	aag	ggc	tcc	cct	tcc	ttc	ggc	cct	1363					
Ala	Gly	Ser	Asn	Asn	Thr	Val	Ile	Lys	Gly	Ser	Pro	Ser	Phe	Gly	Pro						
				410					415					420							
gag	tcc	atc	tcc	acc	gag	acc	tgg	tct	gct	gag	cct	tac	ggc	cgt	aac	1411					
Glu	Ser	Ile	Ser	Thr	Glu	Thr	Trp	Ser	Ala	Glu	Pro	Tyr	Gly	Arg	Asn						
			425					430					435								
ctg	cac	ttc	ggc	atc	cgt	gag	cac	gct	atg	gga	tcc	atc	ctc	aac	ggc	1459					
Leu	His	Phe	Gly	Ile	Arg	Glu	His	Ala	Met	Gly	Ser	Ile	Leu	Asn	Gly						
		440					445					450									
att	tcc	ctc	cac	ggc	ggc	acc	cgc	cca	tac	ggc	gga	acc	ttc	ctc	atc	1507					
Ile	Ser	Leu	His	Gly	Gly	Thr	Arg	Pro	Tyr	Gly	Gly	Thr	Phe	Leu	Ile						
	455					460					465										
ttc	tcc	gac	tac	atg	cgt	cct	gca	gtt	cgt	ctt	gca	gct	ctc	atg	gag	1555					
Phe	Ser	Asp	Tyr	Met	Arg	Pro	Ala	Val	Arg	Leu	Ala	Ala	Leu	Met	Glu						
470					475					480											

atc cca ggt ctg tcc gtc ctg cgt cct gca gat gcg aac gag acc gcc 1699
 Ile Pro Gly Leu Ser Val Leu Arg Pro Ala Asp Ala Asn Glu Thr Ala
 520 525 530

cag gct tgg gct gca gca ctt gag tac aag gaa ggc cct aag ggt ctt 1747
 Gln Ala Trp Ala Ala Ala Leu Glu Tyr Lys Glu Gly Pro Lys Gly Leu
 535 540 545

gca ctg acc cgc cag aac gtt cct gtt ctg gaa ggc acc aag gag aag 1795
 Ala Leu Thr Arg Gln Asn Val Pro Val Leu Glu Gly Thr Lys Glu Lys
 550 555 560 565

gct gct gaa ggc gtt cgc cgc ggt ggc tac gtc ctg gtt gag ggt tcc 1843
 Ala Ala Glu Gly Val Arg Arg Gly Gly Tyr Val Leu Val Glu Gly Ser
 570 575 580

aag gaa acc cca gat gtg atc ctc atg ggc tcc ggc tcc gag gtt cag 1891
 Lys Glu Thr Pro Asp Val Ile Leu Met Gly Ser Gly Ser Glu Val Gln
 585 590 595

ctt gca gtt aac gct gcg aag gct ctg gaa gct gag ggc gtt gca gct 1939
 Leu Ala Val Asn Ala Ala Lys Ala Leu Glu Ala Glu Gly Val Ala Ala
 600 605 610

cgc gtt gtt tcc gtt cct tgc atg gat tgg ttc cag gag cag gac gca 1987
 Arg Val Val Ser Val Pro Cys Met Asp Trp Phe Gln Glu Gln Asp Ala
 615 620 625

gag tac atc gag tcc gtt ctg cct gca gct gtg acc gct cgt gtg tct 2035
 Glu Tyr Ile Glu Ser Val Leu Pro Ala Ala Val Thr Ala Arg Val Ser
 630 635 640 645

gtt gaa gct ggc atc gca atg cct tgg tac cgc ttc ttg ggc acc cag 2083
 Val Glu Ala Gly Ile Ala Met Pro Trp Tyr Arg Phe Leu Gly Thr Gln
 650 655 660

ggc cgt gct gtc tcc ctt gag cac ttc ggt gct tct gcg gat tac cag 2131
 Gly Arg Ala Val Ser Leu Glu His Phe Gly Ala Ser Ala Asp Tyr Gln
 665 670 675

acc ctg ttt gag aag ttc ggc atc acc acc gat gca gtc gtg gca gcg 2179
 Thr Leu Phe Glu Lys Phe Gly Ile Thr Thr Asp Ala Val Val Ala Ala
 680 685 690

gcc aag gac tcc att aac ggt taattgccct gctgttttta gct 2223
 Ala Lys Asp Ser Ile Asn Gly
 695 700

<210> 248

<211> 700

<212> PRT

<213> Corynebacterium glutamicum

<400> 248

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Asn Tyr Pro Ser Asp Trp Ser Asp Val Asp Thr Lys Ala Val Asp Thr
 20 25 30

Val Arg Val Leu Ala Ala Asp Ala Val Glu Asn Cys Gly Ser Gly His
 35 40 45
 Pro Gly Thr Ala Met Ser Leu Ala Pro Leu Ala Tyr Thr Leu Tyr Gln
 50 55 60
 Arg Val Met Asn Val Asp Pro Gln Asp Thr Asn Trp Ala Gly Arg Asp
 65 70 75 80
 Arg Phe Val Leu Ser Cys Gly His Ser Ser Leu Thr Gln Tyr Ile Gln
 85 90 95
 Leu Tyr Leu Gly Gly Phe Gly Leu Glu Met Asp Asp Leu Lys Ala Leu
 100 105 110
 Arg Thr Trp Asp Ser Leu Thr Pro Gly His Pro Glu Tyr Arg His Thr
 115 120 125
 Lys Gly Val Glu Ile Thr Thr Gly Pro Leu Gly Gln Gly Leu Ala Ser
 130 135 140
 Ala Val Gly Met Ala Met Ala Ala Arg Arg Glu Arg Gly Leu Phe Asp
 145 150 155 160
 Pro Thr Ala Ala Glu Gly Glu Ser Pro Phe Asp His His Ile Tyr Val
 165 170 175
 Ile Ala Ser Asp Gly Asp Leu Gln Glu Gly Val Thr Ser Glu Ala Ser
 180 185 190
 Ser Ile Ala Gly Thr Gln Gln Leu Gly Asn Leu Ile Val Phe Trp Asp
 195 200 205
 Asp Asn Arg Ile Ser Ile Glu Asp Asn Thr Glu Ile Ala Phe Asn Glu
 210 215 220
 Asp Val Val Ala Arg Tyr Lys Ala Tyr Gly Trp Gln Thr Ile Glu Val
 225 230 235 240
 Glu Ala Gly Glu Asp Val Ala Ala Ile Glu Ala Ala Val Ala Glu Ala
 245 250 255
 Lys Lys Asp Thr Lys Arg Pro Thr Phe Ile Arg Val Arg Thr Ile Ile
 260 265 270
 Gly Phe Pro Ala Pro Thr Met Met Asn Thr Gly Ala Val His Gly Ala
 275 280 285
 Ala Leu Gly Ala Ala Glu Val Ala Ala Thr Lys Thr Glu Leu Gly Phe
 290 295 300
 Asp Pro Glu Ala His Phe Ala Ile Asp Asp Glu Val Ile Ala His Thr
 305 310 315 320
 Arg Ser Leu Ala Glu Arg Ala Ala Gln Lys Lys Ala Ala Trp Gln Val
 325 330 335
 Lys Phe Asp Glu Trp Ala Ala Ala Asn Pro Glu Asn Lys Ala Leu Phe
 340 345 350

Asp Arg Leu Asn Ser Arg Glu Leu Pro Ala Gly Tyr Ala Asp Glu Leu
 355 360 365
 Pro Thr Trp Asp Ala Asp Glu Lys Gly Val Ala Thr Arg Lys Ala Ser
 370 375 380
 Glu Ala Ala Leu Gln Ala Leu Gly Lys Thr Leu Pro Glu Leu Trp Gly
 385 390 395 400
 Gly Ser Ala Asp Leu Ala Gly Ser Asn Asn Thr Val Ile Lys Gly Ser
 405 410 415
 Pro Ser Phe Gly Pro Glu Ser Ile Ser Thr Glu Thr Trp Ser Ala Glu
 420 425 430
 Pro Tyr Gly Arg Asn Leu His Phe Gly Ile Arg Glu His Ala Met Gly
 435 440 445
 Ser Ile Leu Asn Gly Ile Ser Leu His Gly Gly Thr Arg Pro Tyr Gly
 450 455 460
 Gly Thr Phe Leu Ile Phe Ser Asp Tyr Met Arg Pro Ala Val Arg Leu
 465 470 475 480
 Ala Ala Leu Met Glu Thr Asp Ala Tyr Tyr Val Trp Thr His Asp Ser
 485 490 495
 Ile Gly Leu Gly Glu Asp Gly Pro Thr His Gln Pro Val Glu Thr Leu
 500 505 510
 Ala Ala Leu Arg Ala Ile Pro Gly Leu Ser Val Leu Arg Pro Ala Asp
 515 520 525
 Ala Asn Glu Thr Ala Gln Ala Trp Ala Ala Ala Leu Glu Tyr Lys Glu
 530 535 540
 Gly Pro Lys Gly Leu Ala Leu Thr Arg Gln Asn Val Pro Val Leu Glu
 545 550 555 560
 Gly Thr Lys Glu Lys Ala Ala Glu Gly Val Arg Arg Gly Gly Tyr Val
 565 570 575
 Leu Val Glu Gly Ser Lys Glu Thr Pro Asp Val Ile Leu Met Gly Ser
 580 585 590
 Gly Ser Glu Val Gln Leu Ala Val Asn Ala Ala Lys Ala Leu Glu Ala
 595 600 605
 Glu Gly Val Ala Ala Arg Val Val Ser Val Pro Cys Met Asp Trp Phe
 610 615 620
 Gln Glu Gln Asp Ala Glu Tyr Ile Glu Ser Val Leu Pro Ala Ala Val
 625 630 635 640
 Thr Ala Arg Val Ser Val Glu Ala Gly Ile Ala Met Pro Trp Tyr Arg
 645 650 655
 Phe Leu Gly Thr Gln Gly Arg Ala Val Ser Leu Glu His Phe Gly Ala
 660 665 670
 Ser Ala Asp Tyr Gln Thr Leu Phe Glu Lys Phe Gly Ile Thr Thr Asp

675	680	685	
Ala Val Val Ala Ala Ala	Lys Asp Ser Ile Asn Gly		
690	695	700	
<p><210> 249 <211> 793 <212> DNA <213> Corynebacterium glutamicum</p> <p><220> <221> CDS <222> (48)..(770) <223> RXA00965</p> <p><400> 249 agattgcggg cctcggcttc attgaaaaca agacggtgtt tgaataaatg aca act 56 <div style="text-align: right;">Met Thr Thr 1</div></p> <p>ttc cac gat ctt ccg ctg gag gag cgg ctg aca ctg gcc agg ttg ggc 104 Phe His Asp Leu Pro Leu Glu Glu Arg Leu Thr Leu Ala Arg Leu Gly <div style="display: flex; justify-content: space-around;"><div>5</div><div>10</div><div>15</div></div></p> <p>aca tcc cac tac tcc cgt cag ctc tcc ctc gtg gac aac gct gag ttc 152 Thr Ser His Tyr Ser Arg Gln Leu Ser Leu Val Asp Asn Ala Glu Phe <div style="display: flex; justify-content: space-around;"><div>20</div><div>25</div><div>30</div><div>35</div></div></p> <p>ggc gag cat tcc ctg cta gaa ggg tgg act cgt tcc cac ctc att gcc 200 Gly Glu His Ser Leu Leu Glu Gly Trp Thr Arg Ser His Leu Ile Ala <div style="display: flex; justify-content: space-around;"><div>40</div><div>45</div><div>50</div></div></p> <p>cac gtg gca tac aac gcc atc gca ctg tgc aac ctc atg cac tgg gca 248 His Val Ala Tyr Asn Ala Ile Ala Leu Cys Asn Leu Met His Trp Ala <div style="display: flex; justify-content: space-around;"><div>55</div><div>60</div><div>65</div></div></p> <p>aat act ggt gag gaa acc cca atg tac gtg tgc cca gaa gcg cgc aac 296 Asn Thr Gly Glu Glu Thr Pro Met Tyr Val Ser Pro Glu Ala Arg Asn <div style="display: flex; justify-content: space-around;"><div>70</div><div>75</div><div>80</div></div></p> <p>gag gaa att gcc tac ggt tcc acg ctc aat ccc gat gcg ttg cgt aac 344 Glu Glu Ile Ala Tyr Gly Ser Thr Leu Asn Pro Asp Ala Leu Arg Asn <div style="display: flex; justify-content: space-around;"><div>85</div><div>90</div><div>95</div></div></p> <p>ctg cat gaa cac tcc gtc gca cgc ctg gac gtg gct tgg cgt gaa acg 392 Leu His Glu His Ser Val Ala Arg Leu Asp Val Ala Trp Arg Glu Thr <div style="display: flex; justify-content: space-around;"><div>100</div><div>105</div><div>110</div><div>115</div></div></p> <p>tct gaa gat gct tgg tca cac gag gtt ctg aca gct cag gga cgc act 440 Ser Glu Asp Ala Trp Ser His Glu Val Leu Thr Ala Gln Gly Arg Thr <div style="display: flex; justify-content: space-around;"><div>120</div><div>125</div><div>130</div></div></p> <p>gtc cca gct agt gaa aca ttg tgg atg cgt tcc cgc gaa gtc tgg atc 488 Val Pro Ala Ser Glu Thr Leu Trp Met Arg Ser Arg Glu Val Trp Ile <div style="display: flex; justify-content: space-around;"><div>135</div><div>140</div><div>145</div></div></p> <p>cac gca gtt gac ctc ggt gca gtg gca acc ttt ggc gac atc cca gag 536 His Ala Val Asp Leu Gly Ala Val Ala Thr Phe Gly Asp Ile Pro Glu <div style="display: flex; justify-content: space-around;"><div>150</div><div>155</div><div>160</div></div></p>			

gtc atc ctg cgc acc tta gct gca gaa atc aca caa aag tgg aca agc 584
 Val Ile Leu Arg Thr Leu Ala Ala Glu Ile Thr Gln Lys Trp Thr Ser
 165 170 175

 caa gga gcc ggc gag gga ctt gtg ctt ctc gac gag ccc tcc agc act 632
 Gln Gly Ala Gly Glu Gly Leu Val Leu Leu Asp Glu Pro Ser Ser Thr
 180 185 190 195

 cgc tac ccc gcc gcc cca ggg cag gac gag gta gta gtg tcc ggt agc 680
 Arg Tyr Pro Ala Ala Pro Gly Gln Asp Glu Val Val Val Ser Gly Ser
 200 205 210

 ctt gca ggc att gtt cgc tac gcc gct ggc cgc ggt tcc gat gga gtc 728
 Leu Ala Gly Ile Val Arg Tyr Ala Ala Gly Arg Gly Ser Asp Gly Val
 215 220 225

 act tct tcc act gga gag gtt cca gag cca ccg cgc tgg ctg 770
 Thr Ser Ser Thr Gly Glu Val Pro Glu Pro Pro Arg Trp Leu
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 tagtttccac acattcttaa atg 793

<210> 250

<211> 241

<212> PRT

<213> Corynebacterium glutamicum

<400> 250

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 Arg Leu Gly Thr Ser His Tyr Ser Arg Gln Leu Ser Leu Val Asp Asn
 20 25 30

 Ala Glu Phe Gly Glu His Ser Leu Leu Glu Gly Trp Thr Arg Ser His
 35 40 45

 Leu Ile Ala His Val Ala Tyr Asn Ala Ile Ala Leu Cys Asn Leu Met
 50 55 60

 His Trp Ala Asn Thr Gly Glu Glu Thr Pro Met Tyr Val Ser Pro Glu
 65 70 75 80

 Ala Arg Asn Glu Glu Ile Ala Tyr Gly Ser Thr Leu Asn Pro Asp Ala
 85 90 95

 Leu Arg Asn Leu His Glu His Ser Val Ala Arg Leu Asp Val Ala Trp
 100 105 110

 Arg Glu Thr Ser Glu Asp Ala Trp Ser His Glu Val Leu Thr Ala Gln
 115 120 125

 Gly Arg Thr Val Pro Ala Ser Glu Thr Leu Trp Met Arg Ser Arg Glu
 130 135 140

 Val Trp Ile His Ala Val Asp Leu Gly Ala Val Ala Thr Phe Gly Asp
 145 150 155 160

 Ile Pro Glu Val Ile Leu Arg Thr Leu Ala Ala Glu Ile Thr Gln Lys
 165 170 175

Trp Thr Ser Gln Gly Ala Gly Glu Gly Leu Val Leu Leu Asp Glu Pro
 180 185 190
 Ser Ser Thr Arg Tyr Pro Ala Ala Pro Gly Gln Asp Glu Val Val Val
 195 200 205
 Ser Gly Ser Leu Ala Gly Ile Val Arg Tyr Ala Ala Gly Arg Gly Ser
 210 215 220
 Asp Gly Val Thr Ser Ser Thr Gly Glu Val Pro Glu Pro Pro Arg Trp
 225 230 235 240
 Leu

<210> 251
 <211> 1575
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(1552)
 <223> RXN00999

<400> 251
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 ttgctgacac cgggctatgc cgtcaagtac gatcaataac atg act aat gga gat 115
 Met Thr Asn Gly Asp
 1 5
 aat ctc gca cag atc ggc gtt gta ggc cta gca gta atg ggc tca aac 163
 Asn Leu Ala Gln Ile Gly Val Val Gly Leu Ala Val Met Gly Ser Asn
 10 15 20
 ctc gcc cgc aac ttc gcc cgc aac ggc aac act gtc gct gtc tac aac 211
 Leu Ala Arg Asn Phe Ala Arg Asn Gly Asn Thr Val Ala Val Tyr Asn
 25 30 35
 cgc agc act gac aaa acc gac aag ctc atc gcc gat cac ggc tcc gaa 259
 Arg Ser Thr Asp Lys Thr Asp Lys Leu Ile Ala Asp His Gly Ser Glu
 40 45 50
 ggc aac ttc atc cct tct gca acc gtc gaa gag ttc gta gca tcc ctg 307
 Gly Asn Phe Ile Pro Ser Ala Thr Val Glu Glu Phe Val Ala Ser Leu
 55 60 65
 gaa aag cca cgc cgc gcc atc atc atg gtt cag gct ggt aac gcc acc 355
 Glu Lys Pro Arg Arg Ala Ile Ile Met Val Gln Ala Gly Asn Ala Thr
 70 75 80 85
 gac gca gtc atc aac cag ctg gca gat gcc atg gac gaa ggc gac atc 403
 Asp Ala Val Ile Asn Gln Leu Ala Asp Ala Met Asp Glu Gly Asp Ile
 90 95 100
 atc atc gac ggc ggc aac gcc ctc tac acc gac acc att cgt cgc gag 451
 Ile Ile Asp Gly Gly Asn Ala Leu Tyr Thr Asp Thr Ile Arg Arg Glu
 105 110 115

aag gaa atc tcc gca cgc ggt ctc cac ttc gtc ggt gct ggt atc tcc	499
Lys Glu Ile Ser Ala Arg Gly Leu His Phe Val Gly Ala Gly Ile Ser	
120 125 130	
ggc ggc gaa gaa ggc gca ctc aac ggc cca tcc atc atg cct ggt ggc	547
Gly Gly Glu Glu Gly Ala Leu Asn Gly Pro Ser Ile Met Pro Gly Gly	
135 140 145	
cca gca aag tcc tac gag tcc ctc gga cca ctg ctt gag tcc atc gct	595
Pro Ala Lys Ser Tyr Glu Ser Leu Gly Pro Leu Leu Glu Ser Ile Ala	
150 155 160 165	
gcc aac gtt gac ggc acc cca tgt gtc acc cac atc ggc cca gac ggc	643
Ala Asn Val Asp Gly Thr Pro Cys Val Thr His Ile Gly Pro Asp Gly	
170 175 180	
gcc ggc cac ttc gtc aag atg gtc cac aac ggc atc gag tac gcc gac	691
Ala Gly His Phe Val Lys Met Val His Asn Gly Ile Glu Tyr Ala Asp	
185 190 195	
atg cag gtc atc ggc gag gca tac cac ctt ctc cgc tac gca gca ggc	739
Met Gln Val Ile Gly Glu Ala Tyr His Leu Leu Arg Tyr Ala Ala Gly	
200 205 210	
atg cag cca gct gaa atc gct gag gtt ttc aag gaa tgg aac gca ggc	787
Met Gln Pro Ala Glu Ile Ala Glu Val Phe Lys Glu Trp Asn Ala Gly	
215 220 225	
gac ctg gat tcc tac ctc atc gaa atc acc gca gag gtt ctc tcc cag	835
Asp Leu Asp Ser Tyr Leu Ile Glu Ile Thr Ala Glu Val Leu Ser Gln	
230 235 240 245	
gtg gat gct gaa acc ggc aag cca cta atc gac gtc atc gtt gac gct	883
Val Asp Ala Glu Thr Gly Lys Pro Leu Ile Asp Val Ile Val Asp Ala	
250 255 260	
gca ggt cag aag ggc acc gga cgt tgg acc gtc aag gct gct ctt gat	931
Ala Gly Gln Lys Gly Thr Gly Arg Trp Thr Val Lys Ala Ala Leu Asp	
265 270 275	
ctg ggt att gct acc acc ggc atc ggc gaa gct gtt ttc gca cgt gca	979
Leu Gly Ile Ala Thr Thr Gly Ile Gly Glu Ala Val Phe Ala Arg Ala	
280 285 290	
ctc tcc ggc gca acc agc cag cgc gct gca gca cag ggc aac cta cct	1027
Leu Ser Gly Ala Thr Ser Gln Arg Ala Ala Ala Gln Gly Asn Leu Pro	
295 300 305	
gca ggt gtc ctc acc gat ctg gaa gca ctt ggc gtg gac aag gca cag	1075
Ala Gly Val Leu Thr Asp Leu Glu Ala Leu Gly Val Asp Lys Ala Gln	
310 315 320 325	
ttc gtc gaa gac gtt cgc cgt gca ctg tac gca tcc aag ctt gtt gct	1123
Phe Val Glu Asp Val Arg Arg Ala Leu Tyr Ala Ser Lys Leu Val Ala	
330 335 340	
tac gca cag ggc ttc gac gag atc aag gct ggc tcc gac gag aac aac	1171
Tyr Ala Gln Gly Phe Asp Glu Ile Lys Ala Gly Ser Asp Glu Asn Asn	
345 350 355	

tgg gac gtt gac cct cgc gac ctc gct acc atc tgg cgc ggc ggc tgc 1219
 Trp Asp Val Asp Pro Arg Asp Leu Ala Thr Ile Trp Arg Gly Gly Cys
 360 365 370

 atc att cgc gct aag ttc ctc aac cgc atc gtc gaa gca tac gat gca 1267
 Ile Ile Arg Ala Lys Phe Leu Asn Arg Ile Val Glu Ala Tyr Asp Ala
 375 380 385

 aac gct gaa ctt gag tcc ctg ctg ctc gat cct tac ttc aag agc gag 1315
 Asn Ala Glu Leu Glu Ser Leu Leu Leu Asp Pro Tyr Phe Lys Ser Glu
 390 395 400 405

 ctc ggc gac ctc atc gat tca tgg cgt cgc gtg att gtc acc gcc acc 1363
 Leu Gly Asp Leu Ile Asp Ser Trp Arg Arg Val Ile Val Thr Ala Thr
 410 415 420

 cag ctt ggc ctg cca atc cca gtg ttc gct tcc tcc ctg tcc tac tac 1411
 Gln Leu Gly Leu Pro Ile Pro Val Phe Ala Ser Ser Leu Ser Tyr Tyr
 425 430 435

 gac agc ctg cgt gca gag cgt ctg cca gca gcc ctg atc caa gga cag 1459
 Asp Ser Leu Arg Ala Glu Arg Leu Pro Ala Ala Leu Ile Gln Gly Gln
 440 445 450

 cgc gac ttc ttc ggt gcg cac acc tac aag cgc atc gac aag gat ggc 1507
 Arg Asp Phe Phe Gly Ala His Thr Tyr Lys Arg Ile Asp Lys Asp Gly
 455 460 465

 tcc ttc cac acc gag tgg tcc ggc gac cgc tcc gag gtt gaa gct 1552
 Ser Phe His Thr Glu Trp Ser Gly Asp Arg Ser Glu Val Glu Ala
 470 475 480

 taaaggctct ccttttaaca caa 1575

<210> 252

<211> 484

<212> PRT

<213> Corynebacterium glutamicum

<400> 252

Met Thr Asn Gly Asp Asn Leu Ala Gln Ile Gly Val Val Gly Leu Ala
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Val Met Gly Ser Asn Leu Ala Arg Asn Phe Ala Arg Asn Gly Asn Thr
 20 25 30

Val Ala Val Tyr Asn Arg Ser Thr Asp Lys Thr Asp Lys Leu Ile Ala
 35 40 45

Asp His Gly Ser Glu Gly Asn Phe Ile Pro Ser Ala Thr Val Glu Glu
 50 55 60

Phe Val Ala Ser Leu Glu Lys Pro Arg Arg Ala Ile Ile Met Val Gln
 65 70 75 80

Ala Gly Asn Ala Thr Asp Ala Val Ile Asn Gln Leu Ala Asp Ala Met
 85 90 95

Asp Glu Gly Asp Ile Ile Ile Asp Gly Gly Asn Ala Leu Tyr Thr Asp
 100 105 110

Thr Ile Arg Arg Glu Lys Glu Ile Ser Ala Arg Gly Leu His Phe Val
 115 120 125
 Gly Ala Gly Ile Ser Gly Gly Glu Glu Gly Ala Leu Asn Gly Pro Ser
 130 135 140
 Ile Met Pro Gly Gly Pro Ala Lys Ser Tyr Glu Ser Leu Gly Pro Leu
 145 150 155 160
 Leu Glu Ser Ile Ala Ala Asn Val Asp Gly Thr Pro Cys Val Thr His
 165 170 175
 Ile Gly Pro Asp Gly Ala Gly His Phe Val Lys Met Val His Asn Gly
 180 185 190
 Ile Glu Tyr Ala Asp Met Gln Val Ile Gly Glu Ala Tyr His Leu Leu
 195 200 205
 Arg Tyr Ala Ala Gly Met Gln Pro Ala Glu Ile Ala Glu Val Phe Lys
 210 215 220
 Glu Trp Asn Ala Gly Asp Leu Asp Ser Tyr Leu Ile Glu Ile Thr Ala
 225 230 235 240
 Glu Val Leu Ser Gln Val Asp Ala Glu Thr Gly Lys Pro Leu Ile Asp
 245 250 255
 Val Ile Val Asp Ala Ala Gly Gln Lys Gly Thr Gly Arg Trp Thr Val
 260 265 270
 Lys Ala Ala Leu Asp Leu Gly Ile Ala Thr Thr Gly Ile Gly Glu Ala
 275 280 285
 Val Phe Ala Arg Ala Leu Ser Gly Ala Thr Ser Gln Arg Ala Ala Ala
 290 295 300
 Gln Gly Asn Leu Pro Ala Gly Val Leu Thr Asp Leu Glu Ala Leu Gly
 305 310 315 320
 Val Asp Lys Ala Gln Phe Val Glu Asp Val Arg Arg Ala Leu Tyr Ala
 325 330 335
 Ser Lys Leu Val Ala Tyr Ala Gln Gly Phe Asp Glu Ile Lys Ala Gly
 340 345 350
 Ser Asp Glu Asn Asn Trp Asp Val Asp Pro Arg Asp Leu Ala Thr Ile
 355 360 365
 Trp Arg Gly Gly Cys Ile Ile Arg Ala Lys Phe Leu Asn Arg Ile Val
 370 375 380
 Glu Ala Tyr Asp Ala Asn Ala Glu Leu Glu Ser Leu Leu Leu Asp Pro
 385 390 395 400
 Tyr Phe Lys Ser Glu Leu Gly Asp Leu Ile Asp Ser Trp Arg Arg Val
 405 410 415
 Ile Val Thr Ala Thr Gln Leu Gly Leu Pro Ile Pro Val Phe Ala Ser
 420 425 430

Ser Leu Ser Tyr Tyr Asp Ser Leu Arg Ala Glu Arg Leu Pro Ala Ala
 435 440 445

Leu Ile Gln Gly Gln Arg Asp Phe Phe Gly Ala His Thr Tyr Lys Arg
 450 455 460

Ile Asp Lys Asp Gly Ser Phe His Thr Glu Trp Ser Gly Asp Arg Ser
 465 470 475 480

Glu Val Glu Ala

<210> 253
 <211> 1537
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(1537)
 <223> FRXA00999

<400> 253
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ttgctgacac cgggctatgc cgtcaagtac gatcaataac atg act aat gga gat 115
 Met Thr Asn Gly Asp
 1 5

aat ctc gca cag atc ggc gtt gta ggc cta gca gta atg ggc tca aac 163
 Asn Leu Ala Gln Ile Gly Val Val Gly Leu Ala Val Met Gly Ser Asn
 10 15 20

ctc gcc cgc aac ttc gcc cgc aac ggc aac act gtc gct gtc tac aac 211
 Leu Ala Arg Asn Phe Ala Arg Asn Gly Asn Thr Val Ala Val Tyr Asn
 25 30 35

cgc agc act gac aaa acc gac aag ctc atc gcc gat cac ggc tcc gaa 259
 Arg Ser Thr Asp Lys Thr Asp Lys Leu Ile Ala Asp His Gly Ser Glu
 40 45 50

ggc aac ttc atc cct tct gca acc gtc gaa gag ttc gta gca tcc ctg 307
 Gly Asn Phe Ile Pro Ser Ala Thr Val Glu Glu Phe Val Ala Ser Leu
 55 60 65

gaa aag cca cgc cgc gcc atc atc atg gtt cag gct ggt aac gcc acc 355
 Glu Lys Pro Arg Arg Ala Ile Ile Met Val Gln Ala Gly Asn Ala Thr
 70 75 80 85

gac gca gtc atc aac cag ctg gca gat gcc atg gac gaa ggc gac atc 403
 Asp Ala Val Ile Asn Gln Leu Ala Asp Ala Met Asp Glu Gly Asp Ile
 90 95 100

atc atc gac ggc ggc aac gcc ctc tac acc gac acc att cgt cgc gag 451
 Ile Ile Asp Gly Gly Asn Ala Leu Tyr Thr Asp Thr Ile Arg Arg Glu
 105 110 115

aag gaa atc tcc gca cgc ggt ctc cac ttc gtc ggt gct ggt atc tcc 499
 Lys Glu Ile Ser Ala Arg Gly Leu His Phe Val Gly Ala Gly Ile Ser
 120 125 130

ggc ggc gaa gaa ggc gca ctc aac ggc cca tcc atc atg cct ggt ggc	547
Gly Gly Glu Glu Gly Ala Leu Asn Gly Pro Ser Ile Met Pro Gly Gly	
135 140 145	
cca gca aag tcc tac gag tcc ctc gga cca ctg ctt gag tcc atc gct	595
Pro Ala Lys Ser Tyr Glu Ser Leu Gly Pro Leu Leu Glu Ser Ile Ala	
150 155 160 165	
gcc aac gtt gac ggc acc cca tgt gtc acc cac atc ggc cca gac ggc	643
Ala Asn Val Asp Gly Thr Pro Cys Val Thr His Ile Gly Pro Asp Gly	
170 175 180	
gcc ggc cac ttc gtc aag atg gtc cac aac ggc atc gag tac gcc gac	691
Ala Gly His Phe Val Lys Met Val His Asn Gly Ile Glu Tyr Ala Asp	
185 190 195	
atg cag gtc atc ggc gag gca tac cac ctt ctc cgc tac gca gca ggc	739
Met Gln Val Ile Gly Glu Ala Tyr His Leu Leu Arg Tyr Ala Ala Gly	
200 205 210	
atg cag cca gct gaa atc gct gag gtt ttc aag gaa tgg aac gca ggc	787
Met Gln Pro Ala Glu Ile Ala Glu Val Phe Lys Glu Trp Asn Ala Gly	
215 220 225	
gac ctg gat tcc tac ctc atc gaa atc acc gca gag gtt ctc tcc cag	835
Asp Leu Asp Ser Tyr Leu Ile Glu Ile Thr Ala Glu Val Leu Ser Gln	
230 235 240 245	
gtg gat gct gaa acc ggc aag cca cta atc gac gtc atc gtt gac gct	883
Val Asp Ala Glu Thr Gly Lys Pro Leu Ile Asp Val Ile Val Asp Ala	
250 255 260	
gca ggt cag aag ggc acc gga cgt tgg acc gtc aag gct gct ctt gat	931
Ala Gly Gln Lys Gly Thr Gly Arg Trp Thr Val Lys Ala Ala Leu Asp	
265 270 275	
ctg ggt att gct acc acc ggc atc ggc gaa gct gtt ttc gca cgt gca	979
Leu Gly Ile Ala Thr Thr Gly Ile Gly Glu Ala Val Phe Ala Arg Ala	
280 285 290	
ctc tcc ggc gca acc agc cag cgc gct gca gca cag ggc aac cta cct	1027
Leu Ser Gly Ala Thr Ser Gln Arg Ala Ala Ala Gln Gly Asn Leu Pro	
295 300 305	
gca ggt gtc ctc acc gat ctg gaa gca ctt ggc gtg gac aag gca cag	1075
Ala Gly Val Leu Thr Asp Leu Glu Ala Leu Gly Val Asp Lys Ala Gln	
310 315 320 325	
ttc gtc gaa gac gtt cgc cgt gca ctg tac gca tcc aag ctt gtt gct	1123
Phe Val Glu Asp Val Arg Arg Ala Leu Tyr Ala Ser Lys Leu Val Ala	
330 335 340	
tac gca cag ggc ttc gac gag atc aag gct ggc tcc gac gag aac aac	1171
Tyr Ala Gln Gly Phe Asp Glu Ile Lys Ala Gly Ser Asp Glu Asn Asn	
345 350 355	
tgg gac gtt gac cct cgc gac ctc gct acc atc tgg cgc ggc ggc tgc	1219
Trp Asp Val Asp Pro Arg Asp Leu Ala Thr Ile Trp Arg Gly Gly Cys	
360 365 370	

atc att cgc gct aag ttc ctc aac cgc atc gtc gaa gca tac gat gca 1267
 Ile Ile Arg Ala Lys Phe Leu Asn Arg Ile Val Glu Ala Tyr Asp Ala
 375 380 385

 aac gct gaa ctt gag tcc ctg ctg ctc gat cct tac ttc aag agc gag 1315
 Asn Ala Glu Leu Glu Ser Leu Leu Leu Asp Pro Tyr Phe Lys Ser Glu
 390 395 400 405

 ctc ggc gac ctc atc gat tca tgg cgt cgc gtg att gtc acc gcc acc 1363
 Leu Gly Asp Leu Ile Asp Ser Trp Arg Arg Val Ile Val Thr Ala Thr
 410 415 420

 cag ctt ggc ctg cca atc cca gtg ttc gct tcc tcc ctg tcc tac tac 1411
 Gln Leu Gly Leu Pro Ile Pro Val Phe Ala Ser Ser Leu Ser Tyr Tyr
 425 430 435

 gac agc ctg cgt gca gag cgt ctg cca gca gcc ctg atc caa gga cag 1459
 Asp Ser Leu Arg Ala Glu Arg Leu Pro Ala Ala Leu Ile Gln Gly Gln
 440 445 450

 cgc gac ttc ttc ggt gcg cac acc tac aag cgc atc gac aag gat ggc 1507
 Arg Asp Phe Phe Gly Ala His Thr Tyr Lys Arg Ile Asp Lys Asp Gly
 455 460 465

 tcc ttc cac acc gag tgg tcc ggc gac cgc 1537
 Ser Phe His Thr Glu Trp Ser Gly Asp Arg
 470 475

<210> 254

<211> 479

<212> PRT

<213> Corynebacterium glutamicum

<400> 254

Met Thr Asn Gly Asp Asn Leu Ala Gln Ile Gly Val Val Gly Leu Ala
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 Val Met Gly Ser Asn Leu Ala Arg Asn Phe Ala Arg Asn Gly Asn Thr
 20 25 30

 Val Ala Val Tyr Asn Arg Ser Thr Asp Lys Thr Asp Lys Leu Ile Ala
 35 40 45

 Asp His Gly Ser Glu Gly Asn Phe Ile Pro Ser Ala Thr Val Glu Glu
 50 55 60

 Phe Val Ala Ser Leu Glu Lys Pro Arg Arg Ala Ile Ile Met Val Gln
 65 70 75 80

 Ala Gly Asn Ala Thr Asp Ala Val Ile Asn Gln Leu Ala Asp Ala Met
 85 90 95

 Asp Glu Gly Asp Ile Ile Ile Asp Gly Gly Asn Ala Leu Tyr Thr Asp
 100 105 110

 Thr Ile Arg Arg Glu Lys Glu Ile Ser Ala Arg Gly Leu His Phe Val
 115 120 125

 Gly Ala Gly Ile Ser Gly Gly Glu Glu Gly Ala Leu Asn Gly Pro Ser
 130 135 140

Ile Met Pro Gly Gly Pro Ala Lys Ser Tyr Glu Ser Leu Gly Pro Leu
 145 150 155 160
 Leu Glu Ser Ile Ala Ala Asn Val Asp Gly Thr Pro Cys Val Thr His
 165 170 175
 Ile Gly Pro Asp Gly Ala Gly His Phe Val Lys Met Val His Asn Gly
 180 185 190
 Ile Glu Tyr Ala Asp Met Gln Val Ile Gly Glu Ala Tyr His Leu Leu
 195 200 205
 Arg Tyr Ala Ala Gly Met Gln Pro Ala Glu Ile Ala Glu Val Phe Lys
 210 215 220
 Glu Trp Asn Ala Gly Asp Leu Asp Ser Tyr Leu Ile Glu Ile Thr Ala
 225 230 235 240
 Glu Val Leu Ser Gln Val Asp Ala Glu Thr Gly Lys Pro Leu Ile Asp
 245 250 255
 Val Ile Val Asp Ala Ala Gly Gln Lys Gly Thr Gly Arg Trp Thr Val
 260 265 270
 Lys Ala Ala Leu Asp Leu Gly Ile Ala Thr Thr Gly Ile Gly Glu Ala
 275 280 285
 Val Phe Ala Arg Ala Leu Ser Gly Ala Thr Ser Gln Arg Ala Ala Ala
 290 295 300
 Gln Gly Asn Leu Pro Ala Gly Val Leu Thr Asp Leu Glu Ala Leu Gly
 305 310 315 320
 Val Asp Lys Ala Gln Phe Val Glu Asp Val Arg Arg Ala Leu Tyr Ala
 325 330 335
 Ser Lys Leu Val Ala Tyr Ala Gln Gly Phe Asp Glu Ile Lys Ala Gly
 340 345 350
 Ser Asp Glu Asn Asn Trp Asp Val Asp Pro Arg Asp Leu Ala Thr Ile
 355 360 365
 Trp Arg Gly Gly Cys Ile Ile Arg Ala Lys Phe Leu Asn Arg Ile Val
 370 375 380
 Glu Ala Tyr Asp Ala Asn Ala Glu Leu Glu Ser Leu Leu Leu Asp Pro
 385 390 395 400
 Tyr Phe Lys Ser Glu Leu Gly Asp Leu Ile Asp Ser Trp Arg Arg Val
 405 410 415
 Ile Val Thr Ala Thr Gln Leu Gly Leu Pro Ile Pro Val Phe Ala Ser
 420 425 430
 Ser Leu Ser Tyr Tyr Asp Ser Leu Arg Ala Glu Arg Leu Pro Ala Ala
 435 440 445
 Leu Ile Gln Gly Gln Arg Asp Phe Phe Gly Ala His Thr Tyr Lys Arg
 450 455 460

Ile Asp Lys Asp Gly Ser Phe His Thr Glu Trp Ser Gly Asp Arg
 465 470 475

<210> 255
 <211> 1326
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(1303)
 <223> RXN02596

<400> 255
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 gaaatttcgg caacgccgaa tgtaagttag tgtcgaatgc atg acg gaa tcg aaa 115
 Met Thr Glu Ser Lys
 1 5
 aat tac gac tta atc gtt gta ggc tcc ggc ctc ttc ggg ctc acc gtg 163
 Asn Tyr Asp Leu Ile Val Val Gly Ser Gly Leu Phe Gly Leu Thr Val
 10 15 20
 gct gag cgt gca gct agc cag ctg ggt aag aaa gtc ctc atc gtt gaa 211
 Ala Glu Arg Ala Ala Ser Gln Leu Gly Lys Lys Val Leu Ile Val Glu
 25 30 35
 cgc cgc tcg cac ctc ggt ggc aat gct tac tct gaa gca gaa cca gag 259
 Arg Arg Ser His Leu Gly Gly Asn Ala Tyr Ser Glu Ala Glu Pro Glu
 40 45 50
 acc ggc att gaa atc cac aaa tac ggc gcg cac ctc ttc cac acc tcc 307
 Thr Gly Ile Glu Ile His Lys Tyr Gly Ala His Leu Phe His Thr Ser
 55 60 65
 aac aca cgc gtg tgg gaa tac gtc aac cag ttc acc agt ttc acc ggc 355
 Asn Thr Arg Val Trp Glu Tyr Val Asn Gln Phe Thr Ser Phe Thr Gly
 70 75 80 85
 tac cag cac cgc gtc ttc gca atg cac aac ggc acc gcc tac caa ttc 403
 Tyr Gln His Arg Val Phe Ala Met His Asn Gly Thr Ala Tyr Gln Phe
 90 95 100
 ccc atg gga ctg ggc ctg att aac cag ttc ttc ggc aag tac tac agc 451
 Pro Met Gly Leu Gly Leu Ile Asn Gln Phe Phe Gly Lys Tyr Tyr Ser
 105 110 115
 cca gat gaa gcc cgt gag ctc atc aag gaa cag tct gca gaa atc gat 499
 Pro Asp Glu Ala Arg Glu Leu Ile Lys Glu Gln Ser Ala Glu Ile Asp
 120 125 130
 tcc tcc gac gcc acc aac ctc gaa gaa aag gcc att tcc ctc att ggt 547
 Ser Ser Asp Ala Thr Asn Leu Glu Glu Lys Ala Ile Ser Leu Ile Gly
 135 140 145
 cgc cca ctt tac gag gca ttc atc cgc gac tac acc gca aag cag tgg 595
 Arg Pro Leu Tyr Glu Ala Phe Ile Arg Asp Tyr Thr Ala Lys Gln Trp
 150 155 160 165

cag act gat cca aag aac ctc cca gcc ggc aac atc acc cgc ctg cca	643
Gln Thr Asp Pro Lys Asn Leu Pro Ala Gly Asn Ile Thr Arg Leu Pro	
170 175 180	
gtt cgc tac aac ttc aac aac cgc tat ttc aac gac acc tac gaa ggc	691
Val Arg Tyr Asn Phe Asn Asn Arg Tyr Phe Asn Asp Thr Tyr Glu Gly	
185 190 195	
ctt ccc aca gac ggc tac gcg gca tgg ttg gaa aag atg gca gag cat	739
Leu Pro Thr Asp Gly Tyr Ala Trp Leu Glu Lys Met Ala Glu His	
200 205 210	
gag ctt atc gac gtc cgc ctc gac acc gac tgg ttc gac gtt cgc gat	787
Glu Leu Ile Asp Val Arg Leu Asp Thr Asp Trp Phe Asp Val Arg Asp	
215 220 225	
gac ctc cgc gca agc aac ccc gac gca cct gtg gtc tac acc ggc cca	835
Asp Leu Arg Ala Ser Asn Pro Asp Ala Pro Val Val Tyr Thr Gly Pro	
230 235 240 245	
ctc gac ctc tac ttc aac tac gca gag ggc aag ctg gga tgg cgc acc	883
Leu Asp Leu Tyr Phe Asn Tyr Ala Glu Gly Lys Leu Gly Trp Arg Thr	
250 255 260	
ctc gac ttt gaa acc gaa gta gta gaa acc ggt gac ttc caa gga acc	931
Leu Asp Phe Glu Thr Glu Val Val Glu Thr Gly Asp Phe Gln Gly Thr	
265 270 275	
cca gtg atg aac tac aac gat gcg gac gta cct ttc acc cgc atc cac	979
Pro Val Met Asn Tyr Asn Asp Ala Asp Val Pro Phe Thr Arg Ile His	
280 285 290	
gag ttc cgt cac ttc cac cca gag cgt gat gac agt tac ccc aag gat	1027
Glu Phe Arg His Phe His Pro Glu Arg Asp Asp Ser Tyr Pro Lys Asp	
295 300 305	
aag acc gtc atc atg cgc gag ttc tcc cgt ttc gca gat aac gag gat	1075
Lys Thr Val Ile Met Arg Glu Phe Ser Arg Phe Ala Asp Asn Glu Asp	
310 315 320 325	
gag cct tat tac cca atc aac act cca gac gac cga gac atg ctg aag	1123
Glu Pro Tyr Tyr Pro Ile Asn Thr Pro Asp Asp Arg Asp Met Leu Lys	
330 335 340	
cag tac cgc ctt ctg gct gct gaa gag gct gct aat aat aag gtg ctg	1171
Gln Tyr Arg Leu Leu Ala Ala Glu Glu Ala Ala Asn Asn Lys Val Leu	
345 350 355	
ttc ggc ggt cga ctg ggc acg tac cag tac ctc gac atg cac atg gct	1219
Phe Gly Gly Arg Leu Gly Thr Tyr Gln Tyr Leu Asp Met His Met Ala	
360 365 370	
atc ggt tct gcg ctg agc atg ttt gac aac aag ctg gtg ccg ttc ttt	1267
Ile Gly Ser Ala Leu Ser Met Phe Asp Asn Lys Leu Val Pro Phe Phe	
375 380 385	
gaa gaa ggc aca ccg cta gag cag gaa cgc gga cac taaaaggaag	1313
Glu Glu Gly Thr Pro Leu Glu Gln Glu Arg Gly His	
390 395 400	
ggcatctccc aca	1326

<210> 256

<211> 401

<212> PRT

<213> Corynebacterium glutamicum

<400> 256

Met Thr Glu Ser Lys Asn Tyr Asp Leu Ile Val Val Gly Ser Gly Leu
 1 5 10 15

Phe Gly Leu Thr Val Ala Glu Arg Ala Ala Ser Gln Leu Gly Lys Lys
 20 25 30

Val Leu Ile Val Glu Arg Arg Ser His Leu Gly Gly Asn Ala Tyr Ser
 35 40 45

Glu Ala Glu Pro Glu Thr Gly Ile Glu Ile His Lys Tyr Gly Ala His
 50 55 60

Leu Phe His Thr Ser Asn Thr Arg Val Trp Glu Tyr Val Asn Gln Phe
 65 70 75 80

Thr Ser Phe Thr Gly Tyr Gln His Arg Val Phe Ala Met His Asn Gly
 85 90 95

Thr Ala Tyr Gln Phe Pro Met Gly Leu Gly Leu Ile Asn Gln Phe Phe
 100 105 110

Gly Lys Tyr Tyr Ser Pro Asp Glu Ala Arg Glu Leu Ile Lys Glu Gln
 115 120 125

Ser Ala Glu Ile Asp Ser Ser Asp Ala Thr Asn Leu Glu Glu Lys Ala
 130 135 140

Ile Ser Leu Ile Gly Arg Pro Leu Tyr Glu Ala Phe Ile Arg Asp Tyr
 145 150 155 160

Thr Ala Lys Gln Trp Gln Thr Asp Pro Lys Asn Leu Pro Ala Gly Asn
 165 170 175

Ile Thr Arg Leu Pro Val Arg Tyr Asn Phe Asn Asn Arg Tyr Phe Asn
 180 185 190

Asp Thr Tyr Glu Gly Leu Pro Thr Asp Gly Tyr Ala Ala Trp Leu Glu
 195 200 205

Lys Met Ala Glu His Glu Leu Ile Asp Val Arg Leu Asp Thr Asp Trp
 210 215 220

Phe Asp Val Arg Asp Asp Leu Arg Ala Ser Asn Pro Asp Ala Pro Val
 225 230 235 240

Val Tyr Thr Gly Pro Leu Asp Leu Tyr Phe Asn Tyr Ala Glu Gly Lys
 245 250 255

Leu Gly Trp Arg Thr Leu Asp Phe Glu Thr Glu Val Val Glu Thr Gly
 260 265 270

Asp Phe Gln Gly Thr Pro Val Met Asn Tyr Asn Asp Ala Asp Val Pro
 275 280 285

Phe Thr Arg Ile His Glu Phe Arg His Phe His Pro Glu Arg Asp Asp
 290 295 300
 Ser Tyr Pro Lys Asp Lys Thr Val Ile Met Arg Glu Phe Ser Arg Phe
 305 310 315 320
 Ala Asp Asn Glu Asp Glu Pro Tyr Tyr Pro Ile Asn Thr Pro Asp Asp
 325 330 335
 Arg Asp Met Leu Lys Gln Tyr Arg Leu Leu Ala Ala Glu Glu Ala Ala
 340 345 350
 Asn Asn Lys Val Leu Phe Gly Gly Arg Leu Gly Thr Tyr Gln Tyr Leu
 355 360 365
 Asp Met His Met Ala Ile Gly Ser Ala Leu Ser Met Phe Asp Asn Lys
 370 375 380
 Leu Val Pro Phe Phe Glu Glu Gly Thr Pro Leu Glu Gln Glu Arg Gly
 385 390 395 400
 His

<210> 257
 <211> 512
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (1)..(489)
 <223> FRXA02596

<400> 257
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 Pro Val Val Tyr Thr Gly Pro Leu Asp Leu Tyr Phe Asn Tyr Ala Glu
 1 5 10 15
 ggc aag ctg gga tgg cgc acc ctc gac ttt gaa acc gaa gta gta gaa 96
 Gly Lys Leu Gly Trp Arg Thr Leu Asp Phe Glu Thr Glu Val Val Glu
 20 25 30
 acc ggt gac ttc caa gga acc cca gtg atg aac tac aac gat gcg gac 144
 Thr Gly Asp Phe Gln Gly Thr Pro Val Met Asn Tyr Asn Asp Ala Asp
 35 40 45
 gta cct ttc acc cgc atc cac gag ttc cgt cac ttc cac cca gag cgt 192
 Val Pro Phe Thr Arg Ile His Glu Phe Arg His Phe His Pro Glu Arg
 50 55 60
 gat gac agt tac ccc aag gat aag acc gtc atc atg cgc gag ttc tcc 240
 Asp Asp Ser Tyr Pro Lys Asp Lys Thr Val Ile Met Arg Glu Phe Ser
 65 70 75 80
 cgt ttc gca gat aac gag gat gag cct tat tac cca atc aac act cca 288
 Arg Phe Ala Asp Asn Glu Asp Glu Pro Tyr Tyr Pro Ile Asn Thr Pro
 85 90 95

gac gac cga gac atg ctg aag cag tac cgc ctt ctg gct gct gaa gag 336
 Asp Asp Arg Asp Met Leu Lys Gln Tyr Arg Leu Leu Ala Ala Glu Glu
 100 105 110

 gct gct aat aat aag gtg ctg ttc ggc ggt cga ctg ggc acg tac cag 384
 Ala Ala Asn Asn Lys Val Leu Phe Gly Gly Arg Leu Gly Thr Tyr Gln
 115 120 125

 tac ctc gac atg cac atg gct atc ggt tct gcg ctg agc atg ttt gac 432
 Tyr Leu Asp Met His Met Ala Ile Gly Ser Ala Leu Ser Met Phe Asp
 130 135 140

 aac aag ctg gtg ccg ttc ttt gaa gaa ggc aca ccg cta gag cag gaa 480
 Asn Lys Leu Val Pro Phe Phe Glu Glu Gly Thr Pro Leu Glu Gln Glu
 145 150 155 160

 cgc gga cac taaaaggaag ggcattctccc aca 512
 Arg Gly His

<210> 258
 <211> 163
 <212> PRT
 <213> Corynebacterium glutamicum

<400> 258
 Pro Val Val Tyr Thr Gly Pro Leu Asp Leu Tyr Phe Asn Tyr Ala Glu
 1 5 10 15

 Gly Lys Leu Gly Trp Arg Thr Leu Asp Phe Glu Thr Glu Val Val Glu
 20 25 30

 Thr Gly Asp Phe Gln Gly Thr Pro Val Met Asn Tyr Asn Asp Ala Asp
 35 40 45

 Val Pro Phe Thr Arg Ile His Glu Phe Arg His Phe His Pro Glu Arg
 50 55 60

 Asp Asp Ser Tyr Pro Lys Asp Lys Thr Val Ile Met Arg Glu Phe Ser
 65 70 75 80

 Arg Phe Ala Asp Asn Glu Asp Glu Pro Tyr Tyr Pro Ile Asn Thr Pro
 85 90 95

 Asp Asp Arg Asp Met Leu Lys Gln Tyr Arg Leu Leu Ala Ala Glu Glu
 100 105 110

 Ala Ala Asn Asn Lys Val Leu Phe Gly Gly Arg Leu Gly Thr Tyr Gln
 115 120 125

 Tyr Leu Asp Met His Met Ala Ile Gly Ser Ala Leu Ser Met Phe Asp
 130 135 140

 Asn Lys Leu Val Pro Phe Phe Glu Glu Gly Thr Pro Leu Glu Gln Glu
 145 150 155 160

 Arg Gly His

<400> 259																	
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gaaatttcgg caacgccgaa tgtaagttag tgtcgaatgc atg acg gaa tcg aaa																	115
Met Thr Glu Ser Lys																	
1 5																	
aat tac gac tta atc gtt gta ggc tcc ggc ctc ttc ggg ctc acc gtg																	163
Asn Tyr Asp Leu Ile Val Val Gly Ser Gly Leu Phe Gly Leu Thr Val																	
10 15 20																	
gct gag cgt gca gct agc cag ctg ggt aag aaa gtc ctc atc gtt gaa																	211
Ala Glu Arg Ala Ala Ser Gln Leu Gly Lys Lys Val Leu Ile Val Glu																	
25 30 35																	
cgc cgc tcg cac ctc ggt ggc aat gct tac tct gaa gca gaa cca gag																	259
Arg Arg Ser His Leu Gly Gly Asn Ala Tyr Ser Glu Ala Glu Pro Glu																	
40 45 50																	
acc ggc att gaa atc cac aaa tac ggc gcg cac ctc ttc cac acc tcc																	307
Thr Gly Ile Glu Ile His Lys Tyr Gly Ala His Leu Phe His Thr Ser																	
55 60 65																	
aac aca cgc gtg tgg gaa tac gtc aac cag ttc acc agt ttc acc ggc																	355
Asn Thr Arg Val Trp Glu Tyr Val Asn Gln Phe Thr Ser Phe Thr Gly																	
70 75 80 85																	
tac cag cac cgc gtc ttc gca atg cac aac ggc acc gcc tac caa ttc																	403
Tyr Gln His Arg Val Phe Ala Met His Asn Gly Thr Ala Tyr Gln Phe																	
90 95 100																	
ccc atg gga ctg ggc ctg att aac cag ttc ttc ggc aag tac tac agc																	451
Pro Met Gly Leu Gly Leu Ile Asn Gln Phe Phe Gly Lys Tyr Tyr Ser																	
105 110 115																	
cca gat gaa gcc cgt gag ctc atc aag gaa cag tct gca gaa atc gat																	499
Pro Asp Glu Ala Arg Glu Leu Ile Lys Glu Gln Ser Ala Glu Ile Asp																	
120 125 130																	
tcc tcc gac gcc acc aac ctc gaa gaa aag gcc att tcc ctc att ggt																	547
Ser Ser Asp Ala Thr Asn Leu Glu Glu Lys Ala Ile Ser Leu Ile Gly																	
135 140 145																	
cgc cca ctt tac gag gca ttc atc cgc gac tac acc gca aag cag tgg																	595
Arg Pro Leu Tyr Glu Ala Phe Ile Arg Asp Tyr Thr Ala Lys Gln Trp																	
150 155 160 165																	
cag																	598
Gln																	

<210> 260
 <211> 166
 <212> PRT
 <213> Corynebacterium glutamicum

<400> 260
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 Phe Gly Leu Thr Val Ala Glu Arg Ala Ala Ser Gln Leu Gly Lys Lys
 20 25 30
 Val Leu Ile Val Glu Arg Arg Ser His Leu Gly Gly Asn Ala Tyr Ser
 35 40 45
 Glu Ala Glu Pro Glu Thr Gly Ile Glu Ile His Lys Tyr Gly Ala His
 50 55 60
 Leu Phe His Thr Ser Asn Thr Arg Val Trp Glu Tyr Val Asn Gln Phe
 65 70 75 80
 Thr Ser Phe Thr Gly Tyr Gln His Arg Val Phe Ala Met His Asn Gly
 85 90 95
 Thr Ala Tyr Gln Phe Pro Met Gly Leu Gly Leu Ile Asn Gln Phe Phe
 100 105 110
 Gly Lys Tyr Tyr Ser Pro Asp Glu Ala Arg Glu Leu Ile Lys Glu Gln
 115 120 125
 Ser Ala Glu Ile Asp Ser Ser Asp Ala Thr Asn Leu Glu Glu Lys Ala
 130 135 140
 Ile Ser Leu Ile Gly Arg Pro Leu Tyr Glu Ala Phe Ile Arg Asp Tyr
 145 150 155 160
 Thr Ala Lys Gln Trp Gln
 165

<210> 261
 <211> 668
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (1)..(645)
 <223> RXA02572

<400> 261
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 Ala Val Ala Glu Ile Cys Glu Pro Thr Gly Ala Asp Ala Val Ala Leu
 1 5 10 15
 gtg gat gcc atc ggt cac gac gat cgt atc ggc cga aag ttc tta ggc 96
 Val Asp Ala Ile Gly His Asp Asp Arg Ile Gly Arg Lys Phe Leu Gly
 20 25 30
 gcg ggc ctg gga ttc ggt ggc ggt tgt ttg cct aaa gac atc cgc gct 144

Ala Gly Leu Gly Phe Gly Gly Gly Cys Leu Pro Lys Asp Ile Arg Ala
 35 40 45

ttc atg gca cgc gcg ggc gaa ttg ggt gct gac cag gca tta acg ttc 192
 Phe Met Ala Arg Ala Gly Glu Leu Gly Ala Asp Gln Ala Leu Thr Phe
 50 55 60

ttg cgt gag gtc gat tcc atc aat atg cgt cgt cgc gac cgt gtg gtg 240
 Leu Arg Glu Val Asp Ser Ile Asn Met Arg Arg Asp Arg Val Val
 65 70 75 80

cag ctg gcc aaa gag atg tgt ggc ggt tcg ctg ctg ggc aag cgg gtt 288
 Gln Leu Ala Lys Glu Met Cys Gly Gly Ser Leu Leu Gly Lys Arg Val
 85 90 95

aca gtg ctc ggc gcc gca ttc aaa ccc aac tcg gac gat gtc cgc gat 336
 Thr Val Leu Gly Ala Ala Phe Lys Pro Asn Ser Asp Asp Val Arg Asp
 100 105 110

tct ccg gcg ctg tcg gtc gcg ggt tcg ctg tcg ctc cag ggt gcg gcg 384
 Ser Pro Ala Leu Ser Val Ala Gly Ser Leu Ser Leu Gln Gly Ala Ala
 115 120 125

gtc tcg gtc tac gac ccg gaa gct atg gac aac gct cga cgc gtc ttc 432
 Val Ser Val Tyr Asp Pro Glu Ala Met Asp Asn Ala Arg Arg Val Phe
 130 135 140

ccg acg ctc agc tat gcg tcc agc act aaa gag gcg ctt atc gac gcc 480
 Pro Thr Leu Ser Tyr Ala Ser Ser Thr Lys Glu Ala Leu Ile Asp Ala
 145 150 155 160

cac ctc gtc gtt ctt gcc act gaa tgg caa gaa ttc cgc gac ctt gac 528
 His Leu Val Val Leu Ala Thr Glu Trp Gln Glu Phe Arg Asp Leu Asp
 165 170 175

ccc gaa gtg gcg gga ggg gtc gtc gag aag cgc gct att att gat ggc 576
 Pro Glu Val Ala Gly Gly Val Val Glu Lys Arg Ala Ile Ile Asp Gly
 180 185 190

cga aac gtc ctc gat gtt gcc aaa tgg aag gcc gcc ggt tgg gaa atg 624
 Arg Asn Val Leu Asp Val Ala Lys Trp Lys Ala Ala Gly Trp Glu Met
 195 200 205

gaa gcg ctc ggc cgc aac ctt tagtgcggtg gatcaggcgg ggc 668
 Glu Ala Leu Gly Arg Asn Leu
 210 215

<210> 262

<211> 215

<212> PRT

<213> Corynebacterium glutamicum

<400> 262

Ala Val Ala Glu Ile Cys Glu Pro Thr Gly Ala Asp Ala Val Ala Leu
 1 5 10 15

Val Asp Ala Ile Gly His Asp Asp Arg Ile Gly Arg Lys Phe Leu Gly
 20 25 30

Ala Gly Leu Gly Phe Gly Gly Gly Cys Leu Pro Lys Asp Ile Arg Ala

376

gcc gta cgt tgc cag acc acg gag gcg ctg gtc agc gcc ata aaa ttg	259
Ala Val Arg Cys Gln Thr Thr Glu Ala Leu Val Ser Ala Ile Lys Leu	
40 45 50	
ctt gac gac gcc tcc ctc ccc ctc ctc att gtc ggc ggc ggg tcc aat	307
Leu Asp Asp Ala Ser Leu Pro Leu Leu Ile Val Gly Gly Gly Ser Asn	
55 60 65	
ctc gtc gtg gcc gac ggc gat ctg gat gtt att gcc gtc atc atc gaa	355
Leu Val Val Ala Asp Gly Asp Leu Asp Val Ile Ala Val Ile Ile Glu	
70 75 80 85	
acc gac gac gtc tcc atc aac ctc acc gac ggt ctc ctc acc gcc gat	403
Thr Asp Asp Val Ser Ile Asn Leu Thr Asp Gly Leu Leu Thr Ala Asp	
90 95 100	
gca ggc gct gtt tgg gac gat gtt gtc cac ctt tcg gtg gat gcc ggc	451
Ala Gly Ala Val Trp Asp Asp Val Val His Leu Ser Val Asp Ala Gly	
105 110 115	
ctc ggt gga att gaa tgc ctc tcc gga atc ccc ggc tcc gcc ggc gcc	499
Leu Gly Gly Ile Glu Cys Leu Ser Gly Ile Pro Gly Ser Ala Gly Ala	
120 125 130	
acc cca gtc caa aac gtg ggc gcc tac ggc acg gaa gtt tcc gat gta	547
Thr Pro Val Gln Asn Val Gly Ala Tyr Gly Thr Glu Val Ser Asp Val	
135 140 145	
ctc acc cgc gtc cag ctt ctc gac cgc acc acc cac caa gtc tcc tgg	595
Leu Thr Arg Val Gln Leu Leu Asp Arg Thr Thr His Gln Val Ser Trp	
150 155 160 165	
gtc gac gcc tcc gaa ctc gac ctc tct tac cga tac tcc aat ctc aaa	643
Val Asp Ala Ser Glu Leu Asp Leu Ser Tyr Arg Tyr Ser Asn Leu Lys	
170 175 180	
ttc acc aac cgc gca gtc gtc ttg gcg atc gaa ctc cag ctc ctc acc	691
Phe Thr Asn Arg Ala Val Val Leu Ala Ile Glu Leu Gln Leu Leu Thr	
185 190 195	
gac gga ttg tcc gcg ccg cta cgt ttt ggt gaa ttg gga cgt cga tta	739
Asp Gly Leu Ser Ala Pro Leu Arg Phe Gly Glu Leu Gly Arg Arg Leu	
200 205 210	
gcg atc tcc gag gcc gaa ccc cac cca cgt cgc ccc gtc cgc atg gtc	787
Ala Ile Ser Glu Ala Glu Pro His Pro Arg Arg Pro Val Arg Met Val	
215 220 225	
cgc gac gcc gtc cta gaa ctc cgc cgc gcc aaa ggc atg gtc gtg gaa	835
Arg Asp Ala Val Leu Glu Leu Arg Arg Ala Lys Gly Met Val Val Glu	
230 235 240 245	
cac acc gac cac gac acc tgg tcc gcc gga tcc ttc ttc acc aac cca	883
His Thr Asp His Asp Thr Trp Ser Ala Gly Ser Phe Phe Thr Asn Pro	
250 255 260	
atc gtc gac cca gcc ctt gcc gac gca gtc ttt gaa aaa gtc ggc gaa	931
Ile Val Asp Pro Ala Leu Ala Asp Ala Val Phe Glu Lys Val Gly Glu	
265 270 275	
ccc acc atg ccc cgc ttc cca gcc ggc gat ggc aaa gaa aaa ctc tcc	979

Pro Thr Met Pro Arg Phe Pro Ala Gly Asp Gly Lys Glu Lys Leu Ser
 280 285 290

gca gcc tgg ctc atc gaa cgc gcc ggc ttc aaa aag gga cac ccc ggc 1027
 Ala Ala Trp Leu Ile Glu Arg Ala Gly Phe Lys Lys Gly His Pro Gly
 295 300 305

gca ggc gca aaa gcc tcc ctg agc acc aaa cac acc ctc gca ctc acc 1075
 Ala Gly Ala Lys Ala Ser Leu Ser Thr Lys His Thr Leu Ala Leu Thr
 310 315 320 325

aac cgt ggc gac gcc cgc gcc tcc gac ctc gtc gca tta gcc aaa gaa 1123
 Asn Arg Gly Asp Ala Arg Ala Ser Asp Leu Val Ala Leu Ala Lys Glu
 330 335 340

atc cgc gac gga gtc ctc gaa acc ttc ggc gtc acc ctc gtc cca gaa 1171
 Ile Arg Asp Gly Val Leu Glu Thr Phe Gly Val Thr Leu Val Pro Glu
 345 350 355

ccc gtc tgg att gga atc agc atc gat gac tgaattttcc gacgtccctg 1221
 Pro Val Trp Ile Gly Ile Ser Ile Asp Asp
 360 365

gca 1224

<210> 264
 <211> 367
 <212> PRT
 <213> Corynebacterium glutamicum

<400> 264
 Leu Asp Ser Ser Leu Ala Gln Glu Ile Ala Ala Ile Asp Gly Val Glu
 1 5 10 15

Leu Asp Ser Glu Val Thr Phe Ala Asp Leu Thr Thr Leu Arg Ile Gly
 20 25 30

Gly Lys Pro Arg Ser Ala Val Arg Cys Gln Thr Thr Glu Ala Leu Val
 35 40 45

Ser Ala Ile Lys Leu Leu Asp Asp Ala Ser Leu Pro Leu Leu Ile Val
 50 55 60

Gly Gly Gly Ser Asn Leu Val Val Ala Asp Gly Asp Leu Asp Val Ile
 65 70 75 80

Ala Val Ile Ile Glu Thr Asp Asp Val Ser Ile Asn Leu Thr Asp Gly
 85 90 95

Leu Leu Thr Ala Asp Ala Gly Ala Val Trp Asp Asp Val Val His Leu
 100 105 110

Ser Val Asp Ala Gly Leu Gly Gly Ile Glu Cys Leu Ser Gly Ile Pro
 115 120 125

Gly Ser Ala Gly Ala Thr Pro Val Gln Asn Val Gly Ala Tyr Gly Thr
 130 135 140

Glu Val Ser Asp Val Leu Thr Arg Val Gln Leu Leu Asp Arg Thr Thr
 145 150 155 160

His Gln Val Ser Trp Val Asp Ala Ser Glu Leu Asp Leu Ser Tyr Arg
 165 170 175
 Tyr Ser Asn Leu Lys Phe Thr Asn Arg Ala Val Val Leu Ala Ile Glu
 180 185 190
 Leu Gln Leu Leu Thr Asp Gly Leu Ser Ala Pro Leu Arg Phe Gly Glu
 195 200 205
 Leu Gly Arg Arg Leu Ala Ile Ser Glu Ala Glu Pro His Pro Arg Arg
 210 215 220
 Pro Val Arg Met Val Arg Asp Ala Val Leu Glu Leu Arg Arg Ala Lys
 225 230 235 240
 Gly Met Val Val Glu His Thr Asp His Asp Thr Trp Ser Ala Gly Ser
 245 250 255
 Phe Phe Thr Asn Pro Ile Val Asp Pro Ala Leu Ala Asp Ala Val Phe
 260 265 270
 Glu Lys Val Gly Glu Pro Thr Met Pro Arg Phe Pro Ala Gly Asp Gly
 275 280 285
 Lys Glu Lys Leu Ser Ala Ala Trp Leu Ile Glu Arg Ala Gly Phe Lys
 290 295 300
 Lys Gly His Pro Gly Ala Gly Ala Lys Ala Ser Leu Ser Thr Lys His
 305 310 315 320
 Thr Leu Ala Leu Thr Asn Arg Gly Asp Ala Arg Ala Ser Asp Leu Val
 325 330 335
 Ala Leu Ala Lys Glu Ile Arg Asp Gly Val Leu Glu Thr Phe Gly Val
 340 345 350
 Thr Leu Val Pro Glu Pro Val Trp Ile Gly Ile Ser Ile Asp Asp
 355 360 365

<210> 265
 <211> 1124
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (1)..(1101)
 <223> RXA01216

<400> 265
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 Thr Asp His Thr Leu Ser Ala Leu Leu Asp Ala His Val Glu Val Pro
 1 5 10 15
 acc gct gtc acc gtg ttg acc atg cgt ctg gat gac ccc acc ggc tac 96
 Thr Ala Val Thr Val Leu Thr Met Arg Leu Asp Asp Pro Thr Gly Tyr
 20 25 30
 ggc cgc atc gtg cgc aac gaa gaa ggc gaa gtc acc gcc atc gtt gag 144

Gly	Arg	Ile	Val	Arg	Asn	Glu	Glu	Gly	Glu	Val	Thr	Ala	Ile	Val	Glu		
		35					40					45					
caa	aaa	gat	gct	tca	gca	gaa	gtc	caa	gcc	atc	gat	gag	gtc	aac	tcc	192	
Gln	Lys	Asp	Ala	Ser	Ala	Glu	Val	Gln	Ala	Ile	Asp	Glu	Val	Asn	Ser		
	50					55					60						
ggt	gtc	ttt	gct	ttc	gac	gcc	gcc	atc	ttg	cgt	tcc	gca	ctg	gct	gaa	240	
Gly	Val	Phe	Ala	Phe	Asp	Ala	Ala	Ile	Leu	Arg	Ser	Ala	Leu	Ala	Glu		
	65				70				75					80			
ctg	aag	tcc	gac	aac	gct	cag	ggc	gag	ctg	tac	ctg	acc	gac	gtt	ttg	288	
Leu	Lys	Ser	Asp	Asn	Ala	Gln	Gly	Glu	Leu	Tyr	Leu	Thr	Asp	Val	Leu		
				85					90					95			
ggc	att	gct	cgt	ggc	gag	ggc	cac	cca	gtg	cgc	gcc	cac	acc	gcc	gcc	336	
Gly	Ile	Ala	Arg	Gly	Glu	Gly	His	Pro	Val	Arg	Ala	His	Thr	Ala	Ala		
		100						105					110				
gat	gct	cgt	gaa	ctc	gcc	ggc	gtc	aac	gat	cgt	gtg	cag	ctc	gca	gaa	384	
Asp	Ala	Arg	Glu	Leu	Ala	Gly	Val	Asn	Asp	Arg	Val	Gln	Leu	Ala	Glu		
		115					120					125					
gcc	ggc	gcc	gaa	cta	aac	cgt	cgc	acc	gtc	atc	gcc	gct	atg	cgt	ggt	432	
Ala	Gly	Ala	Glu	Leu	Asn	Arg	Arg	Thr	Val	Ile	Ala	Ala	Met	Arg	Gly		
	130					135					140						
ggc	gca	acc	atc	gtt	gat	cca	gca	acc	acc	tgg	atc	gat	gtg	gag	gtt	480	
Gly	Ala	Thr	Ile	Val	Asp	Pro	Ala	Thr	Thr	Trp	Ile	Asp	Val	Glu	Val		
	145				150					155				160			
tct	atc	gga	cgc	gac	gtg	atc	atc	cac	cct	ggc	acc	cag	ctc	aag	ggc	528	
Ser	Ile	Gly	Arg	Asp	Val	Ile	Ile	His	Pro	Gly	Thr	Gln	Leu	Lys	Gly		
				165					170					175			
gaa	act	gtc	atc	gga	gac	cgc	gtt	gaa	gtt	ggt	cca	gac	acc	acc	ttg	576	
Glu	Thr	Val	Ile	Gly	Asp	Arg	Val	Glu	Val	Gly	Pro	Asp	Thr	Thr	Leu		
		180						185					190				
acc	aac	atg	acc	atc	ggc	gac	ggc	gca	tcc	gta	atc	cgc	acc	cac	ggt	624	
Thr	Asn	Met	Thr	Ile	Gly	Asp	Gly	Ala	Ser	Val	Ile	Arg	Thr	His	Gly		
		195					200					205					
ttc	gac	tcc	acc	atc	ggt	gaa	aac	gcc	acc	gtt	ggc	ccc	ttc	acc	tac	672	
Phe	Asp	Ser	Thr	Ile	Gly	Glu	Asn	Ala	Thr	Val	Gly	Pro	Phe	Thr	Tyr		
	210					215					220						
atc	cgc	cca	gga	acc	aca	ctg	gga	cca	gaa	ggc	aag	ctc	ggt	ggc	ttc	720	
Ile	Arg	Pro	Gly	Thr	Thr	Leu	Gly	Pro	Glu	Gly	Lys	Leu	Gly	Gly	Phe		
	225				230					235				240			
gta	gaa	acc	aag	aag	gcc	aca	atc	ggc	cgt	ggc	tcc	aag	gtt	cca	cac	768	
Val	Glu	Thr	Lys	Lys	Ala	Thr	Ile	Gly	Arg	Gly	Ser	Lys	Val	Pro	His		
				245				250					255				
ctc	acc	tat	gtc	ggc	gac	gcc	acc	atc	ggc	gag	gaa	tcc	aac	atc	gga	816	
Leu	Thr	Tyr	Val	Gly	Asp	Ala	Thr	Ile	Gly	Glu	Glu	Ser	Asn	Ile	Gly		
			260					265					270				
gcc	tcc	tct	gtc	ttc	gtg	aac	tac	gac	ggt	gaa	aac	aag	cac	cac	acc	864	
Ala	Ser	Ser	Val	Phe	Val	Asn	Tyr	Asp	Gly	Glu	Asn	Lys	His	His	Thr		

275	280	285	
acc atc ggc agc cac gtt cgc act ggt tct gac acc atg ttt atc gct			912
Thr Ile Gly Ser His Val Arg Thr Gly Ser Asp Thr Met Phe Ile Ala			
290	295	300	
cca gtg acc gtg ggt gac gga gcg tat tcc gga gcc ggt aca gta att			960
Pro Val Thr Val Gly Asp Gly Ala Tyr Ser Gly Ala Gly Thr Val Ile			
305	310	315	320
aaa gac gat gtt ccg cca gga gcc ctt gcc gtg tcc ggc gga cgc caa			1008
Lys Asp Asp Val Pro Pro Gly Ala Leu Ala Val Ser Gly Gly Arg Gln			
	325	330	335
cga aac atc gaa ggc tgg gtg caa aag aag cgc cct gga acc gct gca			1056
Arg Asn Ile Glu Gly Trp Val Gln Lys Lys Arg Pro Gly Thr Ala Ala			
	340	345	350
gca caa gcc gca gaa gcc gcc caa aac gtc cac aac cag gaa ggc			1101
Ala Gln Ala Ala Glu Ala Ala Gln Asn Val His Asn Gln Glu Gly			
	355	360	365
taagcaggat cctcatgact gct			1124

<210> 266

<211> 367

<212> PRT

<213> Corynebacterium glutamicum

<400> 266

Thr Asp His Thr Leu Ser Ala Leu Leu Asp Ala His Val Glu Val Pro
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Thr Ala Val Thr Val Leu Thr Met Arg Leu Asp Asp Pro Thr Gly Tyr
20 25 30

Gly Arg Ile Val Arg Asn Glu Glu Gly Glu Val Thr Ala Ile Val Glu
35 40 45

Gln Lys Asp Ala Ser Ala Glu Val Gln Ala Ile Asp Glu Val Asn Ser
50 55 60

Gly Val Phe Ala Phe Asp Ala Ala Ile Leu Arg Ser Ala Leu Ala Glu
65 70 75 80

Leu Lys Ser Asp Asn Ala Gln Gly Glu Leu Tyr Leu Thr Asp Val Leu
85 90 95

Gly Ile Ala Arg Gly Glu Gly His Pro Val Arg Ala His Thr Ala Ala
100 105 110

Asp Ala Arg Glu Leu Ala Gly Val Asn Asp Arg Val Gln Leu Ala Glu
115 120 125

Ala Gly Ala Glu Leu Asn Arg Arg Thr Val Ile Ala Ala Met Arg Gly
130 135 140

Gly Ala Thr Ile Val Asp Pro Ala Thr Thr Trp Ile Asp Val Glu Val
145 150 155 160

Ser Ile Gly Arg Asp Val Ile Ile His Pro Gly Thr Gln Leu Lys Gly
 165 170 175

Glu Thr Val Ile Gly Asp Arg Val Glu Val Gly Pro Asp Thr Thr Leu
 180 185 190

Thr Asn Met Thr Ile Gly Asp Gly Ala Ser Val Ile Arg Thr His Gly
 195 200 205

Phe Asp Ser Thr Ile Gly Glu Asn Ala Thr Val Gly Pro Phe Thr Tyr
 210 215 220

Ile Arg Pro Gly Thr Thr Leu Gly Pro Glu Gly Lys Leu Gly Gly Phe
 225 230 235 240

Val Glu Thr Lys Lys Ala Thr Ile Gly Arg Gly Ser Lys Val Pro His
 245 250 255

Leu Thr Tyr Val Gly Asp Ala Thr Ile Gly Glu Glu Ser Asn Ile Gly
 260 265 270

Ala Ser Ser Val Phe Val Asn Tyr Asp Gly Glu Asn Lys His His Thr
 275 280 285

Thr Ile Gly Ser His Val Arg Thr Gly Ser Asp Thr Met Phe Ile Ala
 290 295 300

Pro Val Thr Val Gly Asp Gly Ala Tyr Ser Gly Ala Gly Thr Val Ile
 305 310 315 320

Lys Asp Asp Val Pro Pro Gly Ala Leu Ala Val Ser Gly Gly Arg Gln
 325 330 335

Arg Asn Ile Glu Gly Trp Val Gln Lys Lys Arg Pro Gly Thr Ala Ala
 340 345 350

Ala Gln Ala Ala Glu Ala Ala Gln Asn Val His Asn Gln Glu Gly
 355 360 365

<210> 267

<211> 981

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(958)

<223> RXA01259

<400> 267

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tcaaaatgct gtaaaaactg tcgtggtacc agctgcagga atg gga aca cgg ttc 115
 Met Gly Thr Arg Phe
 1 5

ctt cct gca acg aag aca att cca aag gag ctt ctt cct gta gtt gat 163
 Leu Pro Ala Thr Lys Thr Ile Pro Lys Glu Leu Leu Pro Val Val Asp
 10 15 20

acc ccg ggt att gaa ctt gtt gcc aaa gag gct gct gat ctt ggt gca	211
Thr Pro Gly Ile Glu Leu Val Ala Lys Glu Ala Ala Asp Leu Gly Ala	
25 30 35	
act cgg tta gca att atc act gct ccg aac aaa gac gga att ctt aaa	259
Thr Arg Leu Ala Ile Ile Thr Ala Pro Asn Lys Asp Gly Ile Leu Lys	
40 45 50	
cac ttc gag gag ttc cct gag ctt gag gca act ctt gag gct cgc ggt	307
His Phe Glu Glu Phe Pro Glu Leu Glu Ala Thr Leu Glu Ala Arg Gly	
55 60 65	
aag act gat caa ctg aat aaa gtt cga gca gct cga gaa ttg att gca	355
Lys Thr Asp Gln Leu Asn Lys Val Arg Ala Ala Arg Glu Leu Ile Ala	
70 75 80 85	
aca gtt cca gtg gtt caa gaa aag cca ttg ggg ctt ggt cac gct gtt	403
Thr Val Pro Val Val Gln Glu Lys Pro Leu Gly Leu Gly His Ala Val	
90 95 100	
ggc ctt gct gag tct gtg ctc gat gat gat gaa gat gtt gtg gct gtc	451
Gly Leu Ala Glu Ser Val Leu Asp Asp Asp Glu Asp Val Val Ala Val	
105 110 115	
atg ctg cca gac gat ttg gtg ctg cca ttt ggt gtg acc gag aga atg	499
Met Leu Pro Asp Asp Leu Val Leu Pro Phe Gly Val Thr Glu Arg Met	
120 125 130	
gca gaa gtt cgc gct aag ttt ggc gga tct gtt ctt gca gca att gag	547
Ala Glu Val Arg Ala Lys Phe Gly Gly Ser Val Leu Ala Ala Ile Glu	
135 140 145	
gtg gct gaa gat gaa gtc tca aat tac gga gta ttt aag ctc ggt gaa	595
Val Ala Glu Asp Glu Val Ser Asn Tyr Gly Val Phe Lys Leu Gly Glu	
150 155 160 165	
ctc gat gca gag tcc gaa agt gaa ggc att agg cgt gtt gta gga atg	643
Leu Asp Ala Glu Ser Glu Ser Glu Gly Ile Arg Arg Val Val Gly Met	
170 175 180	
gtt gaa aag cct gcg cct gaa gat gca cca tca agg ttt gcc gca acg	691
Val Glu Lys Pro Ala Pro Glu Asp Ala Pro Ser Arg Phe Ala Ala Thr	
185 190 195	
ggc cgt tat cta ctt gat cga gct att ttt gat gca ctg cgt cga att	739
Gly Arg Tyr Leu Leu Asp Arg Ala Ile Phe Asp Ala Leu Arg Arg Ile	
200 205 210	
gag cct ggt gct ggt gga gaa ctg caa tta aca gat gcc atc gca tta	787
Glu Pro Gly Ala Gly Gly Glu Leu Gln Leu Thr Asp Ala Ile Ala Leu	
215 220 225	
ttg atc gaa gaa ggc cat ccg gta cac att gtg gtt cat gaa gga aag	835
Leu Ile Glu Glu Gly His Pro Val His Ile Val Val His Glu Gly Lys	
230 235 240 245	
cgc cat gac ctt ggt aat cca gct ggg tac att cct gct gtt gtg tac	883
Arg His Asp Leu Gly Asn Pro Ala Gly Tyr Ile Pro Ala Val Val Tyr	
250 255 260	
ttc gga ctt cgt cat gca gag tac ggt tcc aag att cac cgt gcg gtg	931

Phe Gly Leu Arg His Ala Glu Tyr Gly Ser Lys Ile His Arg Ala Val
 265 270 275

aag gaa ata ctc gct gag ttt gaa tct taaaaaggaa accgccttcc 978
 Lys Glu Ile Leu Ala Glu Phe Glu Ser
 280 285

aca 981

<210> 268

<211> 286

<212> PRT

<213> Corynebacterium glutamicum

<400> 268

Met Gly Thr Arg Phe Leu Pro Ala Thr Lys Thr Ile Pro Lys Glu Leu
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Leu Pro Val Val Asp Thr Pro Gly Ile Glu Leu Val Ala Lys Glu Ala
 20 25 30

Ala Asp Leu Gly Ala Thr Arg Leu Ala Ile Ile Thr Ala Pro Asn Lys
 35 40 45

Asp Gly Ile Leu Lys His Phe Glu Glu Phe Pro Glu Leu Glu Ala Thr
 50 55 60

Leu Glu Ala Arg Gly Lys Thr Asp Gln Leu Asn Lys Val Arg Ala Ala
 65 70 75 80

Arg Glu Leu Ile Ala Thr Val Pro Val Val Gln Glu Lys Pro Leu Gly
 85 90 95

Leu Gly His Ala Val Gly Leu Ala Glu Ser Val Leu Asp Asp Asp Glu
 100 105 110

Asp Val Val Ala Val Met Leu Pro Asp Asp Leu Val Leu Pro Phe Gly
 115 120 125

Val Thr Glu Arg Met Ala Glu Val Arg Ala Lys Phe Gly Gly Ser Val
 130 135 140

Leu Ala Ala Ile Glu Val Ala Glu Asp Glu Val Ser Asn Tyr Gly Val
 145 150 155 160

Phe Lys Leu Gly Glu Leu Asp Ala Glu Ser Glu Ser Glu Gly Ile Arg
 165 170 175

Arg Val Val Gly Met Val Glu Lys Pro Ala Pro Glu Asp Ala Pro Ser
 180 185 190

Arg Phe Ala Ala Thr Gly Arg Tyr Leu Leu Asp Arg Ala Ile Phe Asp
 195 200 205

Ala Leu Arg Arg Ile Glu Pro Gly Ala Gly Gly Glu Leu Gln Leu Thr
 210 215 220

Asp Ala Ile Ala Leu Leu Ile Glu Glu Gly His Pro Val His Ile Val
 225 230 235 240

Val His Glu Gly Lys Arg His Asp Leu Gly Asn Pro Ala Gly Tyr Ile
 245 250 255

Pro Ala Val Val Tyr Phe Gly Leu Arg His Ala Glu Tyr Gly Ser Lys
 260 265 270

Ile His Arg Ala Val Lys Glu Ile Leu Ala Glu Phe Glu Ser
 275 280 285

<210> 269

<211> 526

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(526)

<223> RXA02028

<400> 269

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tacgacgatt ggggttgccg gggcaggtac tcttggttcc atg agt ttg cct atc 115
 Met Ser Leu Pro Ile
 1 5

gat gag cac gtg aac gcg gtt aaa acc gtc gta gtg cct gct gca gga 163
 Asp Glu His Val Asn Ala Val Lys Thr Val Val Val Pro Ala Ala Gly
 10 15 20

ctg gga acc cga ttc ctt ccg gcc acc aaa acc gta ccc aag gag ttg 211
 Leu Gly Thr Arg Phe Leu Pro Ala Thr Lys Thr Val Pro Lys Glu Leu
 25 30 35

ctg ccg gtt gtc gat acc cca ggt att gag ctg att gct gct gag gct 259
 Leu Pro Val Val Asp Thr Pro Gly Ile Glu Leu Ile Ala Ala Glu Ala
 40 45 50

gcc gaa ctt ggt gcg acc agg ctg gcg atc atc act gcg cca aac aaa 307
 Ala Glu Leu Gly Ala Thr Arg Leu Ala Ile Ile Thr Ala Pro Asn Lys
 55 60 65

gct ggg gta ctt gca cac ttt gag cgt tct tct gaa ttg gaa gaa acg 355
 Ala Gly Val Leu Ala His Phe Glu Arg Ser Ser Glu Leu Glu Glu Thr
 70 75 80 85

ctg atg gag cgt ggc aag act gac cag gtg gag ata atc cgc cgc gcc 403
 Leu Met Glu Arg Gly Lys Thr Asp Gln Val Glu Ile Ile Arg Arg Ala
 90 95 100

gcc gat tta atc aag gca gtt cca gta acc cag gac aag ccg ctg ggg 451
 Ala Asp Leu Ile Lys Ala Val Pro Val Thr Gln Asp Lys Pro Leu Gly
 105 110 115

cta ggt cat gct gtt ggt ttg gct gag tct gtg ttg gat gat gat gaa 499
 Leu Gly His Ala Val Gly Leu Ala Glu Ser Val Leu Asp Asp Asp Glu
 120 125 130

gat gtc gta gcg gtg atg ttg ccg cac 526
 Asp Val Val Ala Val Met Leu Pro His

135

140

<210> 270

<211> 142

<212> PRT

<213> Corynebacterium glutamicum

<400> 270

Met Ser Leu Pro Ile Asp Glu His Val Asn Ala Val Lys Thr Val Val
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Val Pro Ala Ala Gly Leu Gly Thr Arg Phe Leu Pro Ala Thr Lys Thr
 20 25 30

Val Pro Lys Glu Leu Leu Pro Val Val Asp Thr Pro Gly Ile Glu Leu
 35 40 45

Ile Ala Ala Glu Ala Ala Glu Leu Gly Ala Thr Arg Leu Ala Ile Ile
 50 55 60

Thr Ala Pro Asn Lys Ala Gly Val Leu Ala His Phe Glu Arg Ser Ser
 65 70 75 80

Glu Leu Glu Glu Thr Leu Met Glu Arg Gly Lys Thr Asp Gln Val Glu
 85 90 95

Ile Ile Arg Arg Ala Ala Asp Leu Ile Lys Ala Val Pro Val Thr Gln
 100 105 110

Asp Lys Pro Leu Gly Leu Gly His Ala Val Gly Leu Ala Glu Ser Val
 115 120 125

Leu Asp Asp Asp Glu Asp Val Val Ala Val Met Leu Pro His
 130 135 140

<210> 271

<211> 1284

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(1261)

<223> RXA01262

<400> 271

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aaacttgctg tatcaataaa acacgaaaag gaatactttt atg aaa att gcc gtc 115
 Met Lys Ile Ala Val
 1 5

gca ggg ctc gga tat gtt ggg ctt tca aat gca gct ctc ctc tct aaa 163
 Ala Gly Leu Gly Tyr Val Gly Leu Ser Asn Ala Ala Leu Leu Ser Lys
 10 15 20

aat cat aaa gtt gtt gca gtt gac att gat gaa gaa cga gtg aaa cta 211
 Asn His Lys Val Val Ala Val Asp Ile Asp Glu Glu Arg Val Lys Leu
 25 30 35

gtt caa gaa ttt cgt tgc cca att gtc gat agc gat ctc gaa gaa tat	259
Val Gln Glu Phe Arg Ser Pro Ile Val Asp Ser Asp Leu Glu Glu Tyr	
40 45 50	
ctg tcc act aag cct caa aac tta act gcc aca acg gac gcc gaa gcc	307
Leu Ser Thr Lys Pro Gln Asn Leu Thr Ala Thr Thr Asp Ala Glu Ala	
55 60 65	
gct tac aaa ggc gca gat ttt att gtt att gca acg cca act aat tac	355
Ala Tyr Lys Gly Ala Asp Phe Ile Val Ile Ala Thr Pro Thr Asn Tyr	
70 75 80 85	
gac cca gag tca aac ttt ttt gat act tcc agc gtt gag tcc gta att	403
Asp Pro Glu Ser Asn Phe Phe Asp Thr Ser Ser Val Glu Ser Val Ile	
90 95 100	
gag ata gtc ctt aag gtt tct cct gga tcc aca atc gta att aaa tcg	451
Glu Ile Val Leu Lys Val Ser Pro Gly Ser Thr Ile Val Ile Lys Ser	
105 110 115	
act atc cct gtt ggt ttt aca tcg gaa cta cgc att aag cat cca gaa	499
Thr Ile Pro Val Gly Phe Thr Ser Glu Leu Arg Ile Lys His Pro Glu	
120 125 130	
gct tcg att att ttt tca cct gag ttc ctg cgt gaa ggc cga gca ttc	547
Ala Ser Ile Ile Phe Ser Pro Glu Phe Leu Arg Glu Gly Arg Ala Phe	
135 140 145	
tac gac aat ctc tac cca tcc aga gtt gtc gtt ggt gat cgc agt cct	595
Tyr Asp Asn Leu Tyr Pro Ser Arg Val Val Val Gly Asp Arg Ser Pro	
150 155 160 165	
ctg ggg gaa gaa ttt gcg act ctg tta gct gag ggg gca aaa gaa aag	643
Leu Gly Glu Glu Phe Ala Thr Leu Leu Ala Glu Gly Ala Lys Glu Lys	
170 175 180	
cct ccg att cta ctt acg gac tca act gag gca gag gcg att aaa tta	691
Pro Pro Ile Leu Leu Thr Asp Ser Thr Glu Ala Glu Ala Ile Lys Leu	
185 190 195	
ttt tct aat aca tat ctt gca ctg cga gtt gct ttt ttc aac gaa ctg	739
Phe Ser Asn Thr Tyr Leu Ala Leu Arg Val Ala Phe Phe Asn Glu Leu	
200 205 210	
gat act tat gcg tct gtt cga agc ttg gat act aag cag att att gaa	787
Asp Thr Tyr Ala Ser Val Arg Ser Leu Asp Thr Lys Gln Ile Ile Glu	
215 220 225	
ggg gta ggg ctc gat cca cgt att gga tct cat tac aat aat cct tca	835
Gly Val Gly Leu Asp Pro Arg Ile Gly Ser His Tyr Asn Asn Pro Ser	
230 235 240 245	
ttt gga tat ggc gga tat tgt ctt ccg aaa gat acg aaa cag ctt ctc	883
Phe Gly Tyr Gly Tyr Cys Leu Pro Lys Asp Thr Lys Gln Leu Leu	
250 255 260	
gcc aac tat aag gat gtc ccg cag aat cta atc tct gca gta gtc caa	931
Ala Asn Tyr Lys Asp Val Pro Gln Asn Leu Ile Ser Ala Val Val Gln	
265 270 275	

gca aat aag act cgt aag gac ttt att gca gag gat atc ctc agt aaa 979
 Ala Asn Lys Thr Arg Lys Asp Phe Ile Ala Glu Asp Ile Leu Ser Lys
 280 285 290

 tca cct act gta gtt gga att tac cgc ctt gta atg aag tct gga tca 1027
 Ser Pro Thr Val Val Gly Ile Tyr Arg Leu Val Met Lys Ser Gly Ser
 295 300 305

 gat aac ttt cgt tct tct tct att caa gga gtc atg aaa cga att aag 1075
 Asp Asn Phe Arg Ser Ser Ser Ile Gln Gly Val Met Lys Arg Ile Lys
 310 315 320 325

 gcc aag gga atc gaa att gta gta ttt gaa ccg aat ctc gga gaa gaa 1123
 Ala Lys Gly Ile Glu Ile Val Val Phe Glu Pro Asn Leu Gly Glu Glu
 330 335 340

 act ttc tac aat tcg aag atc ctt aat gac atc gaa gag ttt aag gat 1171
 Thr Phe Tyr Asn Ser Lys Ile Leu Asn Asp Ile Glu Glu Phe Lys Asp
 345 350 355

 tac tgc gac atc att att gca aat cgt cca acc gat gag ctt tct gat 1219
 Tyr Cys Asp Ile Ile Ile Ala Asn Arg Pro Thr Asp Glu Leu Ser Asp
 360 365 370

 gta cca gaa aaa gtt tat aca cgt gat att ttc cag cgt gac 1261
 Val Pro Glu Lys Val Tyr Thr Arg Asp Ile Phe Gln Arg Asp
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<210> 272

<211> 387

<212> PRT

<213> Corynebacterium glutamicum

<400> 272

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 20 25 30

 Glu Arg Val Lys Leu Val Gln Glu Phe Arg Ser Pro Ile Val Asp Ser
 35 40 45

 Asp Leu Glu Glu Tyr Leu Ser Thr Lys Pro Gln Asn Leu Thr Ala Thr
 50 55 60

 Thr Asp Ala Glu Ala Ala Tyr Lys Gly Ala Asp Phe Ile Val Ile Ala
 65 70 75 80

 Thr Pro Thr Asn Tyr Asp Pro Glu Ser Asn Phe Phe Asp Thr Ser Ser
 85 90 95

 Val Glu Ser Val Ile Glu Ile Val Leu Lys Val Ser Pro Gly Ser Thr
 100 105 110

 Ile Val Ile Lys Ser Thr Ile Pro Val Gly Phe Thr Ser Glu Leu Arg
 115 120 125

Ile Lys His Pro Glu Ala Ser Ile Ile Phe Ser Pro Glu Phe Leu Arg
 130 135 140
 Glu Gly Arg Ala Phe Tyr Asp Asn Leu Tyr Pro Ser Arg Val Val Val
 145 150 155 160
 Gly Asp Arg Ser Pro Leu Gly Glu Glu Phe Ala Thr Leu Leu Ala Glu
 165 170 175
 Gly Ala Lys Glu Lys Pro Pro Ile Leu Leu Thr Asp Ser Thr Glu Ala
 180 185 190
 Glu Ala Ile Lys Leu Phe Ser Asn Thr Tyr Leu Ala Leu Arg Val Ala
 195 200 205
 Phe Phe Asn Glu Leu Asp Thr Tyr Ala Ser Val Arg Ser Leu Asp Thr
 210 215 220
 Lys Gln Ile Ile Glu Gly Val Gly Leu Asp Pro Arg Ile Gly Ser His
 225 230 235 240
 Tyr Asn Asn Pro Ser Phe Gly Tyr Gly Gly Tyr Cys Leu Pro Lys Asp
 245 250 255
 Thr Lys Gln Leu Leu Ala Asn Tyr Lys Asp Val Pro Gln Asn Leu Ile
 260 265 270
 Ser Ala Val Val Gln Ala Asn Lys Thr Arg Lys Asp Phe Ile Ala Glu
 275 280 285
 Asp Ile Leu Ser Lys Ser Pro Thr Val Val Gly Ile Tyr Arg Leu Val
 290 295 300
 Met Lys Ser Gly Ser Asp Asn Phe Arg Ser Ser Ser Ile Gln Gly Val
 305 310 315 320
 Met Lys Arg Ile Lys Ala Lys Gly Ile Glu Ile Val Val Phe Glu Pro
 325 330 335
 Asn Leu Gly Glu Glu Thr Phe Tyr Asn Ser Lys Ile Leu Asn Asp Ile
 340 345 350
 Glu Glu Phe Lys Asp Tyr Cys Asp Ile Ile Ile Ala Asn Arg Pro Thr
 355 360 365
 Asp Glu Leu Ser Asp Val Pro Glu Lys Val Tyr Thr Arg Asp Ile Phe
 370 375 380
 Gln Arg Asp
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<211> 1209

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(1186)

<223> RXA01377

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Met Thr Leu Thr Asp															
1 5															
aac agc aaa aac gtt gat gct gtc atc ttg gtc ggt ggc aaa ggt acc															163
Asn Ser Lys Asn Val Asp Ala Val Ile Leu Val Gly Gly Lys Gly Thr															
10 15 20															
cga ctg cgc ccc ctg acc gtc aat act cca aag cca atg ctg cca act															211
Arg Leu Arg Pro Leu Thr Val Asn Thr Pro Lys Pro Met Leu Pro Thr															
25 30 35															
gct ggc cac cca ttc ttg acc cac ctt ttg gcc cgc atc aag gcc gca															259
Ala Gly His Pro Phe Leu Thr His Leu Leu Ala Arg Ile Lys Ala Ala															
40 45 50															
ggc atc aca cac gtc gtg ctg gga acg tca ttc aaa gct gaa gtc ttc															307
Gly Ile Thr His Val Val Leu Gly Thr Ser Phe Lys Ala Glu Val Phe															
55 60 65															
gag gaa tac ttc gga gat ggc tcc gaa atg ggc ttg gaa att gaa tat															355
Glu Glu Tyr Phe Gly Asp Gly Ser Glu Met Gly Leu Glu Ile Glu Tyr															
70 75 80 85															
gtc gtc gag gat cag cct ttg ggc act ggt ggt ggc atc cga aac gtc															403
Val Val Glu Asp Gln Pro Leu Gly Thr Gly Gly Ile Arg Asn Val															
90 95 100															
tac gac aag ctg cgt cac gat act gcg att gtg ttc aac ggc gat gtg															451
Tyr Asp Lys Leu Arg His Asp Thr Ala Ile Val Phe Asn Gly Asp Val															
105 110 115															
ctc tcc ggt gcg gat ctc aac agc att ctg gac acc cac cgc gaa aag															499
Leu Ser Gly Ala Asp Leu Asn Ser Ile Leu Asp Thr His Arg Glu Lys															
120 125 130															
gac gca gat ctg acc atg cat ctc gtg cgc gta gct aac cct cgt gcg															547
Asp Ala Asp Leu Thr Met His Leu Val Arg Val Ala Asn Pro Arg Ala															
135 140 145															
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Phe Gly Cys Val Pro Thr Asp Glu Asp Gly Arg Val Ser Glu Phe Leu															
150 155 160 165															
gaa aag acc gaa gat cca cca acc gat cag atc aac gcc ggc tgc tac															643
Glu Lys Thr Glu Asp Pro Pro Thr Asp Gln Ile Asn Ala Gly Cys Tyr															
170 175 180															
gtg ttc aag aag gaa ctc atc gag cag atc ccg gca ggc cga gca gtt															691
Val Phe Lys Lys Glu Leu Ile Glu Gln Ile Pro Ala Gly Arg Ala Val															
185 190 195															
tcc gtc gag cgc gaa acc ttc cct cag ctg ttg gaa gaa ggc aag cga															739
Ser Val Glu Arg Glu Thr Phe Pro Gln Leu Leu Glu Glu Gly Lys Arg															
200 205 210															
gtc ttc ggc cac gtc gac gct tcc tac tgg cgc gac atg ggc acc cca															787

Val Phe Gly His Val Asp Ala Ser Tyr Trp Arg Asp Met Gly Thr Pro
 215 220 225
 agc gac ttc gtc cgc ggc tcg gct gac ctg gtc cgc ggc att gcg tac 835
 Ser Asp Phe Val Arg Gly Ser Ala Asp Leu Val Arg Gly Ile Ala Tyr
 230 235 240 245
 tcc cca ttg ctc gaa ggc aaa aca gga gag tcg ctt gtc gac gcc tcc 883
 Ser Pro Leu Leu 250 Gly Lys Thr Gly Glu Ser Leu Val Asp Ala Ser
 255 260
 gcc ggc gtt cgc gac ggc gtc ctg ctg ctc ggc gga acc gta gtc ggc 931
 Ala Gly Val Arg Asp Gly Val Leu Leu Leu Gly Gly Thr Val Val Gly
 265 270 275
 cgc ggc act gag atc ggt gcc ggc tgc cgc gtt gac aac act gtt att 979
 Arg Gly Thr Glu Ile Gly Ala Gly Cys Arg Val Asp Asn Thr Val Ile
 280 285 290
 ttc gac ggc gtc acc att gaa cca ggt gcg gtc att gaa aat tcc atc 1027
 Phe Asp Gly Val Thr Ile Glu Pro Gly Ala Val Ile Glu Asn Ser Ile
 295 300 305
 att tcc tcg gga gca cgc atc ggt gct aat gcg cac atc tcc ggt tgc 1075
 Ile Ser Ser Gly Ala Arg Ile Gly Ala Asn Ala His Ile Ser Gly Cys
 310 315 320 325
 atc att ggc gag ggc gca cag gtt ggt gct cgg tgt gaa ctc aac gca 1123
 Ile Ile Gly Glu Gly Ala Gln Val Gly Ala Arg Cys Glu Leu Asn Ala
 330 335 340
 ggg atg cgc gtc ttc cca ggc gtt gtg atc cca gac agc gga att cgt 1171
 Gly Met Arg Val Phe Pro Gly Val Val Ile Pro Asp Ser Gly Ile Arg
 345 350 355
 ttt tcg tct gat cag taggcatttt tagccctttt gga 1209
 Phe Ser Ser Asp Gln
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<210> 274

<211> 362

<212> PRT

<213> Corynebacterium glutamicum

<400> 274

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 20 25 30
 Pro Met Leu Pro Thr Ala Gly His Pro Phe Leu Thr His Leu Leu Ala
 35 40 45
 Arg Ile Lys Ala Ala Gly Ile Thr His Val Val Leu Gly Thr Ser Phe
 50 55 60
 Lys Ala Glu Val Phe Glu Tyr Phe Gly Asp Gly Ser Glu Met Gly
 65 70 75 80

Leu Glu Ile Glu Tyr Val Val Glu Asp Gln Pro Leu Gly Thr Gly Gly
 85 90 95
 Gly Ile Arg Asn Val Tyr Asp Lys Leu Arg His Asp Thr Ala Ile Val
 100 105 110
 Phe Asn Gly Asp Val Leu Ser Gly Ala Asp Leu Asn Ser Ile Leu Asp
 115 120 125
 Thr His Arg Glu Lys Asp Ala Asp Leu Thr Met His Leu Val Arg Val
 130 135 140
 Ala Asn Pro Arg Ala Phe Gly Cys Val Pro Thr Asp Glu Asp Gly Arg
 145 150 155 160
 Val Ser Glu Phe Leu Glu Lys Thr Glu Asp Pro Pro Thr Asp Gln Ile
 165 170 175
 Asn Ala Gly Cys Tyr Val Phe Lys Lys Glu Leu Ile Glu Gln Ile Pro
 180 185 190
 Ala Gly Arg Ala Val Ser Val Glu Arg Glu Thr Phe Pro Gln Leu Leu
 195 200 205
 Glu Glu Gly Lys Arg Val Phe Gly His Val Asp Ala Ser Tyr Trp Arg
 210 215 220
 Asp Met Gly Thr Pro Ser Asp Phe Val Arg Gly Ser Ala Asp Leu Val
 225 230 235 240
 Arg Gly Ile Ala Tyr Ser Pro Leu Leu Glu Gly Lys Thr Gly Glu Ser
 245 250 255
 Leu Val Asp Ala Ser Ala Gly Val Arg Asp Gly Val Leu Leu Leu Gly
 260 265 270
 Gly Thr Val Val Gly Arg Gly Thr Glu Ile Gly Ala Gly Cys Arg Val
 275 280 285
 Asp Asn Thr Val Ile Phe Asp Gly Val Thr Ile Glu Pro Gly Ala Val
 290 295 300
 Ile Glu Asn Ser Ile Ile Ser Ser Gly Ala Arg Ile Gly Ala Asn Ala
 305 310 315 320
 His Ile Ser Gly Cys Ile Ile Gly Glu Gly Ala Gln Val Gly Ala Arg
 325 330 335
 Cys Glu Leu Asn Ala Gly Met Arg Val Phe Pro Gly Val Val Ile Pro
 340 345 350
 Asp Ser Gly Ile Arg Phe Ser Ser Asp Gln
 355 360

<210> 275

<211> 1350

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(1327)

<223> RXA02063

<400> 275

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ttgttaccca gctttcatgc gggatagtta ttttgccttt atg gtt aag ggt gtg 115
                                         Met Val Lys Gly Val
                                         1                               5

aag ggt aga cca aat gtt cta gca atc gtt ctc gca ggt ggc gag ggc 163
Lys Gly Arg Pro Asn Val Leu Ala Ile Val Leu Ala Gly Gly Glu Gly
                               10                               15                               20

aaa cga ctt ttt ccg ttg acg gag gac cga gct aag cct gcg gtc cca 211
Lys Arg Leu Phe Pro Leu Thr Glu Asp Arg Ala Lys Pro Ala Val Pro
                               25                               30                               35

ttc ggc gga act tac aga ttg atc gac ttt gtt ttg tcg aac ctg gtg 259
Phe Gly Gly Thr Tyr Arg Leu Ile Asp Phe Val Leu Ser Asn Leu Val
                               40                               45                               50

aac tcc gga ttc ctc aag atc gcg gta ctg act cag tac aag tcg cat 307
Asn Ser Gly Phe Leu Lys Ile Ala Val Leu Thr Gln Tyr Lys Ser His
                               55                               60                               65

tca ttg gat agg cat att tca ttg tcg tgg aac gtg tct ggt cca acg 355
Ser Leu Asp Arg His Ile Ser Leu Ser Trp Asn Val Ser Gly Pro Thr
                               70                               75                               80                               85

ggg cag tac att gct tct gtt cct gcg cag cag cgc ctg ggc aag cga 403
Gly Gln Tyr Ile Ala Ser Val Pro Ala Gln Gln Arg Leu Gly Lys Arg
                               90                               95                               100

tgg ttc act ggt tcc gcg gat gca att ttg cag tct ctg aac ttg atc 451
Trp Phe Thr Gly Ser Ala Asp Ala Ile Leu Gln Ser Leu Asn Leu Ile
                               105                               110                               115

tct gat gag aaa ccg gat tat gtc atc gtt ttc ggc gcg gac cac gtg 499
Ser Asp Glu Lys Pro Asp Tyr Val Ile Val Phe Gly Ala Asp His Val
                               120                               125                               130

tat cgc atg gac cca agc cag atg cta gat gag cac att gca tct ggt 547
Tyr Arg Met Asp Pro Ser Gln Met Leu Asp Glu His Ile Ala Ser Gly
                               135                               140                               145

cgc gcg gtg tct gtg gca ggt att cgc gtt cca cgt gag gaa gca act 595
Arg Ala Val Ser Val Ala Gly Ile Arg Val Pro Arg Glu Glu Ala Thr
                               150                               155                               160                               165

gcg ttt ggt tgc atc cag tcc gat gtc gac ggc aac ata acc gag ttc 643
Ala Phe Gly Cys Ile Gln Ser Asp Val Asp Gly Asn Ile Thr Glu Phe
                               170                               175                               180

ttg gaa aag cca gct gac cct ccg gga acc cct gat gat cct gac atg 691
Leu Glu Lys Pro Ala Asp Pro Pro Gly Thr Pro Asp Asp Pro Asp Met
                               185                               190                               195

act tac gcg tcg atg ggt aac tac att ttc acc act gaa gcc ctg atc 739
Thr Tyr Ala Ser Met Gly Asn Tyr Ile Phe Thr Thr Glu Ala Leu Ile

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200	205	210	
cag gcg ctg aaa gat gat	gaa aat aac gag aac agt gat cat gac atg		787
Gln Ala Leu Lys Asp Asp	Glu Asn Asn Glu Asn Ser Asp His Asp Met		
215	220	225	
ggc gga gac atc att ccg tac ttc gtc tct cgc aat gat gcg cat gtt			835
Gly Gly Asp Ile Ile Pro Tyr Phe Val Ser Arg Asn Asp Ala His Val			
230	235	240	245
tat gat ttc tcc gga aac att gtt cct ggc gca act gag cgt gac aag			883
Tyr Asp Phe Ser Gly Asn Ile Val Pro Gly Ala Thr Glu Arg Asp Lys			
250	255	260	
ggc tac tgg cgc gac gtc ggt acc att gat gcg ttc tac gag tgc cac			931
Gly Tyr Trp Arg Asp Val Gly Thr Ile Asp Ala Phe Tyr Glu Cys His			
265	270	275	
atg gac ctg att tcc gtg cac cca atc ttc aat ctg tat aac tct gag			979
Met Asp Leu Ile Ser Val His Pro Ile Phe Asn Leu Tyr Asn Ser Glu			
280	285	290	
tgg cca atc cac acg acc tct gaa ggt aac ttg cct ccg gct aag ttc			1027
Trp Pro Ile His Thr Thr Ser Glu Gly Asn Leu Pro Pro Ala Lys Phe			
295	300	305	
gtt cgg ggc ggt atc gcg cag tcg tcg atg gtg tct tca ggt tcc atc			1075
Val Arg Gly Gly Ile Ala Gln Ser Ser Met Val Ser Ser Gly Ser Ile			
310	315	320	325
att tct gct ggg act gtt cgc aac tcc gtg ctg tcc aac aac gtt gtc			1123
Ile Ser Ala Gly Thr Val Arg Asn Ser Val Leu Ser Asn Asn Val Val			
330	335	340	
gtc gaa gag ggc gca acg gtg gaa ggt gca gtg ctg atg cca ggc gtg			1171
Val Glu Glu Gly Ala Thr Val Glu Gly Ala Val Leu Met Pro Gly Val			
345	350	355	
cgc atc ggt aag ggt gct gtt gtc cgc cat gcg att ctg gac aag aac			1219
Arg Ile Gly Lys Gly Ala Val Val Arg His Ala Ile Leu Asp Lys Asn			
360	365	370	
gtg gtt gtc cgc gac gga gag ctc atc ggt gtc gac caa gtg cgc gat			1267
Val Val Val Arg Asp Gly Glu Leu Ile Gly Val Asp Gln Val Arg Asp			
375	380	385	
gcg cag cgc ttc aag gtg agc gcc ggc ggc gtc gtg gtt gtc ggt aag			1315
Ala Gln Arg Phe Lys Val Ser Ala Gly Gly Val Val Val Val Gly Lys			
390	395	400	405
aac cag gta gtc taaacgggaa agggacctta aaa			1350
Asn Gln Val Val			

<210> 276

<211> 409

<212> PRT

<213> Corynebacterium glutamicum

<400> 276

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 20 25 30
 Lys Pro Ala Val Pro Phe Gly Gly Thr Tyr Arg Leu Ile Asp Phe Val
 35 40 45
 Leu Ser Asn Leu Val Asn Ser Gly Phe Leu Lys Ile Ala Val Leu Thr
 50 55 60
 Gln Tyr Lys Ser His Ser Leu Asp Arg His Ile Ser Leu Ser Trp Asn
 65 70 75 80
 Val Ser Gly Pro Thr Gly Gln Tyr Ile Ala Ser Val Pro Ala Gln Gln
 85 90 95
 Arg Leu Gly Lys Arg Trp Phe Thr Gly Ser Ala Asp Ala Ile Leu Gln
 100 105 110
 Ser Leu Asn Leu Ile Ser Asp Glu Lys Pro Asp Tyr Val Ile Val Phe
 115 120 125
 Gly Ala Asp His Val Tyr Arg Met Asp Pro Ser Gln Met Leu Asp Glu
 130 135 140
 His Ile Ala Ser Gly Arg Ala Val Ser Val Ala Gly Ile Arg Val Pro
 145 150 155 160
 Arg Glu Glu Ala Thr Ala Phe Gly Cys Ile Gln Ser Asp Val Asp Gly
 165 170 175
 Asn Ile Thr Glu Phe Leu Glu Lys Pro Ala Asp Pro Pro Gly Thr Pro
 180 185 190
 Asp Asp Pro Asp Met Thr Tyr Ala Ser Met Gly Asn Tyr Ile Phe Thr
 195 200 205
 Thr Glu Ala Leu Ile Gln Ala Leu Lys Asp Asp Glu Asn Asn Glu Asn
 210 215 220
 Ser Asp His Asp Met Gly Gly Asp Ile Ile Pro Tyr Phe Val Ser Arg
 225 230 235 240
 Asn Asp Ala His Val Tyr Asp Phe Ser Gly Asn Ile Val Pro Gly Ala
 245 250 255
 Thr Glu Arg Asp Lys Gly Tyr Trp Arg Asp Val Gly Thr Ile Asp Ala
 260 265 270
 Phe Tyr Glu Cys His Met Asp Leu Ile Ser Val His Pro Ile Phe Asn
 275 280 285
 Leu Tyr Asn Ser Glu Trp Pro Ile His Thr Thr Ser Glu Gly Asn Leu
 290 295 300
 Pro Pro Ala Lys Phe Val Arg Gly Gly Ile Ala Gln Ser Ser Met Val
 305 310 315 320
 Ser Ser Gly Ser Ile Ile Ser Ala Gly Thr Val Arg Asn Ser Val Leu

325	330	335	
Ser Asn Asn Val Val Val Glu Glu Gly Ala Thr Val Glu Gly Ala Val			
340	345	350	
Leu Met Pro Gly Val Arg Ile Gly Lys Gly Ala Val Val Arg His Ala			
355	360	365	
Ile Leu Asp Lys Asn Val Val Val Arg Asp Gly Glu Leu Ile Gly Val			
370	375	380	
Asp Gln Val Arg Asp Ala Gln Arg Phe Lys Val Ser Ala Gly Gly Val			
385	390	395	400
Val Val Val Gly Lys Asn Gln Val Val			
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<223> RXN00014			
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		Met Ser Lys Tyr Ala	
		1 5	
gac gat tta gcc tta gcc ctc gaa ctt gcc gaa ctt gcc gat tcc atc			163
Asp Asp Leu Ala Leu Ala Leu Glu Leu Ala Glu Leu Ala Asp Ser Ile			
10 15 20			
acc ctc gac cgc ttc gaa gcc tct gac ctg gaa gta tcc tcc aag cca			211
Thr Leu Asp Arg Phe Glu Ala Ser Asp Leu Glu Val Ser Ser Lys Pro			
25 30 35			
gac atg act ccc gtc agc gat gcc gac ctg gcg acc gaa gaa gca ctc			259
Asp Met Thr Pro Val Ser Asp Ala Asp Leu Ala Thr Glu Glu Ala Leu			
40 45 50			
cgt gag aaa atc gcc acc gcc cgc ccc gcc gac tcc atc ctc ggt gaa			307
Arg Glu Lys Ile Ala Thr Ala Arg Pro Ala Asp Ser Ile Leu Gly Glu			
55 60 65			
gaa ttc ggt ggc gac gta gaa ttc agc ggc cgc cag tgg atc atc gac			355
Glu Phe Gly Gly Asp Val Glu Phe Ser Gly Arg Gln Trp Ile Ile Asp			
70 75 80 85			
ccc atc gac ggc acc aaa aac tac gtc cgc ggc gtc ccc gta tgg gca			403
Pro Ile Asp Gly Thr Lys Asn Tyr Val Arg Gly Val Pro Val Trp Ala			
90 95 100			
acc ctg atc gcg ctg ctc gac aac ggc aaa ccc gtc gca ggt gtc atc			451
Thr Leu Ile Ala Leu Leu Asp Asn Gly Lys Pro Val Ala Gly Val Ile			

105	110	115	
tcc gca ccc gca ctg gct agg cgt tgg tgg gca tcc gaa ggg gcc ggc			499
Ser Ala Pro Ala Leu Ala Arg Arg Trp Trp Ala Ser Glu Gly Ala Gly			
120	125	130	
gca tgg cgc acc ttc aac ggc agc tcc cca cgc aaa ctg tcc gtg tcc			547
Ala Trp Arg Thr Phe Asn Gly Ser Ser Pro Arg Lys Leu Ser Val Ser			
135	140	145	
cag gtg tcc aag ctt gac gac gcc tcc ctc tcc ttc tcc tcc ctc tcc			595
Gln Val Ser Lys Leu Asp Asp Ala Ser Leu Ser Phe Ser Ser Leu Ser			
150	155	160	165
ggc tgg gcc gaa cga gat ttg cgc gat cag ttc gtc tcc cta act gat			643
Gly Trp Ala Glu Arg Asp Leu Arg Asp Gln Phe Val Ser Leu Thr Asp			
170	175	180	
acc acc tgg cga ctc cgc ggc tac ggc gac ttc ttc tcc tac tgc ctc			691
Thr Thr Trp Arg Leu Arg Gly Tyr Gly Asp Phe Phe Ser Tyr Cys Leu			
185	190	195	
gtc gcc gaa ggt gcc gtc gat atc gcc gct gaa cca gaa gtc agc ctc			739
Val Ala Glu Gly Ala Val Asp Ile Ala Ala Glu Pro Glu Val Ser Leu			
200	205	210	
tgg gat ctt gct ccc ctg tcc atc ctg gtc acc gaa gcc gga gga aag			787
Trp Asp Leu Ala Pro Leu Ser Ile Leu Val Thr Glu Ala Gly Gly Lys			
215	220	225	
ttc acc tca ctg gct ggc gtc gat gga cca cac ggt ggc gat gca gta			835
Phe Thr Ser Leu Ala Gly Val Asp Gly Pro His Gly Gly Asp Ala Val			
230	235	240	245
gcc acc aac ggc atc ctg cac gat gag acg ctg gat cgt tta aaa			880
Ala Thr Asn Gly Ile Leu His Asp Glu Thr Leu Asp Arg Leu Lys			
250	255	260	
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Leu Ala Asp Ser Ile Thr Leu Asp Arg Phe Glu Ala Ser Asp Leu Glu			
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Val Ser Ser Lys Pro Asp Met Thr Pro Val Ser Asp Ala Asp Leu Ala			
35	40	45	
Thr Glu Glu Ala Leu Arg Glu Lys Ile Ala Thr Ala Arg Pro Ala Asp			
50	55	60	
Ser Ile Leu Gly Glu Glu Phe Gly Gly Asp Val Glu Phe Ser Gly Arg			
65	70	75	80

Gln	Trp	Ile	Ile	Asp	Pro	Ile	Asp	Gly	Thr	Lys	Asn	Tyr	Val	Arg	Gly	
				85					90					95		
Val	Pro	Val	Trp	Ala	Thr	Leu	Ile	Ala	Leu	Leu	Asp	Asn	Gly	Lys	Pro	
				100					105					110		
Val	Ala	Gly	Val	Ile	Ser	Ala	Pro	Ala	Leu	Ala	Arg	Arg	Trp	Trp	Ala	
				115					120					125		
Ser	Glu	Gly	Ala	Gly	Ala	Trp	Arg	Thr	Phe	Asn	Gly	Ser	Ser	Pro	Arg	
				130					135					140		
Lys	Leu	Ser	Val	Ser	Gln	Val	Ser	Lys	Leu	Asp	Asp	Ala	Ser	Leu	Ser	
				145					150					155		
Phe	Ser	Ser	Leu	Ser	Gly	Trp	Ala	Glu	Arg	Asp	Leu	Arg	Asp	Gln	Phe	
				165					170					175		
Val	Ser	Leu	Thr	Asp	Thr	Thr	Trp	Arg	Leu	Arg	Gly	Tyr	Gly	Asp	Phe	
				180					185					190		
Phe	Ser	Tyr	Cys	Leu	Val	Ala	Glu	Gly	Ala	Val	Asp	Ile	Ala	Ala	Glu	
				195					200					205		
Pro	Glu	Val	Ser	Leu	Trp	Asp	Leu	Ala	Pro	Leu	Ser	Ile	Leu	Val	Thr	
				210					215					220		
Glu	Ala	Gly	Gly	Lys	Phe	Thr	Ser	Leu	Ala	Gly	Val	Asp	Gly	Pro	His	
				225					230					235		
Gly	Gly	Asp	Ala	Val	Ala	Thr	Asn	Gly	Ile	Leu	His	Asp	Glu	Thr	Leu	
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Asp	Arg	Leu	Lys													
				260												

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<212> DNA
<213> Corynebacterium glutamicum
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<222> (101)..(880)  
<223> FRXA00014
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Met Ser Lys Tyr Ala
1 5

gac gat tta gcc tta gcc ctc gaa ctc gcc gaa ctt gcc gat tcc atc 163
Asp Asp Leu Ala Leu Ala Leu Glu Leu Ala Glu Leu Ala Asp Ser Ile
10 15 20

acc ctc gac cgc ttc gaa gcc tct gac ctg gaa gta tcc tcc aag cca 211
Thr Leu Asp Arg Phe Glu Ala Ser Asp Leu Glu Val Ser Ser Lys Pro

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25	30	35	
gac atg act ccc gtc agc gat gcc gac ctg gcg acc gaa gaa gca ctc Asp Met Thr Pro Val Ser Asp Ala Asp Leu Ala Thr Glu Glu Ala Leu 40 45 50			259
cgc gag aaa atc gcc acc gcc cgc ccc gcc gac tcc atc ctc ggt gaa Arg Glu Lys Ile Ala Thr Ala Arg Pro Ala Asp Ser Ile Leu Gly Glu 55 60 65			307
gaa ttc ggt ggc gac gta gaa ttc agc ggc cgc cag tgg atc atc gac Glu Phe Gly Gly Asp Val Glu Phe Ser Gly Arg Gln Trp Ile Ile Asp 70 75 80 85			355
ccc atc gac ggc acc aaa aac tac gtc cgc ggc gtc ccc gta tgg gca Pro Ile Asp Gly Thr Lys Asn Tyr Val Arg Gly Val Pro Val Trp Ala 90 95 100			403
acc ctg atc gcg ctg ctc gac aac ggc aaa ccc gtc gca ggt gtc atc Thr Leu Ile Ala Leu Leu Asp Asn Gly Lys Pro Val Ala Gly Val Ile 105 110 115			451
tcc gca ccc gca ctg gct agg cgt tgg tgg gca tcc gaa ggg gcc ggc Ser Ala Pro Ala Leu Ala Arg Arg Trp Trp Ala Ser Glu Gly Ala Gly 120 125 130			499
gca tgg cgc acc ttc aac ggc agc tcc cca cgc aaa ctg tcc gtg tcc Ala Trp Arg Thr Phe Asn Gly Ser Ser Pro Arg Lys Leu Ser Val Ser 135 140 145			547
cag gtg tcc aag ctt gac gac gcc tcc ctc tcc ttc tcc tcc ctc tcc Gln Val Ser Lys Leu Asp Asp Ala Ser Leu Ser Phe Ser Ser Leu Ser 150 155 160 165			595
ggc tgg gcc gaa cga gat ttg cgc gat cag ttc gtc tcc cta act gat Gly Trp Ala Glu Arg Asp Leu Arg Asp Gln Phe Val Ser Leu Thr Asp 170 175 180			643
acc acc tgg cga ctc cgc ggc tac ggc gac ttc ttc tcc tac tgc ctc Thr Thr Trp Arg Leu Arg Gly Tyr Gly Asp Phe Phe Ser Tyr Cys Leu 185 190 195			691
gtc gcc gaa ggt gcc gtc gat atc gcc gct gaa cca gaa gtc agc ctc Val Ala Glu Gly Ala Val Asp Ile Ala Ala Glu Pro Glu Val Ser Leu 200 205 210			739
tgg gat ctt gct ccc ctg tcc atc ctg gtc acc gaa gcc gga gga aag Trp Asp Leu Ala Pro Leu Ser Ile Leu Val Thr Glu Ala Gly Gly Lys 215 220 225			787
ttc acc tca ctg gct ggc gtc gat gga cca cac ggt ggc gat gca gta Phe Thr Ser Leu Ala Gly Val Asp Gly Pro His Gly Gly Asp Ala Val 230 235 240 245			835
gcc acc aac ggc atc ctg cac gat gag acg ctg gat cgt tta aaa Ala Thr Asn Gly Ile Leu His Asp Glu Thr Leu Asp Arg Leu Lys 250 255 260			880
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<210> 280
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 <212> PRT
 <213> Corynebacterium glutamicum

<400> 280
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 Leu Ala Asp Ser Ile Thr Leu Asp Arg Phe Glu Ala Ser Asp Leu Glu
 20 25 30
 Val Ser Ser Lys Pro Asp Met Thr Pro Val Ser Asp Ala Asp Leu Ala
 35 40 45
 Thr Glu Glu Ala Leu Arg Glu Lys Ile Ala Thr Ala Arg Pro Ala Asp
 50 55 60
 Ser Ile Leu Gly Glu Glu Phe Gly Gly Asp Val Glu Phe Ser Gly Arg
 65 70 75 80
 Gln Trp Ile Ile Asp Pro Ile Asp Gly Thr Lys Asn Tyr Val Arg Gly
 85 90 95
 Val Pro Val Trp Ala Thr Leu Ile Ala Leu Leu Asp Asn Gly Lys Pro
 100 105 110
 Val Ala Gly Val Ile Ser Ala Pro Ala Leu Ala Arg Arg Trp Trp Ala
 115 120 125
 Ser Glu Gly Ala Gly Ala Trp Arg Thr Phe Asn Gly Ser Ser Pro Arg
 130 135 140
 Lys Leu Ser Val Ser Gln Val Ser Lys Leu Asp Asp Ala Ser Leu Ser
 145 150 155 160
 Phe Ser Ser Leu Ser Gly Trp Ala Glu Arg Asp Leu Arg Asp Gln Phe
 165 170 175
 Val Ser Leu Thr Asp Thr Thr Trp Arg Leu Arg Gly Tyr Gly Asp Phe
 180 185 190
 Phe Ser Tyr Cys Leu Val Ala Glu Gly Ala Val Asp Ile Ala Ala Glu
 195 200 205
 Pro Glu Val Ser Leu Trp Asp Leu Ala Pro Leu Ser Ile Leu Val Thr
 210 215 220
 Glu Ala Gly Gly Lys Phe Thr Ser Leu Ala Gly Val Asp Gly Pro His
 225 230 235 240
 Gly Gly Asp Ala Val Ala Thr Asn Gly Ile Leu His Asp Glu Thr Leu
 245 250 255
 Asp Arg Leu Lys
 260

<210> 281
 <211> 978
 <212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(955)

<223> RXA01570

<400> 281

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ggcagaccgc cctcaacgac tacctcaagg aactctcaaa gtg aaa ggc atc atc 115
                               Val Lys Gly Ile Ile
                               1 5

ctc gca ggt ggc tcc ggc acc cgg ctc tac ccc atc acc aag ggc atc 163
Leu Ala Gly Gly Ser Gly Thr Arg Leu Tyr Pro Ile Thr Lys Gly Ile
                               10 15 20

tcc aag caa ctg atg ccg att tac gac aaa ccc atg gtc tac tac cca 211
Ser Lys Gln Leu Met Pro Ile Tyr Asp Lys Pro Met Val Tyr Tyr Pro
                               25 30 35

ctg acc acg ctc att cag gcc ggc atc aaa gac atc ctg att atc acc 259
Leu Thr Thr Leu Ile Gln Ala Gly Ile Lys Asp Ile Leu Ile Ile Thr
                               40 45 50

acc cct gaa gac agc gcc tcc ttt gaa cgc ttg ctt ggc gac ggc tcc 307
Thr Pro Glu Asp Ser Ala Ser Phe Glu Arg Leu Leu Gly Asp Gly Ser
                               55 60 65

tcc tgg ggc atc aac ctc acc tac gcc gtc caa ccc tcc ccc gac gga 355
Ser Trp Gly Ile Asn Leu Thr Tyr Ala Val Gln Pro Ser Pro Asp Gly
70 75 80 85

cta gcc caa gca ttc atc atc ggc gag gaa ttc atc ggt gac gac gac 403
Leu Ala Gln Ala Phe Ile Ile Gly Glu Glu Phe Ile Gly Asp Asp Asp
90 95 100

gtc gcg ttg gtg ctt ggc gat aac atc ttc gac ggc gca caa ctt ggc 451
Val Ala Leu Val Leu Gly Asp Asn Ile Phe Asp Gly Ala Gln Leu Gly
105 110 115

cac gca cta aag cag tgc tcc aac ccc gac ggt ggc att gtc ttt gct 499
His Ala Leu Lys Gln Cys Ser Asn Pro Asp Gly Gly Ile Val Phe Ala
120 125 130

tat gag gtc tcc gat cct gag cgt tat ggc gtg gtg gaa ttt gat gct 547
Tyr Glu Val Ser Asp Pro Glu Arg Tyr Gly Val Val Glu Phe Asp Ala
135 140 145

gct aat aag gcg gtg tct att gaa gaa aag ccc acc gcg cca aaa tcc 595
Ala Asn Lys Ala Val Ser Ile Glu Glu Lys Pro Thr Ala Pro Lys Ser
150 155 160 165

aac ttt gcc gtg gta gga cta tat ttc tac gac aat cgc gtg gtg gac 643
Asn Phe Ala Val Val Gly Leu Tyr Phe Tyr Asp Asn Arg Val Val Asp
170 175 180

atc gcc aag tca atc aag cct tcc tcg cgt ggc gaa ctg gaa atc acc 691
Ile Ala Lys Ser Ile Lys Pro Ser Ser Arg Gly Glu Leu Glu Ile Thr
185 190 195

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tcc gtt aac gat gcc tac ctc cag caa ggt gct tta act gtg cag cgc 739
 Ser Val Asn Asp Ala Tyr Leu Gln Gln Gly Ala Leu Thr Val Gln Arg
 200 205 210

ctg gac cgt ggc gat gtc tgg tta gat acc ggc aca atc gat tcc atg 787
 Leu Asp Arg Gly Asp Val Trp Leu Asp Thr Gly Thr Ile Asp Ser Met
 215 220 225

tcc gag gcg tct tcc tat gtt gag gtc ctg caa aaa cgt acc ggc aac 835
 Ser Glu Ala Ser Ser Tyr Val Glu Val Leu Gln Lys Arg Thr Gly Asn
 230 235 240 245

atc atc gga tcc ccc gaa gtc gct gcg tac cgc gaa ggt ttc atc aca 883
 Ile Ile Gly Ser Pro Glu Val Ala Ala Tyr Arg Glu Gly Phe Ile Thr
 250 255 260

gct gaa gaa ctc aca gtg ctt ggt gag gaa ctg aag aaa tca ggc tac 931
 Ala Glu Glu Leu Thr Val Leu Gly Glu Glu Leu Lys Lys Ser Gly Tyr
 265 270 275

gga aac tac ctg ctg aga gct ttg taatttacgg tgtggtgtg gag 978
 Gly Asn Tyr Leu Leu Arg Ala Leu
 280 285

<210> 282

<211> 285

<212> PRT

<213> Corynebacterium glutamicum

<400> 282

Val Lys Gly Ile Ile Leu Ala Gly Gly Ser Gly Thr Arg Leu Tyr Pro
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Ile Thr Lys Gly Ile Ser Lys Gln Leu Met Pro Ile Tyr Asp Lys Pro
 20 25 30

Met Val Tyr Tyr Pro Leu Thr Thr Leu Ile Gln Ala Gly Ile Lys Asp
 35 40 45

Ile Leu Ile Ile Thr Thr Pro Glu Asp Ser Ala Ser Phe Glu Arg Leu
 50 55 60

Leu Gly Asp Gly Ser Ser Trp Gly Ile Asn Leu Thr Tyr Ala Val Gln
 65 70 75 80

Pro Ser Pro Asp Gly Leu Ala Gln Ala Phe Ile Ile Gly Glu Glu Phe
 85 90 95

Ile Gly Asp Asp Asp Val Ala Leu Val Leu Gly Asp Asn Ile Phe Asp
 100 105 110

Gly Ala Gln Leu Gly His Ala Leu Lys Gln Cys Ser Asn Pro Asp Gly
 115 120 125

Gly Ile Val Phe Ala Tyr Glu Val Ser Asp Pro Glu Arg Tyr Gly Val
 130 135 140

Val Glu Phe Asp Ala Ala Asn Lys Ala Val Ser Ile Glu Glu Lys Pro
 145 150 155 160

Thr Ala Pro Lys Ser Asn Phe Ala Val Val Gly Leu Tyr Phe Tyr Asp
 165 170 175

Asn Arg Val Val Asp Ile Ala Lys Ser Ile Lys Pro Ser Ser Arg Gly
 180 185 190

Glu Leu Glu Ile Thr Ser Val Asn Asp Ala Tyr Leu Gln Gln Gly Ala
 195 200 205

Leu Thr Val Gln Arg Leu Asp Arg Gly Asp Val Trp Leu Asp Thr Gly
 210 215 220

Thr Ile Asp Ser Met Ser Glu Ala Ser Ser Tyr Val Glu Val Leu Gln
 225 230 235 240

Lys Arg Thr Gly Asn Ile Ile Gly Ser Pro Glu Val Ala Ala Tyr Arg
 245 250 255

Glu Gly Phe Ile Thr Ala Glu Glu Leu Thr Val Leu Gly Glu Glu Leu
 260 265 270

Lys Lys Ser Gly Tyr Gly Asn Tyr Leu Leu Arg Ala Leu
 275 280 285

<210> 283

<211> 891

<212> DNA

<213> *Corynebacterium glutamicum*

<220>

<221> CDS

<222> (101)..(868)

<223> RXA02666

<400> 283

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 Met Ser Ser Thr Arg
 1 5

atc ccc gtc atc gca ctc ctc gcg gcg gcg ggg cgc gga acc cgc ctc 163
 Ile Pro Val Ile Ala Leu Leu Ala Ala Ala Gly Arg Gly Thr Arg Leu
 10 15 20

ggc gga ccc atc ccc aaa gca ttc gtc acg ttg cgt gaa cgc aca ctt 211
 Gly Gly Pro Ile Pro Lys Ala Phe Val Thr Leu Arg Glu Arg Thr Leu
 25 30 35

tta gag cgc tcg ctc caa gcc atg ctc acc tcc gaa agc gtc gac gaa 259
 Leu Glu Arg Ser Leu Gln Ala Met Leu Thr Ser Glu Ser Val Asp Glu
 40 45 50

atc atc atc ctc gtc agc ccc gac atg gaa acc tac gcc cgc gat ttg 307
 Ile Ile Ile Leu Val Ser Pro Asp Met Glu Thr Tyr Ala Arg Asp Leu
 55 60 65

ctg cgc aaa cgc ggt ctt ttg aac gac ccc gaa ggg gta cgc gta cgg 355
 Leu Arg Lys Arg Gly Leu Leu Asn Asp Pro Glu Gly Val Arg Val Arg

70	75	80	85	
ctc gtg cac ggc ggc ggg gag cgc gcg gac tcg gtc tgg gca ggc ctt				403
Leu Val His Gly Gly Gly Glu Arg Ala Asp Ser Val Trp Ala Gly Leu	90	95	100	
cag gca att tcg ctt gac gac gcc acc ccc gat gca att gtc tta atc				451
Gln Ala Ile Ser Leu Asp Asp Ala Thr Pro Asp Ala Ile Val Leu Ile	105	110	115	
cac gac agc gcc cga gcg ctc aca cca ccc ggc atg att gcg cgc gtg				499
His Asp Ser Ala Arg Ala Leu Thr Pro Pro Gly Met Ile Ala Arg Val	120	125	130	
gtg cgc aaa gtc cac gaa ggc gcc acc gca gtc atc cca gta ctg cca				547
Val Arg Lys Val His Glu Gly Ala Thr Ala Val Ile Pro Val Leu Pro	135	140	145	
gta tcg gac acc atc aaa cga gtg tcc cct gat ggc gga gta gtt gtc				595
Val Ser Asp Thr Ile Lys Arg Val Ser Pro Asp Gly Gly Val Val Val	150	155	160	165
gac aca ccc aac cgt gca gaa ctt cgc gcc gtc caa acc cca caa ggc				643
Asp Thr Pro Asn Arg Ala Glu Leu Arg Ala Val Gln Thr Pro Gln Gly	170	175	180	
ttc ctg ctg tcc gaa ctt gtt gca gcg aat gag aaa ttc ttc gcc gac				691
Phe Leu Leu Ser Glu Leu Val Ala Ala Asn Glu Lys Phe Phe Ala Asp	185	190	195	
ccc aac cca ggc ttc atc cca acc gat gac gcc agc ttg atg gaa tgg				739
Pro Asn Pro Gly Phe Ile Pro Thr Asp Asp Ala Ser Leu Met Glu Trp	200	205	210	
tac ggc gca gat gta gtc tgc gta caa ggc gac cca atg gcg ttt aaa				787
Tyr Gly Ala Asp Val Val Cys Val Gln Gly Asp Pro Met Ala Phe Lys	215	220	225	
gta aca acc ccc att gat atg atg ctg gca caa cgc atc acc gac gaa				835
Val Thr Thr Pro Ile Asp Met Met Leu Ala Gln Arg Ile Thr Asp Glu	230	235	240	245
gcc gaa ccc aca ata ttt gag gta cca ggt gac taacccaatc atccccgcg				888
Ala Glu Pro Thr Ile Phe Glu Val Pro Gly Asp	250	255		
tag				891
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<211> 256				
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<213> Corynebacterium glutamicum				
<400> 284				
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Arg Gly Thr Arg Leu Gly Gly Pro Ile Pro Lys Ala Phe Val Thr Leu	20	25	30	

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<400> 285
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               Met Arg Thr Val Val

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acc ggc ggt gcc ggc ttc atc gga tcc cat ctc gtt gac ctt ttg atc	163																
Thr Gly Gly Ala Gly Phe Ile Gly Ser His Leu Val Asp Leu Leu Ile																	
	10	15	20														
aag gaa ggc cac gag gtc gtt gtg atc gat aac ctc tcc cgc gga cgc	211																
Lys Glu Gly His Glu Val Val Val Ile Asp Asn Leu Ser Arg Gly Arg																	
	25	30	35														
ctg gag aat ctc tcc gat gcg gaa gcc acc gga aaa ctc acc ttt gtg	259																
Leu Glu Asn Leu Ser Asp Ala Glu Ala Thr Gly Lys Leu Thr Phe Val																	
	40	45	50														
gaa gcc gat ctt ctc gac gtt gat ttc aac gag ttt cta gga acc cac	307																
Glu Ala Asp Leu Leu Asp Val Asp Phe Asn Glu Phe Leu Gly Thr His																	
	55	60	65														
aag cct gag gtt att ttc cac ctg gca gcg caa atc gat gtg cgc cac	355																
Lys Pro Glu Val Ile Phe His Leu Ala Ala Gln Ile Asp Val Arg His																	
	70	75	80	85													
tct gtt gta gat cct ctt cac gac gcc gaa acc aac att ttg tcc acc	403																
Ser Val Val Asp Pro Leu His Asp Ala Glu Thr Asn Ile Leu Ser Thr																	
	90	95	100														
atc cgc atc gct gac gct gcc cgc cag cac ggt gtt cgc aag gtt gtc	451																
Ile Arg Ile Ala Asp Ala Ala Arg Gln His Gly Val Arg Lys Val Val																	
	105	110	115														
ttt acc tcc tca ggc ggt tcc att tac ggt gag cct tcg gaa ttc cca	499																
Phe Thr Ser Ser Gly Gly Ser Ile Tyr Gly Glu Pro Ser Glu Phe Pro																	
	120	125	130														
gtt gat gaa acc gtg cca gtg gat cca cat tcc cct tat gcg gca tcc	547																
Val Asp Glu Thr Val Pro Val Asp Pro His Ser Pro Tyr Ala Ala Ser																	
	135	140	145														
aag gtg tcc ggt gaa att tac ctg aac acc ttc cgc cac ctg tac ggc	595																
Lys Val Ser Gly Glu Ile Tyr Leu Asn Thr Phe Arg His Leu Tyr Gly																	
	150	155	160	165													
tta gac tgt tct cac atc gca ccg gca aat gtt tac ggc cca cgc caa	643																
Leu Asp Cys Ser His Ile Ala Pro Ala Asn Val Tyr Gly Pro Arg Gln																	
	170	175	180														
gat cca cac ggt gaa gca gga gtt gtg gcc att ttc gcg ctg cga ctt	691																
Asp Pro His Gly Glu Ala Gly Val Val Ala Ile Phe Ala Leu Arg Leu																	
	185	190	195														
ctg gga ggc ctg gac acc aag gta ttc ggc gac ggc gga aac acc cgc	739																
Leu Gly Gly Leu Asp Thr Lys Val Phe Gly Asp Gly Gly Asn Thr Arg																	
	200	205	210														
gac tac gtc tac gtc ggt gac gta gtt cgt gct ttc tac ctg gct tct	787																
Asp Tyr Val Tyr Val Gly Asp Val Val Arg Ala Phe Tyr Leu Ala Ser																	
	215	220	225														
ggg gaa atc ggt ggg gga gag cgc ttc aac att ggc acc tct gtg gaa	835																
Gly Glu Ile Gly Gly Gly Glu Arg Phe Asn Ile Gly Thr Ser Val Glu																	
	230	235	240	245													

acc tct gac cgc cag ctg cac acc ctc gtg gcc act gcg gca ggt tcc 883
 Thr Ser Asp Arg Gln Leu His Thr Leu Val Ala Thr Ala Ala Gly Ser
 250 255 260

aaa gat gat cct gaa tat gca cct gca cgt ctc ggc gat gtg cca cgc 931
 Lys Asp Asp Pro Glu Tyr Ala Pro Ala Arg Leu Gly Asp Val Pro Arg
 265 270 275

agt gca ctc agc ttc ggc aag gcc aaa gag gtg ctt ggt tgg gag cct 979
 Ser Ala Leu Ser Phe Gly Lys Ala Lys Glu Val Leu Gly Trp Glu Pro
 280 285 290

gag gtg aac atc gaa caa ggt gtg gcc aag act gtg gag tac ttc cgc 1027
 Glu Val Asn Ile Glu Gln Gly Val Ala Lys Thr Val Glu Tyr Phe Arg
 295 300 305

act cac taggggaaaa tccaccacaa atc 1056
 Thr His
 310

<210> 286

<211> 311

<212> PRT

<213> Corynebacterium glutamicum

<400> 286

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Leu Ser Arg Gly Arg Leu Glu Asn Leu Ser Asp Ala Glu Ala Thr Gly
 35 40 45

Lys Leu Thr Phe Val Glu Ala Asp Leu Leu Asp Val Asp Phe Asn Glu
 50 55 60

Phe Leu Gly Thr His Lys Pro Glu Val Ile Phe His Leu Ala Ala Gln
 65 70 75 80

Ile Asp Val Arg His Ser Val Val Asp Pro Leu His Asp Ala Glu Thr
 85 90 95

Asn Ile Leu Ser Thr Ile Arg Ile Ala Asp Ala Ala Arg Gln His Gly
 100 105 110

Val Arg Lys Val Val Phe Thr Ser Ser Gly Gly Ser Ile Tyr Gly Glu
 115 120 125

Pro Ser Glu Phe Pro Val Asp Glu Thr Val Pro Val Asp Pro His Ser
 130 135 140

Pro Tyr Ala Ala Ser Lys Val Ser Gly Glu Ile Tyr Leu Asn Thr Phe
 145 150 155 160

Arg His Leu Tyr Gly Leu Asp Cys Ser His Ile Ala Pro Ala Asn Val
 165 170 175

<400> 287																
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ttatagtaga acgttctagt aaaacttggga aggatgaaaa																
															atg tca gtc aaa ctt	115
															Met Ser Val Lys Leu	
															1 5	
gcc ctc atc ggt gct gga cgc atc gga tca aat cac gca cgc ctg atc															163	
Ala Leu Ile Gly Ala Gly Arg Ile Gly Ser Asn His Ala Arg Leu Ile																
															10 15 20	
aca aac cac gtg atc ggc tct gaa ctg gtc gcc gtc gtt gac cca act															211	
Thr Asn His Val Ile Gly Ser Glu Leu Val Ala Val Val Asp Pro Thr																
															25 30 35	
ccc aac gca gaa acc ctc gct gat gaa ttg ggc gcc gtt gcg ttc tct															259	
Pro Asn Ala Glu Thr Leu Ala Asp Glu Leu Gly Ala Val Ala Phe Ser																
															40 45 50	
aac cca gat gac gtc ctg acc cgc gat gac att gac gcg gtt ttg att															307	
Asn Pro Asp Asp Val Leu Thr Arg Asp Asp Ile Asp Ala Val Leu Ile																
															55 60 65	

gct aca cca gca cga acc cac gcg gat ctc gtg gtc aaa gca gcg gca	355
Ala Thr Pro Ala Arg Thr His Ala Asp Leu Val Val Lys Ala Ala Ala	
70 75 80 85	
gcg ggc aag cac gtg ttt gtg gaa aag ccc atg gcc gtc acc ctc gag	403
Ala Gly Lys His Val Phe Val Glu Lys Pro Met Ala Val Thr Leu Glu	
90 95 100	
gac gca gat cgt gcc atc aac gca gca cgc gaa gca aac act gtc ctg	451
Asp Ala Asp Arg Ala Ile Asn Ala Ala Arg Glu Ala Asn Thr Val Leu	
105 110 115	
cag gtg ggc ttc aat cgt cgt ttc gcg gca ggt ttc gct gca gca cgc	499
Gln Val Gly Phe Asn Arg Arg Phe Ala Ala Gly Phe Ala Ala Ala Arg	
120 125 130	
gca cgc att gac gca ggc gat atc ggc acc cca cag ctg ctt cgt tcc	547
Ala Arg Ile Asp Ala Gly Asp Ile Gly Thr Pro Gln Leu Leu Arg Ser	
135 140 145	
gtg acc cgc gat cca gga cca ttc acc gct gac ccc aac aag atc cct	595
Val Thr Arg Asp Pro Gly Pro Phe Thr Ala Asp Pro Asn Lys Ile Pro	
150 155 160 165	
cag tgg acc atc ttc ctg gaa acc ctc atc cac gat ttc gat gcg ctg	643
Gln Trp Thr Ile Phe Leu Glu Thr Leu Ile His Asp Phe Asp Ala Leu	
170 175 180	
tgc tac ctc aac cca ggc gca acc cca gtg gaa gta acc gct cac gct	691
Cys Tyr Leu Asn Pro Gly Ala Thr Pro Val Glu Val Thr Ala His Ala	
185 190 195	
gat tgc ctc gtc gtt cca gaa gct gct ggc act ggc ttc ctc gac acc	739
Asp Cys Leu Val Val Pro Glu Ala Ala Gly Thr Gly Phe Leu Asp Thr	
200 205 210	
gca gtg gtg act gtc cgt ttt gat aac gga gca att ggt act gca gaa	787
Ala Val Val Thr Val Arg Phe Asp Asn Gly Ala Ile Gly Thr Ala Glu	
215 220 225	
gca agc ttc agc gca gcc tat ggt tat gac gtt cgc ggt gaa gtc ttc	835
Ala Ser Phe Ser Ala Ala Tyr Gly Tyr Asp Val Arg Gly Glu Val Phe	
230 235 240 245	
gga tcc aag ggc atg atg acc gca ggc gac gcg cgc gca acc aac atg	883
Gly Ser Lys Gly Met Met Thr Ala Gly Asp Ala Arg Ala Thr Asn Met	
250 255 260	
act ttc tac ggc gct gag ggc atc gcg gct gcc acc tca cgc gcg gat	931
Thr Phe Tyr Gly Ala Glu Gly Ile Ala Ala Ala Thr Ser Arg Ala Asp	
265 270 275	
acc gat ctg ctc tcc gat gct tac cga gct gaa ttc caa gct ttc gtc	979
Thr Asp Leu Leu Ser Asp Ala Tyr Arg Ala Glu Phe Gln Ala Phe Val	
280 285 290	
gac tcc atc cgt acc aac acc cct tcc aag gtt cca ggc gaa gct gca	1027
Asp Ser Ile Arg Thr Asn Thr Pro Ser Lys Val Pro Gly Glu Ala Ala	
295 300 305	
cgc acc gca cta ctc atc gca ctc ggc gcc atc cga agc gta gaa acc	1075

Arg Thr Ala Leu Leu Ile Ala Leu Gly Ala Ile Arg Ser Val Glu Thr
 310 315 320 325
 ggc gca acc atc aac ctt gct gaa agc atc gag gtt taaccatgac 1121
 Gly Ala Thr Ile Asn Leu Ala Glu Ser Ile Glu Val
 330 335

ttttaaaactc gca 1134

<210> 288

<211> 337

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 288

Met Ser Val Lys Leu Ala Leu Ile Gly Ala Gly Arg Ile Gly Ser Asn
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 His Ala Arg Leu Ile Thr Asn His Val Ile Gly Ser Glu Leu Val Ala
 20 25 30
 Val Val Asp Pro Thr Pro Asn Ala Glu Thr Leu Ala Asp Glu Leu Gly
 35 40 45
 Ala Val Ala Phe Ser Asn Pro Asp Asp Val Leu Thr Arg Asp Asp Ile
 50 55 60
 Asp Ala Val Leu Ile Ala Thr Pro Ala Arg Thr His Ala Asp Leu Val
 65 70 75 80
 Val Lys Ala Ala Ala Gly Lys His Val Phe Val Glu Lys Pro Met
 85 90 95
 Ala Val Thr Leu Glu Asp Ala Asp Arg Ala Ile Asn Ala Ala Arg Glu
 100 105 110
 Ala Asn Thr Val Leu Gln Val Gly Phe Asn Arg Arg Phe Ala Ala Gly
 115 120 125
 Phe Ala Ala Ala Arg Ala Arg Ile Asp Ala Gly Asp Ile Gly Thr Pro
 130 135 140
 Gln Leu Leu Arg Ser Val Thr Arg Asp Pro Gly Pro Phe Thr Ala Asp
 145 150 155 160
 Pro Asn Lys Ile Pro Gln Trp Thr Ile Phe Leu Glu Thr Leu Ile His
 165 170 175
 Asp Phe Asp Ala Leu Cys Tyr Leu Asn Pro Gly Ala Thr Pro Val Glu
 180 185 190
 Val Thr Ala His Ala Asp Cys Leu Val Val Pro Glu Ala Ala Gly Thr
 195 200 205
 Gly Phe Leu Asp Thr Ala Val Val Thr Val Arg Phe Asp Asn Gly Ala
 210 215 220
 Ile Gly Thr Ala Glu Ala Ser Phe Ser Ala Ala Tyr Gly Tyr Asp Val
 225 230 235 240

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<210> 289
<211> 996
<212> DNA
<213> Corynebacterium glutamicum
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<220>  
<221> CDS  
<222> (101)..(973)  
<223> RXN00013
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<400> 289																
ctgcagaaaa ttcgggacgc atgattgcac atattaccgcg caccgattgt gattcttaga																60
acgccacctt attcagcaca cttggccgac ggcattgcaca																
										atg	gaa	ggc	atg	act		115
										Met	Glu	Gly	Met	Thr		
										1				5		
aat cca gag cag aca cat ccc gct gca agc ctc gaa gac atg atc aaa																163
Asn	Pro	Glu	Gln	Thr	His	Pro	Ala	Ala	Ser	Leu	Glu	Asp	Met	Ile	Lys	
				10				15						20		
acc atc aca aag acc ttc gtg att gct cac gat cag gat tct gat gag																211
Thr	Ile	Thr	Lys	Thr	Phe	Val	Ile	Ala	His	Asp	Gln	Asp	Ser	Asp	Glu	
			25				30						35			
cat ctt gcg cag gca ctg gtg tac aac gct gga cgt ttg gca tgg cgc																259
His	Leu	Ala	Gln	Ala	Leu	Val	Tyr	Asn	Ala	Gly	Arg	Leu	Ala	Trp	Arg	
		40				45						50				
atg cgc gaa aac ggt gtg gat acg gat tac aag act tct gtg tct gat																307
Met	Arg	Glu	Asn	Gly	Val	Asp	Thr	Asp	Tyr	Lys	Thr	Ser	Val	Ser	Asp	
	55					60					65					
gtg gtc acg gat gcc gat cgt gcg gcc gag gcc ttc gtc gca ggc gtt																355
Val	Val	Thr	Asp	Ala	Asp	Arg	Ala	Ala	Glu	Ala	Phe	Val	Ala	Gly	Val	
	70				75					80				85		
ctt gaa gcg ttg cgg cct gag gac ggc gtg ctt ggc gag gaa ggc gcg																403
Leu	Glu	Ala	Leu	Arg	Pro	Glu	Asp	Gly	Val	Leu	Gly	Glu	Glu	Gly	Ala	

90	95	100	
gac cgg gcg tcg aaa agc gga aaa acc tgg gtc atc gac ccg gtt gat			451
Asp Arg Ala Ser Lys Ser Gly Lys Thr Trp Val Ile Asp Pro Val Asp			
105	110	115	
ggc acc tac aac ttc acc cag ggc tca gat tat tgg tgc tcg gcg ctc			499
Gly Thr Tyr Asn Phe Thr Gln Gly Ser Asp Tyr Trp Cys Ser Ala Leu			
120	125	130	
gcg ctg gtc gag ggc gat cca tcc gcg cca tcg cgc gtg ctt ttc ggc			547
Ala Leu Val Glu Gly Asp Pro Ser Ala Pro Ser Arg Val Leu Phe Gly			
135	140	145	
gcc gta cac cgc cca gcc atg ggt tat acg tgg ttc ggt ggc ccg gga			595
Ala Val His Arg Pro Ala Met Gly Tyr Thr Trp Phe Gly Gly Pro Gly			
150	155	160	165
atc cgc acc acg ctc gac ggc aag gag cta gat ttg ctt gtc gac gcc			643
Ile Arg Thr Thr Leu Asp Gly Lys Glu Leu Asp Leu Leu Val Asp Ala			
170	175	180	
ccc ctc aat caa atc tcc ctg gcc acc tac atc cac ccg tca cgc atc			691
Pro Leu Asn Gln Ile Ser Leu Ala Thr Tyr Ile His Pro Ser Arg Ile			
185	190	195	
gcg gaa cct gat att caa aag gcg tgg atg agc gtt gcc acc cac cct			739
Ala Glu Pro Asp Ile Gln Lys Ala Trp Met Ser Val Ala Thr His Pro			
200	205	210	
gca acg ctg cgc atg ttc ggc gcc ggc tcc atc gat ttg gcc aac atc			787
Ala Thr Leu Arg Met Phe Gly Ala Gly Ser Ile Asp Leu Ala Asn Ile			
215	220	225	
gcc gac ggc agc atg ggc gca tgg gtg cag cac agc gtc gca gat tgg			835
Ala Asp Gly Ser Met Gly Ala Trp Val Gln His Ser Val Ala Asp Trp			
230	235	240	245
gac tgg cta ccc ggc cgc gca ctc atc gaa ggc gtc ggc gga gca tgc			883
Asp Trp Leu Pro Gly Arg Ala Leu Ile Glu Gly Val Gly Gly Ala Cys			
250	255	260	
atc aaa gtg acc gcc ggc ggc gtc gaa tgg tcc gtt gca gga aac gcg			931
Ile Lys Val Thr Ala Gly Gly Val Glu Trp Ser Val Ala Gly Asn Ala			
265	270	275	
gaa gca gtt agt gag atc tcc gaa act tta agc gca cta gac			973
Glu Ala Val Ser Glu Ile Ser Glu Thr Leu Ser Ala Leu Asp			
280	285	290	
taacaacaca tgagcaaata tgc			996

<210> 290

<211> 291

<212> PRT

<213> Corynebacterium glutamicum

<400> 290

Met	Glu	Gly	Met	Thr	Asn	Pro	Glu	Gln	Thr	His	Pro	Ala	Ala	Ser	Leu
1				5					10					15	

Glu Asp Met Ile Lys Thr Ile Thr Lys Thr Phe Val Ile Ala His Asp
 20 25 30
 Gln Asp Ser Asp Glu His Leu Ala Gln Ala Leu Val Tyr Asn Ala Gly
 35 40 45
 Arg Leu Ala Trp Arg Met Arg Glu Asn Gly Val Asp Thr Asp Tyr Lys
 50 55 60
 Thr Ser Val Ser Asp Val Val Thr Asp Ala Asp Arg Ala Ala Glu Ala
 65 70 75 80
 Phe Val Ala Gly Val Leu Glu Ala Leu Arg Pro Glu Asp Gly Val Leu
 85 90 95
 Gly Glu Glu Gly Ala Asp Arg Ala Ser Lys Ser Gly Lys Thr Trp Val
 100 105 110
 Ile Asp Pro Val Asp Gly Thr Tyr Asn Phe Thr Gln Gly Ser Asp Tyr
 115 120 125
 Trp Cys Ser Ala Leu Ala Leu Val Glu Gly Asp Pro Ser Ala Pro Ser
 130 135 140
 Arg Val Leu Phe Gly Ala Val His Arg Pro Ala Met Gly Tyr Thr Trp
 145 150 155 160
 Phe Gly Gly Pro Gly Ile Arg Thr Thr Leu Asp Gly Lys Glu Leu Asp
 165 170 175
 Leu Leu Val Asp Ala Pro Leu Asn Gln Ile Ser Leu Ala Thr Tyr Ile
 180 185 190
 His Pro Ser Arg Ile Ala Glu Pro Asp Ile Gln Lys Ala Trp Met Ser
 195 200 205
 Val Ala Thr His Pro Ala Thr Leu Arg Met Phe Gly Ala Gly Ser Ile
 210 215 220
 Asp Leu Ala Asn Ile Ala Asp Gly Ser Met Gly Ala Trp Val Gln His
 225 230 235 240
 Ser Val Ala Asp Trp Asp Trp Leu Pro Gly Arg Ala Leu Ile Glu Gly
 245 250 255
 Val Gly Gly Ala Cys Ile Lys Val Thr Ala Gly Gly Val Glu Trp Ser
 260 265 270
 Val Ala Gly Asn Ala Glu Ala Val Ser Glu Ile Ser Glu Thr Leu Ser
 275 280 285
 Ala Leu Asp
 290

<210> 291

<211> 996

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(973)

<223> FRXA00013

<400> 291

ctgcagaaaa ttcgggacgc atgattgcac atattacccg caccgattgt gattcttaga 60

acgccacctt attcagcaca cttggccgac ggcatgcaca atg gaa ggc atg act 115
 Met Glu Gly Met Thr
 1 5

aat cca gag cag aca cat ccc gct gca agc ctc gaa gac atg atc aaa 163
 Asn Pro Glu Gln Thr His Pro Ala Ala Ser Leu Glu Asp Met Ile Lys
 10 15 20

acc atc aca aag acc ttc gtg att gct cac gat cag gat tct gat gag 211
 Thr Ile Thr Lys Thr Phe Val Ile Ala His Asp Gln Asp Ser Asp Glu
 25 30 35

cat ctt gcg cag gca ctg gtg tac aac gct gga cgt ttg gca tgg cgc 259
 His Leu Ala Gln Ala Leu Val Tyr Asn Ala Gly Arg Leu Ala Trp Arg
 40 45 50

atg cgc gaa aac ggt gtg gat acg gat tac aag act tct gtg tct gat 307
 Met Arg Glu Asn Gly Val Asp Thr Asp Tyr Lys Thr Ser Val Ser Asp
 55 60 65

gtg gtc acg gat gcc gat cgt gcg gcc gag gcc ttc gtc gca ggc gtt 355
 Val Val Thr Asp Ala Asp Arg Ala Ala Glu Ala Phe Val Ala Gly Val
 70 75 80 85

ctt gaa gcg ttg cgg cct gag gac ggc gtg ctt ggc gag gaa ggc gcg 403
 Leu Glu Ala Leu Arg Pro Glu Asp Gly Val Leu Gly Glu Glu Gly Ala
 90 95 100

gac cgg gcg tcg aaa agc gga aaa acc tgg gtc atc gac ccg gtt gat 451
 Asp Arg Ala Ser Lys Ser Gly Lys Thr Trp Val Ile Asp Pro Val Asp
 105 110 115

ggc acc tac aac ttc acc cag ggc tca gat tat tgg tgc tcg gcg ctc 499
 Gly Thr Tyr Asn Phe Thr Gln Gly Ser Asp Tyr Trp Cys Ser Ala Leu
 120 125 130

gcg ctg gtc gag ggc gat cca tcc gcg cca tcg cgc gtg ctt ttc ggc 547
 Ala Leu Val Glu Gly Asp Pro Ser Ala Pro Ser Arg Val Leu Phe Gly
 135 140 145

gcc gta cac cgc cca gcc atg ggt tat acg tgg ttc ggt ggc ccg gga 595
 Ala Val His Arg Pro Ala Met Gly Tyr Thr Trp Phe Gly Gly Pro Gly
 150 155 160 165

atc cgc acc acg ctc gac ggc aag gag cta gat ttg ctt gtc gac gcc 643
 Ile Arg Thr Thr Leu Asp Gly Lys Glu Leu Asp Leu Leu Val Asp Ala
 170 175 180

ccc ctc aat caa atc tcc ctg gcc acc tac atc cac ccg tca cgc atc 691
 Pro Leu Asn Gln Ile Ser Leu Ala Thr Tyr Ile His Pro Ser Arg Ile
 185 190 195

gcg gaa cct gat att caa aag gcg tgg atg agc gtt gcc acc cac cct 739

Ala Glu Pro Asp Ile Gln Lys Ala Trp Met Ser Val Ala Thr His Pro
 200 205 210

gca acg ctg cgc atg ttc ggc gcc ggc tcc atc gat ttg gcc aac atc 787
 Ala Thr Leu Arg Met Phe Gly Ala Gly Ser Ile Asp Leu Ala Asn Ile
 215 220 225

gcc gac ggc agc atg ggc gca tgg gtg cag cac agc gtc gca gat tgg 835
 Ala Asp Gly Ser Met Gly Ala Trp Val Gln His Ser Val Ala Asp Trp
 230 235 240 245

gac tgg cta ccc ggc cgc gca ctc atc gaa ggc gtc ggc gga gcg tgc 883
 Asp Trp Leu Pro Gly Arg Ala Leu Ile Glu Gly Val Gly Gly Ala Cys
 250 255 260

atc aaa gtg acc gcc ggc ggc gtc gaa tgg tcc gtt gca gga aac gcg 931
 Ile Lys Val Thr Ala Gly Gly Val Glu Trp Ser Val Ala Gly Asn Ala
 265 270 275

gaa gca gtt agt gag atc tcc gaa act tta agc gca cta gac 973
 Glu Ala Val Ser Glu Ile Ser Glu Thr Leu Ser Ala Leu Asp
 280 285 290

tagcaacaca tgagcaaata tgc 996

<210> 292

<211> 291

<212> PRT

<213> Corynebacterium glutamicum

<400> 292

Met Glu Gly Met Thr Asn Pro Glu Gln Thr His Pro Ala Ala Ser Leu
 1 5 10 15

Glu Asp Met Ile Lys Thr Ile Thr Lys Thr Phe Val Ile Ala His Asp
 20 25 30

Gln Asp Ser Asp Glu His Leu Ala Gln Ala Leu Val Tyr Asn Ala Gly
 35 40 45

Arg Leu Ala Trp Arg Met Arg Glu Asn Gly Val Asp Thr Asp Tyr Lys
 50 55 60

Thr Ser Val Ser Asp Val Val Thr Asp Ala Asp Arg Ala Ala Glu Ala
 65 70 75 80

Phe Val Ala Gly Val Leu Glu Ala Leu Arg Pro Glu Asp Gly Val Leu
 85 90 95

Gly Glu Glu Gly Ala Asp Arg Ala Ser Lys Ser Gly Lys Thr Trp Val
 100 105 110

Ile Asp Pro Val Asp Gly Thr Tyr Asn Phe Thr Gln Gly Ser Asp Tyr
 115 120 125

Trp Cys Ser Ala Leu Ala Leu Val Glu Gly Asp Pro Ser Ala Pro Ser
 130 135 140

Arg Val Leu Phe Gly Ala Val His Arg Pro Ala Met Gly Tyr Thr Trp
 145 150 155 160

[illegible]

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<210> 293
<211> 948
<212> DNA
<213> Corynebacterium glutamicum
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<220>  
<221> CDS  
<222> (101)..(925)  
<223> RXA01099
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<400> 293
gggatgaggggc attgattccg tcatcattgg caaggcactt tatgagcaca agttcaccct 60

cgaagagggt ttggctgcag tagaaaagct cggttaatac atg gat gct cgt ggg 115
Met Asp Ala Arg Gly
1 5

atg ttg gcc att gcg gag gcc gtt gta gat gat gcc gaa gcc ctc ttc 163
Met Leu Ala Ile Ala Glu Ala Val Val Asp Asp Ala Glu Ala Leu Phe
10 15 20

atg cag ggc ttc gga gct gca cct gcc cat atg aaa tcc ccg ggg gat 211
Met Gln Gly Phe Gly Ala Ala Pro Ala His Met Lys Ser Pro Gly Asp
25 30 35

ttt gcc acg gaa gtg gat atg gcc atc gaa tcc cat atg cgt tcg atg 259
Phe Ala Thr Glu Val Asp Met Ala Ile Glu Ser His Met Arg Ser Met
40 45 50

ctg aac atg atg aca ggc att gct gtc atc ggt gaa gaa ggt ggc ggt 307
Leu Asn Met Met Thr Gly Ile Ala Val Ile Gly Glu Glu Gly Gly Gly
55 60 65

```

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gcg acc tcc ggc acg cgc tgg gtg att gat ccc atc gac ggc acc gcc 355
Ala Thr Ser Gly Thr Arg Trp Val Ile Asp Pro Ile Asp Gly Thr Ala
 70                      75                      80                      85

aac ttc gcg gcg tcc aac ccg atg agc gcg atc ctg gtg tct ttg ctt 403
Asn Phe Ala Ala Ser Asn Pro Met Ser Ala Ile Leu Val Ser Leu Leu
          90                      95                      100

gtc gac gac cag ccc gtc ctg ggt att acc tcc atg ccc atg ctg ggt 451
Val Asp Asp Gln Pro Val Leu Gly Ile Thr Ser Met Pro Met Leu Gly
          105                      110                      115

aaa cgc ctc acc gct ttt gaa ggt tca ccg ctg atg atc aac ggt gaa 499
Lys Arg Leu Thr Ala Phe Glu Gly Ser Pro Leu Met Ile Asn Gly Glu
          120                      125                      130

cct cag gaa cca ttg caa gaa caa tcc agt ttg gta tcc cac att ggt 547
Pro Gln Glu Pro Leu Gln Glu Gln Ser Ser Leu Val Ser His Ile Gly
          135                      140                      145

ttt agt tcc atg gcc tcc ccg cgc aat aca gcg ttt cct gtg gag ttg 595
Phe Ser Ser Met Ala Ser Pro Arg Asn Thr Ala Phe Pro Val Glu Leu
150                      155                      160                      165

cgt cgg gat ctt ctg acc gag ctc acg gaa tcg tat ctt cgt ccc cgc 643
Arg Arg Asp Leu Leu Thr Glu Leu Thr Glu Ser Tyr Leu Arg Pro Arg
          170                      175                      180

att aca ggt tcg gtg ggt gtt gat ctc gcg ttc act gcg cag ggc att 691
Ile Thr Gly Ser Val Gly Val Asp Leu Ala Phe Thr Ala Gln Gly Ile
          185                      190                      195

ttt gga gca tgc gta tcg ttt agt cct cat gtt tgg gac aat tcc gca 739
Phe Gly Ala Cys Val Ser Phe Ser Pro His Val Trp Asp Asn Ser Ala
          200                      205                      210

ggc gtg atg ttg atg cgc gct gct ggt gca caa gtt act gac acc gaa 787
Gly Val Met Leu Met Arg Ala Ala Gly Ala Gln Val Thr Asp Thr Glu
          215                      220                      225

ggc cat ccg tgg gca cca ggt agg gga gtc gtg gcc gga aca aaa agg 835
Gly His Pro Trp Ala Pro Gly Arg Gly Val Val Ala Gly Thr Lys Arg
230                      235                      240                      245

gct cac gat gtg ctg tta agt aag att gaa aaa gtt cgg ttg atg cat 883
Ala His Asp Val Leu Leu Ser Lys Ile Glu Lys Val Arg Leu Met His
          250                      255                      260

gca gat gca ggt aat gac cag tcg tta aat gag gag tac aag 925
Ala Asp Ala Gly Asn Asp Gln Ser Leu Asn Glu Glu Tyr Lys
          265                      270                      275

taaaatgggc gtggcaattc gag 948

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<210> 294

<211> 275

<212> PRT

<213> Corynebacterium glutamicum

<400> 294

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Met Asp Ala Arg Gly Met Leu Ala Ile Ala Glu Ala Val Val Asp Asp
 1           5           10           15
Ala Glu Ala Leu Phe Met Gln Gly Phe Gly Ala Ala Pro Ala His Met
          20           25           30
Lys Ser Pro Gly Asp Phe Ala Thr Glu Val Asp Met Ala Ile Glu Ser
          35           40           45
His Met Arg Ser Met Leu Asn Met Met Thr Gly Ile Ala Val Ile Gly
          50           55           60
Glu Glu Gly Gly Gly Ala Thr Ser Gly Thr Arg Trp Val Ile Asp Pro
 65           70           75           80
Ile Asp Gly Thr Ala Asn Phe Ala Ala Ser Asn Pro Met Ser Ala Ile
          85           90           95
Leu Val Ser Leu Leu Val Asp Asp Gln Pro Val Leu Gly Ile Thr Ser
          100          105          110
Met Pro Met Leu Gly Lys Arg Leu Thr Ala Phe Glu Gly Ser Pro Leu
          115          120          125
Met Ile Asn Gly Glu Pro Gln Glu Pro Leu Gln Glu Gln Ser Ser Leu
          130          135          140
Val Ser His Ile Gly Phe Ser Ser Met Ala Ser Pro Arg Asn Thr Ala
          145          150          155          160
Phe Pro Val Glu Leu Arg Arg Asp Leu Leu Thr Glu Leu Thr Glu Ser
          165          170          175
Tyr Leu Arg Pro Arg Ile Thr Gly Ser Val Gly Val Asp Leu Ala Phe
          180          185          190
Thr Ala Gln Gly Ile Phe Gly Ala Cys Val Ser Phe Ser Pro His Val
          195          200          205
Trp Asp Asn Ser Ala Gly Val Met Leu Met Arg Ala Ala Gly Ala Gln
          210          215          220
Val Thr Asp Thr Glu Gly His Pro Trp Ala Pro Gly Arg Gly Val Val
          225          230          235          240
Ala Gly Thr Lys Arg Ala His Asp Val Leu Leu Ser Lys Ile Glu Lys
          245          250          255
Val Arg Leu Met His Ala Asp Ala Gly Asn Asp Gln Ser Leu Asn Glu
          260          265          270
Glu Tyr Lys
          275

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<210> 295

<211> 576

<212> DNA

<213> *Corynebacterium glutamicum*

<220>

<221> CDS

<222> (1)..(576)

<223> RXN01332

<400> 295

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cac atc tct gcc att att gag ccc gac gca gca cgt gcc gct gca gct 48
His Ile Ser Ala Ile Ile Glu Pro Asp Ala Ala Arg Ala Ala Ala Ala
  1             5             10             15

gca gaa gac gcg ccg ggt gca cag gcc ttc act cgc att gaa gat gct 96
Ala Glu Asp Ala Pro Gly Ala Gln Ala Phe Thr Arg Ile Glu Asp Ala
      20             25             30

atc gca gcc gat gct gtc gac gca gtg ctg atc gcc gta cca ggt cag 144
Ile Ala Ala Asp Ala Val Asp Ala Val Leu Ile Ala Val Pro Gly Gln
      35             40             45

ttc cat gag cca gta ctt gtc cca gca cta gaa gca ggc ctt ccc atc 192
Phe His Glu Pro Val Leu Val Pro Ala Leu Glu Ala Gly Leu Pro Ile
      50             55             60

ctg tgt gaa aag cca ctg acc cca gat tct gaa tcc tca ctg cgc atc 240
Leu Cys Glu Lys Pro Leu Thr Pro Asp Ser Glu Ser Ser Leu Arg Ile
      65             70             75             80

gtc gag ctg gag cag aag ctg gac aag cca cac atc cag gtt ggt ttc 288
Val Glu Leu Glu Gln Lys Leu Asp Lys Pro His Ile Gln Val Gly Phe
      85             90             95

atg cgc cgc ttc gac cct gag tac aac aac ttg cgc aaa ttg gtg gaa 336
Met Arg Arg Phe Asp Pro Glu Tyr Asn Asn Leu Arg Lys Leu Val Glu
      100             105             110

tcc ggc gaa gct ggc gaa ctg ctc atg ctc cgc ggc ctg cac cgc aac 384
Ser Gly Glu Ala Gly Glu Leu Leu Met Leu Arg Gly Leu His Arg Asn
      115             120             125

cca agt gtt ggt gag agc tac acc cag tcc atg ctg atc acc gac tcc 432
Pro Ser Val Gly Glu Ser Tyr Thr Gln Ser Met Leu Ile Thr Asp Ser
      130             135             140

gtc gtc cac gaa ttc gat gtc atc cca tgg ctc gca ggc tcc cga gtt 480
Val Val His Glu Phe Asp Val Ile Pro Trp Leu Ala Gly Ser Arg Val
      145             150             155             160

gtc tcc gtt gaa gtg aag tac cca aag acc tcc tca ctg gcg cac tcc 528
Val Ser Val Glu Val Lys Tyr Pro Lys Thr Ser Ser Leu Ala His Ser
      165             170             175

ggc ctc aag gaa cca atc ctg gtg atc atg gag ctc gaa aac ggc gtg 576
Gly Leu Lys Glu Pro Ile Leu Val Ile Met Glu Leu Glu Asn Gly Val
      180             185             190

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<210> 296

<211> 192

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 296

His Ile Ser Ala Ile Ile Glu Pro Asp Ala Ala Arg Ala Ala Ala Ala
 1 5 10 15
 Ala Glu Asp Ala Pro Gly Ala Gln Ala Phe Thr Arg Ile Glu Asp Ala
 20 25 30
 Ile Ala Ala Asp Ala Val Asp Ala Val Leu Ile Ala Val Pro Gly Gln
 35 40 45
 Phe His Glu Pro Val Leu Val Pro Ala Leu Glu Ala Gly Leu Pro Ile
 50 55 60
 Leu Cys Glu Lys Pro Leu Thr Pro Asp Ser Glu Ser Ser Leu Arg Ile
 65 70 75 80
 Val Glu Leu Glu Gln Lys Leu Asp Lys Pro His Ile Gln Val Gly Phe
 85 90 95
 Met Arg Arg Phe Asp Pro Glu Tyr Asn Asn Leu Arg Lys Leu Val Glu
 100 105 110
 Ser Gly Glu Ala Gly Glu Leu Leu Met Leu Arg Gly Leu His Arg Asn
 115 120 125
 Pro Ser Val Gly Glu Ser Tyr Thr Gln Ser Met Leu Ile Thr Asp Ser
 130 135 140
 Val Val His Glu Phe Asp Val Ile Pro Trp Leu Ala Gly Ser Arg Val
 145 150 155 160
 Val Ser Val Glu Val Lys Tyr Pro Lys Thr Ser Ser Leu Ala His Ser
 165 170 175
 Gly Leu Lys Glu Pro Ile Leu Val Ile Met Glu Leu Glu Asn Gly Val
 180 185 190

<210> 297
 <211> 549
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (1)..(549)
 <223> FRXA01332

<400> 297
 gca gca cgt gcc gct gca gct gca gaa gac gcg ccg ggt gca cag gcc 48
 Ala Ala Arg Ala Ala Ala Ala Glu Asp Ala Pro Gly Ala Gln Ala
 1 5 10 15
 ttc act cgc att gaa gat gct atc gca gcc gat gct gtc gac gca gtg 96
 Phe Thr Arg Ile Glu Asp Ala Ile Ala Ala Asp Ala Val Asp Ala Val
 20 25 30
 ctg atc gcc gta cca ggt cag ttc cat gag cca gta ctt gtc cca gca 144
 Leu Ile Ala Val Pro Gly Gln Phe His Glu Pro Val Leu Val Pro Ala

35	40	45	
cta gaa gca ggc ctt ccc atc ctg tgt gaa aag cca ctg acc cca gat			192
Leu Glu Ala Gly Leu Pro Ile Leu Cys Glu Lys Pro Leu Thr Pro Asp			
50	55	60	
tct gaa tcc tca ctg cgc atc gtc gag ctg gag cag aag ctg gac aag			240
Ser Glu Ser Ser Leu Arg Ile Val Glu Leu Glu Gln Lys Leu Asp Lys			
65	70	75	80
cca cac atc cag gtt ggt ttc atg cgc cgc ttc gac cct gag tac aac			288
Pro His Ile Gln Val Gly Phe Met Arg Arg Phe Asp Pro Glu Tyr Asn			
	85	90	95
aac ttg cgc aaa ttg gtg gaa tcc ggc gaa gct ggc gaa ctg ctc atg			336
Asn Leu Arg Lys Leu Val Glu Ser Gly Glu Ala Gly Glu Leu Leu Met			
	100	105	110
ctc cgc ggc ctg cac cgc aac cca agt gtt ggt gag agc tac acc cag			384
Leu Arg Gly Leu His Arg Asn Pro Ser Val Gly Glu Ser Tyr Thr Gln			
	115	120	125
tcc atg ctg atc acc gac tcc gtc gtc cac gaa ttc gat gtc atc cca			432
Ser Met Leu Ile Thr Asp Ser Val Val His Glu Phe Asp Val Ile Pro			
	130	135	140
tgg ctc gca ggc tcc cga gtt gtc tcc gtt gaa gtg aag tac cca aag			480
Trp Leu Ala Gly Ser Arg Val Val Ser Val Glu Val Lys Tyr Pro Lys			
	145	150	155
acc tcc tca ctg gcg cac tcc ggc ctc aag gaa cca atc ctg gtg atc			528
Thr Ser Ser Leu Ala His Ser Gly Leu Lys Glu Pro Ile Leu Val Ile			
	165	170	175
atg gag ctc gaa aac ggc gtg			549
Met Glu Leu Glu Asn Gly Val			
	180		

<210> 298

<211> 183

<212> PRT

<213> Corynebacterium glutamicum

<400> 298

Ala	Ala	Arg	Ala	Ala	Ala	Ala	Ala	Glu	Asp	Ala	Pro	Gly	Ala	Gln	Ala
1				5						10				15	

Phe	Thr	Arg	Ile	Glu	Asp	Ala	Ile	Ala	Ala	Asp	Ala	Val	Asp	Ala	Val
			20					25					30		

Leu	Ile	Ala	Val	Pro	Gly	Gln	Phe	His	Glu	Pro	Val	Leu	Val	Pro	Ala
		35						40				45			

Leu	Glu	Ala	Gly	Leu	Pro	Ile	Leu	Cys	Glu	Lys	Pro	Leu	Thr	Pro	Asp
	50					55					60				

Ser	Glu	Ser	Ser	Leu	Arg	Ile	Val	Glu	Leu	Glu	Gln	Lys	Leu	Asp	Lys
65					70					75				80	

Pro	His	Ile	Gln	Val	Gly	Phe	Met	Arg	Arg	Phe	Asp	Pro	Glu	Tyr	Asn
-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----

85 90 95

Asn Leu Arg Lys Leu Val Glu Ser Gly Glu Ala Gly Glu Leu Leu Met
100 105 110

Leu Arg Gly Leu His Arg Asn Pro Ser Val Gly Glu Ser Tyr Thr Gln
115 120 125

Ser Met Leu Ile Thr Asp Ser Val Val His Glu Phe Asp Val Ile Pro
130 135 140

Trp Leu Ala Gly Ser Arg Val Val Ser Val Glu Val Lys Tyr Pro Lys
145 150 155 160

Thr Ser Ser Leu Ala His Ser Gly Leu Lys Glu Pro Ile Leu Val Ile
165 170 175

Met Glu Leu Glu Asn Gly Val
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<223> RXA01632

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Met Thr Leu Arg Ile
1 5

gcc ctt ttc ggc gct ggc cgc atc ggt cac gtc cac gct gcc aac att 163
Ala Leu Phe Gly Ala Gly Arg Ile Gly His Val His Ala Ala Asn Ile
10 15 20

gct gca aac cct gat ctt gaa ctc gtt gtt atc gcc gat cct ttc att 211
Ala Ala Asn Pro Asp Leu Glu Leu Val Val Ile Ala Asp Pro Phe Ile
25 30 35

gaa ggc gca cag cgt ttg gca gaa gcc aat ggg gca gaa gcg gtt gca 259
Glu Gly Ala Gln Arg Leu Ala Glu Ala Asn Gly Ala Glu Ala Val Ala
40 45 50

tca cca gat gag gtg ttc gcc cgc gat gat atc gat ggc atc gtg atc 307
Ser Pro Asp Glu Val Phe Ala Arg Asp Asp Ile Asp Gly Ile Val Ile
55 60 65

ggt tca cca acc agc acc cac gtt gat ctg atc acc cgc gcc gtg gaa 355
Gly Ser Pro Thr Ser Thr His Val Asp Leu Ile Thr Arg Ala Val Glu
70 75 80 85

cgt ggc att cct gca ctg tgc gaa aaa ccc att gat tta gac att gaa 403
Arg Gly Ile Pro Ala Leu Cys Glu Lys Pro Ile Asp Leu Asp Ile Glu
90 95 100

atg gtg cgt gcc tgc aaa gag aag atc ggc gac ggc gct tcc aag gtg	451
Met Val Arg Ala Cys Lys Glu Lys Ile Gly Asp Gly Ala Ser Lys Val	
105 110 115	
atg ctg ggg ttt aac cga cgc ttc gat cct tct ttc gct gcc atc aat	499
Met Leu Gly Phe Asn Arg Arg Phe Asp Pro Ser Phe Ala Ala Ile Asn	
120 125 130	
gcg cga gtg gca aac cag gag atc ggc aac ctg gag cag ttg gtg atc	547
Ala Arg Val Ala Asn Gln Glu Ile Gly Asn Leu Glu Gln Leu Val Ile	
135 140 145	
atc agc cgc gat cca gcg ccc gca ccg aag gac tac atc gca ggt tcc	595
Ile Ser Arg Asp Pro Ala Pro Ala Pro Lys Asp Tyr Ile Ala Gly Ser	
150 155 160 165	
ggt gga atc ttc cgc gat atg acc atc cac gat ctg gat atg gcg cgt	643
Gly Gly Ile Phe Arg Asp Met Thr Ile His Asp Leu Asp Met Ala Arg	
170 175 180	
ttc ttt gtg ccc aat atc gtg gaa gtg act gca acc ggc gcc aat gtt	691
Phe Phe Val Pro Asn Ile Val Glu Val Thr Ala Thr Gly Ala Asn Val	
185 190 195	
ttc agc cag gaa atc gcg gag ttc aat gac tac gac cag gtt atc gtc	739
Phe Ser Gln Glu Ile Ala Glu Phe Asn Asp Tyr Asp Gln Val Ile Val	
200 205 210	
acg ctt cgt ggc tca aag ggc gag ttg atc aac atc gtg aac tcc cgc	787
Thr Leu Arg Gly Ser Lys Gly Glu Leu Ile Asn Ile Val Asn Ser Arg	
215 220 225	
cac tgc tcc tac ggc tac gac cag cga ctt gag gct ttc ggc tct aag	835
His Cys Ser Tyr Gly Tyr Asp Gln Arg Leu Glu Ala Phe Gly Ser Lys	
230 235 240 245	
ggc atg ctc gcc gcc gac aac atc agg ccc acc acg gtg cgc aag cac	883
Gly Met Leu Ala Ala Asp Asn Ile Arg Pro Thr Thr Val Arg Lys His	
250 255 260	
aat gcg gaa agc acc gag cag gca gat ccg att ttc aac ttc ttc ctc	931
Asn Ala Glu Ser Thr Glu Gln Ala Asp Pro Ile Phe Asn Phe Phe Leu	
265 270 275	
gag cgc tac gac gcc gct tac aag gca gag ctc gca act ttt gct caa	979
Glu Arg Tyr Asp Ala Ala Tyr Lys Ala Glu Leu Ala Thr Phe Ala Gln	
280 285 290	
gga atc cgc gac gcc ggc caa ggc ttc tca cca aac ttc gag gac ggc gtc	1027
Gly Ile Arg Asp Gly Gln Gly Phe Ser Pro Asn Phe Glu Asp Gly Val	
295 300 305	
atc gcc ctt gaa cta gcg aat gca tgc ctt gaa tca gct caa acc ggc	1075
Ile Ala Leu Glu Leu Ala Asn Ala Cys Leu Glu Ser Ala Gln Thr Gly	
310 315 320 325	
cgc acc gtc acc ctc aac cct gcc aac gtt tagtcaacgt ctagttaatg	1125
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cct

1128

<210> 300

<211> 335

<212> PRT

<213> Corynebacterium glutamicum

<400> 300

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 20 25 30

Ala Asp Pro Phe Ile Glu Gly Ala Gln Arg Leu Ala Glu Ala Asn Gly
 35 40 45

Ala Glu Ala Val Ala Ser Pro Asp Glu Val Phe Ala Arg Asp Asp Ile
 50 55 60

Asp Gly Ile Val Ile Gly Ser Pro Thr Ser Thr His Val Asp Leu Ile
 65 70 75 80

Thr Arg Ala Val Glu Arg Gly Ile Pro Ala Leu Cys Glu Lys Pro Ile
 85 90 95

Asp Leu Asp Ile Glu Met Val Arg Ala Cys Lys Glu Lys Ile Gly Asp
 100 105 110

Gly Ala Ser Lys Val Met Leu Gly Phe Asn Arg Arg Phe Asp Pro Ser
 115 120 125

Phe Ala Ala Ile Asn Ala Arg Val Ala Asn Gln Glu Ile Gly Asn Leu
 130 135 140

Glu Gln Leu Val Ile Ile Ser Arg Asp Pro Ala Pro Ala Pro Lys Asp
 145 150 155 160

Tyr Ile Ala Gly Ser Gly Gly Ile Phe Arg Asp Met Thr Ile His Asp
 165 170 175

Leu Asp Met Ala Arg Phe Phe Val Pro Asn Ile Val Glu Val Thr Ala
 180 185 190

Thr Gly Ala Asn Val Phe Ser Gln Glu Ile Ala Glu Phe Asn Asp Tyr
 195 200 205

Asp Gln Val Ile Val Thr Leu Arg Gly Ser Lys Gly Glu Leu Ile Asn
 210 215 220

Ile Val Asn Ser Arg His Cys Ser Tyr Gly Tyr Asp Gln Arg Leu Glu
 225 230 235 240

Ala Phe Gly Ser Lys Gly Met Leu Ala Ala Asp Asn Ile Arg Pro Thr
 245 250 255

Thr Val Arg Lys His Asn Ala Glu Ser Thr Glu Gln Ala Asp Pro Ile
 260 265 270

Phe Asn Phe Phe Leu Glu Arg Tyr Asp Ala Ala Tyr Lys Ala Glu Leu

275	280	285	
Ala Thr Phe Ala Gln Gly Ile Arg Asp Gly Gln Gly Phe Ser Pro Asn 290 295 300			
Phe Glu Asp Gly Val Ile Ala Leu Glu Leu Ala Asn Ala Cys Leu Glu 305 310 315 320			
Ser Ala Gln Thr Gly Arg Thr Val Thr Leu Asn Pro Ala Asn Val 325 330 335			
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<211> 1206			
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<223> RXA01633			
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gtttagtcaa cgtctagtta atgcctaagg agaaaaacctc	atg aaa aac atc acc	115	
	Met Lys Asn Ile Thr		
	1 5		
atc gga atg gtc ggc gtc ggc cgc att ggc cgc atg cac gtc gcc aac	163		
Ile Gly Met Val Gly Val Gly Arg Ile Gly Arg Met His Val Ala Asn			
	10 15 20		
atg ctt gcc gtt gct gaa act ttg aag gaa cgc gac ctc aac att gag	211		
Met Leu Ala Val Ala Glu Thr Leu Lys Glu Arg Asp Leu Asn Ile Glu			
	25 30 35		
atc gtg ctc gca gac gca atg ccc ggt ttt gcg gag cag gtg ggc gcg	259		
Ile Val Leu Ala Asp Ala Met Pro Gly Phe Ala Glu Gln Val Gly Ala			
	40 45 50		
gac atg ggc gtg aag gcg gcg gca agc gtc gat aag ctt att gag gac	307		
Asp Met Gly Val Lys Ala Ala Ser Val Asp Lys Leu Ile Glu Asp			
	55 60 65		
ggg gtg gat gcc ctt ttc att gcc acc agc acc gct ggc cac gtc gat	355		
Gly Val Asp Ala Leu Phe Ile Ala Thr Ser Thr Ala Gly His Val Asp			
	70 75 80 85		
gtt ttg cgc aag ggc atc gcg gca aag ctg ccg atg ttc tgc gag aag	403		
Val Leu Arg Lys Gly Ile Ala Ala Lys Leu Pro Met Phe Cys Glu Lys			
	90 95 100		
ccg atc gcg tcg gat gtg cct gag tcg ctg aac atc atc cgc gaa att	451		
Pro Ile Ala Ser Asp Val Pro Glu Ser Leu Asn Ile Ile Arg Glu Ile			
	105 110 115		
gat gcg gct ggc gcg acg gtt cag gtc ggc cac cag cgc cgt ttt gac	499		
Asp Ala Ala Gly Ala Thr Val Gln Val Gly His Gln Arg Phe Asp			
	120 125 130		

ctc ggt tac cag gaa gct aaa cga cgc cta gat gca ggc gac ctc ggc	547
Leu Gly Tyr Gln Glu Ala Lys Arg Arg Leu Asp Ala Gly Asp Leu Gly	
135 140 145	
tggttt cat tcg ctc aag gcc gta tcg agc gat gcg ttt ccg cca ccg	595
Trp Leu His Ser Leu Lys Ala Val Ser Ser Asp Ala Phe Pro Pro Pro	
150 155 160 165	
gtg tcc tac tgc gct acc tct ggt gga ctt ttc cgc gat gtg tcg ctg	643
Val Ser Tyr Cys Ala Thr Ser Gly Gly Leu Phe Arg Asp Val Ser Leu	
170 175 180	
cac gat ttc gac atc att cgc tgg ctg acc ggc cag gat att gtc gag	691
His Asp Phe Asp Ile Ile Arg Trp Leu Thr Gly Gln Asp Ile Val Glu	
185 190 195	
gtg tac gcc aag ggc agc aac aac ggc gac cca gaa atc ggc gca gtc	739
Val Tyr Ala Lys Gly Ser Asn Asn Gly Asp Pro Glu Ile Gly Ala Val	
200 205 210	
ggt gac atc gat acc gga gcg gcc cta ctc acg ctt gcc gac ggc acc	787
Gly Asp Ile Asp Thr Gly Ala Ala Leu Leu Thr Leu Ala Asp Gly Thr	
215 220 225	
ctc gcc acc gcc atc gcc act cgt tac aac ggt gca ggc cac gac gtt	835
Leu Ala Thr Ala Ile Ala Thr Arg Tyr Asn Gly Ala Gly His Asp Val	
230 235 240 245	
cgc ctc gat gtt atg ggc tct aaa gat tcc acg atc gtt ggc ctg gat	883
Arg Leu Asp Val Met Gly Ser Lys Asp Ser Thr Ile Val Gly Leu Asp	
250 255 260	
gaa aag tct gcg ttc gct tct gcg gag gag ggc atc gat ttc cca acc	931
Glu Lys Ser Ala Phe Ala Ser Ala Glu Glu Gly Ile Asp Phe Pro Thr	
265 270 275	
ggc gaa tcg cac cca acg ttt gcc gag cgc ttc gcc gac gca tac aag	979
Gly Glu Ser His Pro Thr Phe Ala Glu Arg Phe Ala Asp Ala Tyr Lys	
280 285 290	
aat gag tgc att gcg ttc gtg gag ttg atc ctg gga gag cgg gaa aac	1027
Asn Glu Cys Ile Ala Phe Val Glu Leu Ile Leu Gly Glu Arg Glu Asn	
295 300 305	
cct tgt acc cct gca gac gct gtg gct gcg gcg att gtt gcc gat gca	1075
Pro Cys Thr Pro Ala Asp Ala Val Ala Ala Ala Ile Val Ala Asp Ala	
310 315 320 325	
gct cag ctg tcg ctg gtc act ggc gag cca gtg aag att cct act gta	1123
Ala Gln Leu Ser Leu Val Thr Gly Glu Pro Val Lys Ile Pro Thr Val	
330 335 340	
cgg gaa att ctt gaa ggt tct gcg cag cca gtt gag gtg cgt gcg ctg	1171
Arg Glu Ile Leu Glu Gly Ser Ala Gln Pro Val Glu Val Arg Ala Leu	
345 350 355	
gtt cca tct gct taaaacctta ctgcttatct aaa	1206
Val Pro Ser Ala	
360	

<210> 302

<211> 361

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 302

Met Lys Asn Ile Thr Ile Gly Met Val Gly Val Gly Arg Ile Gly Arg
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Met His Val Ala Asn Met Leu Ala Val Ala Glu Thr Leu Lys Glu Arg
 20 25 30

Asp Leu Asn Ile Glu Ile Val Leu Ala Asp Ala Met Pro Gly Phe Ala
 35 40 45

Glu Gln Val Gly Ala Asp Met Gly Val Lys Ala Ala Ala Ser Val Asp
 50 55 60

Lys Leu Ile Glu Asp Gly Val Asp Ala Leu Phe Ile Ala Thr Ser Thr
 65 70 75 80

Ala Gly His Val Asp Val Leu Arg Lys Gly Ile Ala Ala Lys Leu Pro
 85 90 95

Met Phe Cys Glu Lys Pro Ile Ala Ser Asp Val Pro Glu Ser Leu Asn
 100 105 110

Ile Ile Arg Glu Ile Asp Ala Ala Gly Ala Thr Val Gln Val Gly His
 115 120 125

Gln Arg Arg Phe Asp Leu Gly Tyr Gln Glu Ala Lys Arg Arg Leu Asp
 130 135 140

Ala Gly Asp Leu Gly Trp Leu His Ser Leu Lys Ala Val Ser Ser Asp
 145 150 155 160

Ala Phe Pro Pro Pro Val Ser Tyr Cys Ala Thr Ser Gly Gly Leu Phe
 165 170 175

Arg Asp Val Ser Leu His Asp Phe Asp Ile Ile Arg Trp Leu Thr Gly
 180 185 190

Gln Asp Ile Val Glu Val Tyr Ala Lys Gly Ser Asn Asn Gly Asp Pro
 195 200 205

Glu Ile Gly Ala Val Gly Asp Ile Asp Thr Gly Ala Ala Leu Leu Thr
 210 215 220

Leu Ala Asp Gly Thr Leu Ala Thr Ala Ile Ala Thr Arg Tyr Asn Gly
 225 230 235 240

Ala Gly His Asp Val Arg Leu Asp Val Met Gly Ser Lys Asp Ser Thr
 245 250 255

Ile Val Gly Leu Asp Glu Lys Ser Ala Phe Ala Ser Ala Glu Glu Gly
 260 265 270

Ile Asp Phe Pro Thr Gly Glu Ser His Pro Thr Phe Ala Glu Arg Phe
 275 280 285

Ala Asp Ala Tyr Lys Asn Glu Cys Ile Ala Phe Val Glu Leu Ile Leu

290 295 300

Gly Glu Arg Glu Asn Pro Cys Thr Pro Ala Asp Ala Val Ala Ala Ala
305 310 315 320

Ile Val Ala Asp Ala Ala Gln Leu Ser Leu Val Thr Gly Glu Pro Val
325 330 335

Lys Ile Pro Thr Val Arg Glu Ile Leu Glu Gly Ser Ala Gln Pro Val
340 345 350

Glu Val Arg Ala Leu Val Pro Ser Ala
355 360

<210> 303
<211> 1146
<212> DNA
<213> *Corynebacterium glutamicum*

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<222> (101)..(1123)
<223> RXN01406

<400> 303
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ttcctcctct tagaaaccca cttctgaaag gtataaaaac atg act att cga atc 115
Met Thr Ile Arg Ile
1 5

gga ctc gtt ggc tac ggt gtc ggc ggc agg ctc ttt cac acc cct tac 163
Gly Leu Val Gly Tyr Gly Val Gly Gly Arg Leu Phe His Thr Pro Tyr
10 15 20

atc caa gct tct acg cac tgc gaa tta gta ggc gta gtt gct cgt tcc 211
Ile Gln Ala Ser Thr His Cys Glu Leu Val Gly Val Val Ala Arg Ser
25 30 35

gaa ggc acc aaa gca gcc gtt gca gaa gat ctt cca gat gtt gcc atc 259
Glu Gly Thr Lys Ala Ala Val Ala Glu Asp Leu Pro Asp Val Ala Ile
40 45 50

gtg gga tcg ctg aca gaa ctc ctc gaa ctg ggc gtc gat gca gtg gtg 307
Val Gly Ser Leu Thr Glu Leu Leu Glu Leu Gly Val Asp Ala Val Val
55 60 65

atc tcc acc cct cca gcc acg cgc cgg gaa ctg gcc ttg gaa gca atc 355
Ile Ser Thr Pro Pro Ala Thr Arg Arg Glu Leu Ala Leu Glu Ala Ile
70 75 80 85

aac gca ggt gtc gca gtg gtt gcc gat aaa ccg ttt gca cca tca gcc 403
Asn Ala Gly Val Ala Val Val Ala Asp Lys Pro Phe Ala Pro Ser Ala
90 95 100

gca gat gcc atg gaa ctt gtc gaa gcc gcc gaa aag gct gga gtg ctg 451
Ala Asp Ala Met Glu Leu Val Glu Ala Ala Glu Lys Ala Gly Val Leu
105 110 115

ctc aac gtc ttc cac aac agg cgc aac gac acc cac att gtc acg gca 499

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Leu Asn Val Phe His Asn Arg Arg Asn Asp Thr His Ile Val Thr Ala
      120                      125                      130

ctg gga atc caa gaa gaa ctt ggt gcg atg cgt gga ctg gac ctg cga   547
Leu Gly Ile Gln Glu Glu Leu Gly Ala Met Arg Gly Leu Asp Leu Arg
      135                      140                      145

cta gac ctg atc gaa cct gat tcc ttg gag gca ggt cct gaa ggt ggt   595
Leu Asp Leu Ile Glu Pro Asp Ser Leu Glu Ala Gly Pro Glu Gly Gly
      150                      155                      160                      165

ttg ctg cgc gat ctg ggc tca cac gta gtc gat cag acc ctg gtt ctc   643
Leu Leu Arg Asp Leu Gly Ser His Val Val Asp Gln Thr Leu Val Leu
      170                      175                      180

atg ggg ccg gct acc tct gtc acc gcc caa ctt gga tcc atc gac ctt   691
Met Gly Pro Ala Thr Ser Val Thr Ala Gln Leu Gly Ser Ile Asp Leu
      185                      190                      195

cca gaa ggc cca acc aac gca agg ttc cgc atc gtg ttg gaa cat gaa   739
Pro Glu Gly Pro Thr Asn Ala Arg Phe Arg Ile Val Leu Glu His Glu
      200                      205                      210

tcg ggc gcc gta tcg cac att tct gcc agc aag att gac cgc ttg gag   787
Ser Gly Ala Val Ser His Ile Ser Ala Ser Lys Ile Asp Arg Leu Glu
      215                      220                      225

tcc tgg gaa atc cgc ttg gtg ggc gag cgc ggc tcc tac gta tcc aac   835
Ser Trp Glu Ile Arg Leu Val Gly Glu Arg Gly Ser Tyr Val Ser Asn
      230                      235                      240                      245

tac acc gac gtg cag acc gtg gcg atc aaa cag gga ctt cga cca acc   883
Tyr Thr Asp Val Gln Thr Val Ala Ile Lys Gln Gly Leu Arg Pro Thr
      250                      255                      260

aat gac cgc gaa cac tgg ggc tac gaa tcg gag gag cgg tgg ggc acc   931
Asn Asp Arg Glu His Trp Gly Tyr Glu Ser Glu Glu Arg Trp Gly Thr
      265                      270                      275

ttg gtt acc gat gaa ggc tca aag gtg att cct tca gca caa ggc gat   979
Leu Val Thr Asp Glu Gly Ser Lys Val Ile Pro Ser Ala Gln Gly Asp
      280                      285                      290

tac acc cgc ttc tac gat gcc ttt gcc ttg gct gtg gaa aac ggt ggc   1027
Tyr Thr Arg Phe Tyr Asp Ala Phe Ala Leu Ala Val Glu Asn Gly Gly
      295                      300                      305

gca ggg ccg gtg cct gca cgt gaa ggt gtt gca gtg ctc aag gtg ttg   1075
Ala Gly Pro Val Pro Ala Arg Glu Gly Val Ala Val Leu Lys Val Leu
      310                      315                      320                      325

gat gct gta gcc cag agc gct gcg gaa aaa cgc acc att gag ttg agc   1123
Asp Ala Val Ala Gln Ser Ala Ala Glu Lys Arg Thr Ile Glu Leu Ser
      330                      335                      340

taaggagaag tgctgctggc tgc   1146

<210> 304
<211> 341
<212> PRT

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<213> *Corynebacterium glutamicum*

<400> 304

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 Phe His Thr Pro Tyr Ile Gln Ala Ser Thr His Cys Glu Leu Val Gly
 20 25 30
 Val Val Ala Arg Ser Glu Gly Thr Lys Ala Ala Val Ala Glu Asp Leu
 35 40 45
 Pro Asp Val Ala Ile Val Gly Ser Leu Thr Glu Leu Leu Glu Leu Gly
 50 55 60
 Val Asp Ala Val Val Ile Ser Thr Pro Pro Ala Thr Arg Arg Glu Leu
 65 70 75 80
 Ala Leu Glu Ala Ile Asn Ala Gly Val Ala Val Val Ala Asp Lys Pro
 85 90 95
 Phe Ala Pro Ser Ala Ala Asp Ala Met Glu Leu Val Glu Ala Ala Glu
 100 105 110
 Lys Ala Gly Val Leu Leu Asn Val Phe His Asn Arg Arg Asn Asp Thr
 115 120 125
 His Ile Val Thr Ala Leu Gly Ile Gln Glu Glu Leu Gly Ala Met Arg
 130 135 140
 Gly Leu Asp Leu Arg Leu Asp Leu Ile Glu Pro Asp Ser Leu Glu Ala
 145 150 155 160
 Gly Pro Glu Gly Gly Leu Leu Arg Asp Leu Gly Ser His Val Val Asp
 165 170 175
 Gln Thr Leu Val Leu Met Gly Pro Ala Thr Ser Val Thr Ala Gln Leu
 180 185 190
 Gly Ser Ile Asp Leu Pro Glu Gly Pro Thr Asn Ala Arg Phe Arg Ile
 195 200 205
 Val Leu Glu His Glu Ser Gly Ala Val Ser His Ile Ser Ala Ser Lys
 210 215 220
 Ile Asp Arg Leu Glu Ser Trp Glu Ile Arg Leu Val Gly Glu Arg Gly
 225 230 235 240
 Ser Tyr Val Ser Asn Tyr Thr Asp Val Gln Thr Val Ala Ile Lys Gln
 245 250 255
 Gly Leu Arg Pro Thr Asn Asp Arg Glu His Trp Gly Tyr Glu Ser Glu
 260 265 270
 Glu Arg Trp Gly Thr Leu Val Thr Asp Glu Gly Ser Lys Val Ile Pro
 275 280 285
 Ser Ala Gln Gly Asp Tyr Thr Arg Phe Tyr Asp Ala Phe Ala Leu Ala
 290 295 300
 Val Glu Asn Gly Gly Ala Gly Pro Val Pro Ala Arg Glu Gly Val Ala

305 310 315 320
Val Leu Lys Val Leu Asp Ala Val Ala Gln Ser Ala Ala Glu Lys Arg
 325 330 335

Thr Ile Glu Leu Ser
 340

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<210> 305
<211> 1200
<212> DNA
<213> Corynebacterium glutamicum
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<222> (101)..(1177)
<223> RXN01630
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Met Ser Asp Gln Lys 5																
1																
att gtt gtt ggc ctg cta ggc atc acc cac ccg cat gcg tcg gcg cgg 163																
Ile Val Val Gly Leu Leu Gly Ile Thr His Pro His Ala Ser Ala Arg																
10 15 20																
gtg cgt gcc ctc cgt gaa att gat ggg gta gag gtc gtc gcc gcc gcg 211																
Val Arg Ala Leu Arg Glu Ile Asp Gly Val Glu Val Val Ala Ala Ala																
25 30 35																
gat act gat tcc cgc ctc cag tac ttc acc gac aaa tat gat gtt gaa 259																
Asp Thr Asp Ser Arg Leu Gln Tyr Phe Thr Asp Lys Tyr Asp Val Glu																
40 45 50																
ccc cgc gag atc gat gac gtc ttg aac gac gat cgc atc aac gcc atc 307																
Pro Arg Glu Ile Asp Asp Val Leu Asn Asp Asp Arg Ile Asn Ala Ile																
55 60 65																
atg gtt cac tcc aag agc aag gac atg gtc cct cac gcc aag cgc gcg 355																
Met Val His Ser Lys Ser Lys Asp Met Val Pro His Ala Lys Arg Ala																
70 75 80 85																
ctc gcg gcc gga aaa tcc gtc gtc gtg gag aag ccc gcc ggg gga aca 403																
Leu Ala Ala Gly Lys Ser Val Val Val Glu Lys Pro Gly Gly Gly Thr																
90 95 100																
gtg gcg gat ctt gag gag ctc ctg gcc ctc aaa gaa gct gcc gat cct 451																
Val Ala Asp Leu Glu Glu Leu Leu Ala Leu Lys Glu Ala Ala Asp Pro																
105 110 115																
cag cga atc gtg cag gtc ggg tac aac gtc cgc ctg tct gaa tcg gtt 499																
Gln Arg Ile Val Gln Val Gly Tyr Asn Val Arg Leu Ser Glu Ser Val																
120 125 130																
cag aga tta aaa gag ctt ctc gac gcc ggc ctc atc gcc gaa gtc gtc 547																
Gln Arg Leu Lys Glu Leu Leu Asp Ala Gly Leu Ile Gly Glu Val Val																
135 140 145																

agc gtg caa gca cgc ggc gcc gca aaa gta ggt gag cat atc acc gag 595
 Ser Val Gln Ala Arg Gly Ala Ala Lys Val Gly Glu His Ile Thr Glu
 150 155 160 165

cac ctc aac caa ccc gca gac atg ggc ggt gtg ttg tgg att ctt ggc 643
 His Leu Asn Gln Pro Ala Asp Met Gly Gly Val Leu Trp Ile Leu Gly
 170 175 180

tgc cac atg ctc gat gca ttg gtg gaa gtc ttc gga gct cca gaa tcc 691
 Cys His Met Leu Asp Ala Leu Val Glu Val Phe Gly Ala Pro Glu Ser
 185 190 195

gtg aac gcc cga gtg cat aag acc gca aaa ctc tct gac gac acc agc 739
 Val Asn Ala Arg Val His Lys Thr Ala Lys Leu Ser Asp Asp Thr Ser
 200 205 210

cgc gaa gac tca gcc tcc gca ctg ctg tac tac cca gat ttc tcc gtc 787
 Arg Glu Asp Ser Ala Ser Ala Leu Leu Tyr Tyr Pro Asp Phe Ser Val
 215 220 225

agc ttc agc ttc gac ggc cac gat gat ctg gaa tgg ttc gaa agc tcc 835
 Ser Phe Ser Phe Asp Gly His Asp Asp Leu Glu Trp Phe Glu Ser Ser
 230 235 240 245

cga ctc acg gtc tat gga acc aag ggc atg atc gaa gcc gga atc ctc 883
 Arg Leu Thr Val Tyr Gly Thr Lys Gly Met Ile Glu Ala Gly Ile Leu
 250 255 260

cct cag aca ctg cgc gta tac ctc aat gag tca cgc cag ggc tgg cca 931
 Pro Gln Thr Leu Arg Val Tyr Leu Asn Glu Ser Arg Gln Gly Trp Pro
 265 270 275

cag ggt tgg acc gag tgg acc cag agc tac ttc acc cca ccg ttt gct 979
 Gln Gly Trp Thr Glu Trp Thr Gln Ser Tyr Phe Thr Pro Pro Phe Ala
 280 285 290

cgc aca gaa tcc aac aaa ttc tca gag ctt cca gag cta gaa aac atc 1027
 Arg Thr Glu Ser Asn Lys Phe Ser Glu Leu Pro Glu Leu Glu Asn Ile
 295 300 305

agc aac ttc cgc aca gaa atg cag ggg tgg gtg aat tcc att cgc act 1075
 Ser Asn Phe Arg Thr Glu Met Gln Gly Trp Val Asn Ser Ile Arg Thr
 310 315 320 325

gga tcc cgc aat gtg gcg cca gtt gag gat gct ctc aca gtc gct cgc 1123
 Gly Ser Arg Asn Val Ala Pro Val Glu Asp Ala Leu Thr Val Ala Arg
 330 335 340

att gtc agt gca tgc tac gaa tcc gac aac aac cag ggc att tcc gta 1171
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<210> 306

<211> 359

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 306

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Val Val Ala Ala Ala Asp Thr Asp Ser Arg Leu Gln Tyr Phe Thr Asp
 35 40 45

Lys Tyr Asp Val Glu Pro Arg Glu Ile Asp Asp Val Leu Asn Asp Asp
 50 55 60

Arg Ile Asn Ala Ile Met Val His Ser Lys Ser Lys Asp Met Val Pro
 65 70 75 80

His Ala Lys Arg Ala Leu Ala Ala Gly Lys Ser Val Val Val Glu Lys
 85 90 95

Pro Gly Gly Gly Thr Val Ala Asp Leu Glu Glu Leu Leu Ala Leu Lys
 100 105 110

Glu Ala Ala Asp Pro Gln Arg Ile Val Gln Val Gly Tyr Asn Val Arg
 115 120 125

Leu Ser Glu Ser Val Gln Arg Leu Lys Glu Leu Leu Asp Ala Gly Leu
 130 135 140

Ile Gly Glu Val Val Ser Val Gln Ala Arg Gly Ala Ala Lys Val Gly
 145 150 155 160

Glu His Ile Thr Glu His Leu Asn Gln Pro Ala Asp Met Gly Gly Val
 165 170 175

Leu Trp Ile Leu Gly Cys His Met Leu Asp Ala Leu Val Glu Val Phe
 180 185 190

Gly Ala Pro Glu Ser Val Asn Ala Arg Val His Lys Thr Ala Lys Leu
 195 200 205

Ser Asp Asp Thr Ser Arg Glu Asp Ser Ala Ser Ala Leu Leu Tyr Tyr
 210 215 220

Pro Asp Phe Ser Val Ser Phe Ser Phe Asp Gly His Asp Asp Leu Glu
 225 230 235 240

Trp Phe Glu Ser Ser Arg Leu Thr Val Tyr Gly Thr Lys Gly Met Ile
 245 250 255

Glu Ala Gly Ile Leu Pro Gln Thr Leu Arg Val Tyr Leu Asn Glu Ser
 260 265 270

Arg Gln Gly Trp Pro Gln Gly Trp Thr Glu Trp Thr Gln Ser Tyr Phe
 275 280 285

Thr Pro Pro Phe Ala Arg Thr Glu Ser Asn Lys Phe Ser Glu Leu Pro
 290 295 300

Glu Leu Glu Asn Ile Ser Asn Phe Arg Thr Glu Met Gln Gly Trp Val

305						310													320
Asn	Ser	Ile	Arg	Thr	Gly	Ser	Arg	Asn	Val	Ala	Pro	Val	Glu	Asp	Ala				
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Leu	Thr	Val	Ala	Arg	Ile	Val	Ser	Ala	Cys	Tyr	Glu	Ser	Asp	Asn	Asn				
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				Met	Ser	Thr	Ser	Thr											
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Ile	Arg	Val	Ala	Ile	Ala	Gly	Val	Gly	Asn	Cys	Ala	Thr	Ser	Leu	Ile				
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Gln	Gly	Val	Glu	Tyr	Tyr	Arg	Asn	Ala	Asp	Pro	Ser	Glu	Thr	Val	Pro				
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Gly	Leu	Met	His	Val	Lys	Phe	Gly	Asp	Tyr	His	Val	Gly	Asp	Ile	Glu				
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Phe	Val	Ala	Ala	Phe	Asp	Val	Asp	Ala	Glu	Lys	Val	Gly	Ile	Asp	Leu				
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Ala	Asp	Ala	Thr	Glu	Ala	Ser	Gln	Asn	Cys	Thr	Ile	Lys	Ile	Ala	Asp				
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Val	Pro	Gln	Thr	Gly	Ile	Asn	Val	Leu	Arg	Gly	Pro	Thr	Leu	Asp	Gly				
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ctg	ggc	gat	cat	tac	cgc	gcg	acc	atc	gac	gag	tcc	acc	gcc	gag	cca				451
Leu	Gly	Asp	His	Tyr	Arg	Ala	Thr	Ile	Asp	Glu	Ser	Thr	Ala	Glu	Pro				
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Ser Tyr Leu Pro Val Gly Ser Glu Glu Ala Asp Lys Phe Tyr Ala Gln	
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Ala Ala Ile Asp Ala Gly Cys Ala Phe Val Asn Ala Leu Pro Val Phe	
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Ile Ala Ser Asp Pro Glu Trp Ala Lys Lys Phe Thr Asp Ala Gly Ile	
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cca att gtt ggc gat gac atc aaa tcc cag atc ggt gca acc atc acc	691
Pro Ile Val Gly Asp Asp Ile Lys Ser Gln Ile Gly Ala Thr Ile Thr	
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His Arg Val Leu Ala Arg Leu Phe Glu Glu Arg Gly Val Arg Val Asp	
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Arg Thr Met Gln Leu Asn Val Gly Gly Asn Met Asp Phe Lys Asn Met	
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Leu Asp Arg Asn Arg Leu Glu Ser Lys Lys Val Ser Lys Thr Gln Ala	
230 235 240 245	
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Val Thr Ser Asn Ile Pro Asp Gly Pro Leu Ser Gly Lys Val Glu Asp	
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Arg Asn Val His Ile Gly Pro Ser Asp His Val Gln Trp Leu Asp Asp	
265 270 275	
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Arg Lys Trp Ala Tyr Val Arg Leu Glu Gly Thr Ala Phe Gly Gly Val	
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ccc ctc aac ctt gag tac aaa ctc gag gtg tgg gat tca ccc aac tct	1027
Pro Leu Asn Leu Glu Tyr Lys Leu Glu Val Trp Asp Ser Pro Asn Ser	
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Ala Gly Ile Ile Ile Asp Ala Val Arg Ala Ala Lys Ile Ala Leu Asp	
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Arg Gly Ile Gly Gly Pro Ile Met Pro Ala Ser Ser Tyr Leu Met Lys	
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Ser Pro Pro Glu Gln Leu Pro Asp Asp Val Ala Cys Glu Arg Leu Glu	
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Ala Phe Ile Ile Glu Ala	
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<210> 308
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 <213> Corynebacterium glutamicum

<400> 308

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Ser Glu Thr Val Pro Gly Leu Met His Val Lys Phe Gly Asp Tyr His
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Val Gly Asp Ile Glu Phe Val Ala Ala Phe Asp Val Asp Ala Glu Lys
      50              55              60

Val Gly Ile Asp Leu Ala Asp Ala Thr Glu Ala Ser Gln Asn Cys Thr
      65              70              75              80

Ile Lys Ile Ala Asp Val Pro Gln Thr Gly Ile Asn Val Leu Arg Gly
      85              90              95

Pro Thr Leu Asp Gly Leu Gly Asp His Tyr Arg Ala Thr Ile Asp Glu
      100             105             110

Ser Thr Ala Glu Pro Val Asp Val Val Gln Ala Leu Ile Asp Ala Lys
      115             120             125

Ala Asp Val Leu Val Ser Tyr Leu Pro Val Gly Ser Glu Glu Ala Asp
      130             135             140

Lys Phe Tyr Ala Gln Ala Ala Ile Asp Ala Gly Cys Ala Phe Val Asn
      145             150             155             160

Ala Leu Pro Val Phe Ile Ala Ser Asp Pro Glu Trp Ala Lys Lys Phe
      165             170             175

Thr Asp Ala Gly Ile Pro Ile Val Gly Asp Asp Ile Lys Ser Gln Ile
      180             185             190

Gly Ala Thr Ile Thr His Arg Val Leu Ala Arg Leu Phe Glu Glu Arg
      195             200             205

Gly Val Arg Val Asp Arg Thr Met Gln Leu Asn Val Gly Gly Asn Met
      210             215             220

Asp Phe Lys Asn Met Leu Asp Arg Asn Arg Leu Glu Ser Lys Lys Val
      225             230             235             240

Ser Lys Thr Gln Ala Val Thr Ser Asn Ile Pro Asp Gly Pro Leu Ser
      245             250             255

Gly Lys Val Glu Asp Arg Asn Val His Ile Gly Pro Ser Asp His Val
      260             265             270

Gln Trp Leu Asp Asp Arg Lys Trp Ala Tyr Val Arg Leu Glu Gly Thr
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Ala Phe Gly Gly Val Pro Leu Asn Leu Glu Tyr Lys Leu Glu Val Trp

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290 295 300

Asp Ser Pro Asn Ser Ala Gly Ile Ile Ile Asp Ala Val Arg Ala Ala
305 310 315 320

Lys Ile Ala Leu Asp Arg Gly Ile Gly Gly Pro Ile Met Pro Ala Ser
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Ser Tyr Leu Met Lys Ser Pro Pro Glu Gln Leu Pro Asp Asp Val Ala
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Cys Glu Arg Leu Glu Ala Phe Ile Ile Glu Ala
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Leu Ala Ser Asp Leu
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Gly Ile Lys Phe Val Ala Val Val Asp Lys Asp Leu Glu Thr Ala Glu
10 15 20
aaa ttt gcg acg gga ctt gga gct gct ggc gat tct tca gaa agc agc 211
Lys Phe Ala Thr Gly Leu Gly Ala Ala Gly Asp Ser Ser Glu Ser Ser
25 30 35
gtc aag gcc cac ggc agc ctg ccg gct ttg ttc tcc aaa aag aag atc 259
Val Lys Ala His Gly Ser Leu Pro Ala Leu Phe Ser Lys Lys Lys Ile
40 45 50
gat gtt cta cac atc acc acc ccc cac gac caa cac att ggt ttg gct 307
Asp Val Leu His Ile Thr Thr Pro His Asp Gln His Ile Gly Leu Ala
55 60 65
ctc gaa gcg cta cac cac ggt gta aat gtc atc ctg gaa aag ccg ttg 355
Leu Glu Ala Leu His His Gly Val Asn Val Ile Leu Glu Lys Pro Leu
70 75 80 85
gct aat gag ttg gac cag gcg cag cgt ctc atc gac tac ttg gat gaa 403
Ala Asn Glu Leu Asp Gln Ala Gln Arg Leu Ile Asp Tyr Leu Asp Glu
90 95 100
aac ccc gat ggt cca aag att gca gtg tgc tat cag aac cgt tac aac 451
Asn Pro Asp Gly Pro Lys Ile Ala Val Cys Tyr Gln Asn Arg Tyr Asn
105 110 115
gtt tcc tcc cag gaa ctg cgt cgt ctg ctc gat tca ggt gac ctc ggt 499

Val Ser Ser Gln Glu Leu Arg Arg Leu Leu Asp Ser Gly Asp Leu Gly
 120 125 130

gcc atc aat ggt gca tat tcc tct gtg gtg tgg acc cgc acc cca ggc 547
 Ala Ile Asn Gly Ala Tyr Ser Ser Val Val Trp Thr Arg Thr Pro Gly
 135 140 145

tac tac acc cag aaa cct tgg cgt ggc cag caa gca cac tcc ggt ggt 595
 Tyr Tyr Thr Gln Lys Pro Trp Arg Gly Gln Gln Ala His Ser Gly Gly
 150 155 160 165

ggc ctg ctg atg aac caa gca att cac acc ctg gat ctg ctg cag tgg 643
 Gly Leu Leu Met Asn Gln Ala Ile His Thr Leu Asp Leu Leu Gln Trp
 170 175 180

ttc ctt gga aag gca aca gaa gtc aag ggc act gtc tcc acc gat aag 691
 Phe Leu Gly Lys Ala Thr Glu Val Lys Gly Thr Val Ser Thr Asp Lys
 185 190 195

tat gcc gat gtc atc gat gtt gaa gac acc gca cac gca tac atc ggt 739
 Tyr Ala Asp Val Ile Asp Val Glu Asp Thr Ala His Ala Tyr Ile Gly
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 His Glu Ser Gly Val His Thr Ser Glu Val Ser
 215 220

aca 795

<210> 310

<211> 224

<212> PRT

<213> Corynebacterium glutamicum

<400> 310

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Leu Glu Thr Ala Glu Lys Phe Ala Thr Gly Leu Gly Ala Ala Gly Asp
 20 25 30

Ser Ser Glu Ser Ser Val Lys Ala His Gly Ser Leu Pro Ala Leu Phe
 35 40 45

Ser Lys Lys Lys Ile Asp Val Leu His Ile Thr Thr Pro His Asp Gln
 50 55 60

His Ile Gly Leu Ala Leu Glu Ala Leu His His Gly Val Asn Val Ile
 65 70 75 80

Leu Glu Lys Pro Leu Ala Asn Glu Leu Asp Gln Ala Gln Arg Leu Ile
 85 90 95

Asp Tyr Leu Asp Glu Asn Pro Asp Gly Pro Lys Ile Ala Val Cys Tyr
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Gln Asn Arg Tyr Asn Val Ser Ser Gln Glu Leu Arg Arg Leu Leu Asp
 115 120 125

Ser Gly Asp Leu Gly Ala Ile Asn Gly Ala Tyr Ser Ser Val Val Trp

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Ala His Ser Gly Gly Gly Leu Leu Met Asn Gln Ala Ile His Thr Leu		
	165	170 175
Asp Leu Leu Gln Trp Phe Leu Gly Lys Ala Thr Glu Val Lys Gly Thr		
	180	185 190
Val Ser Thr Asp Lys Tyr Ala Asp Val Ile Asp Val Glu Asp Thr Ala		
	195	200 205
His Ala Tyr Ile Gly His Glu Ser Gly Val His Thr Ser Glu Val Ser		
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 Leu Ala Ser Asp Leu
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 Gly Ile Lys Phe Val Ala Val Val Asp Lys Asp Leu Glu Thr Ala Glu
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 Lys Phe Ala Thr Gly Leu Gly Ala Ala Gly Asp Ser Ser Glu Ser Ser
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 Val Lys Ala His Gly Ser Leu Pro Ala Leu Phe Ser Lys Lys Lys Ile
 40 45 50
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 Asp Val Leu His Ile Thr Thr Pro His Asp Gln His Ile Gly Leu Ala
 55 60 65
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 Leu Glu Ala Leu His His Gly Val Asn Val Ile Leu Glu Lys Pro Leu
 70 75 80 85
 gct aat gag ttg gac cag gcg cag cgt ctc atc gac tac ttg gat gaa 403
 Ala Asn Glu Leu Asp Gln Ala Gln Arg Leu Ile Asp Tyr Leu Asp Glu
 90 95 100

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 Asn Pro Asp Gly Pro Lys Ile Ala Val Cys Tyr Gln Asn Arg Tyr Asn
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 Ala Ile Asn Gly Ala Tyr Ser Ser Val Val Trp Thr Arg Thr Pro Gly
 135 140 145
 tac tac acc cag aaa cct tgg cgt ggc cag caa gca cac tcc ggt ggt 595
 Tyr Tyr Thr Gln Lys Pro Trp Arg Gly Gln Gln Ala His Ser Gly Gly
 150 155 160 165
 ggc ctg ctg atg aac caa gca att cac acc ctg gat ctg ctg cag tgg 643
 Gly Leu Leu Met Asn Gln Ala Ile His Thr Leu Asp Leu Leu Gln Trp
 170 175 180
 ttc ctt gga aag gca aca gaa gtc aag ggc act gtc tcc acc gat aag 691
 Phe Leu Gly Lys Ala Thr Glu Val Lys Gly Thr Val Ser Thr Asp Lys
 185 190 195
 tat gcc gat gtc atc gat gtt gaa gac acc gca cac gca tac atc ggt 739
 Tyr Ala Asp Val Ile Asp Val Glu Asp Thr Ala His Ala Tyr Ile Gly
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 cac gag tcc gga gtc cac acc agt gaa gtg agt tgaaccatgc tattggtgat 792
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 aca 795

<210> 312
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 <213> Corynebacterium glutamicum

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 35 40 45
 Ser Lys Lys Lys Ile Asp Val Leu His Ile Thr Thr Pro His Asp Gln
 50 55 60
 His Ile Gly Leu Ala Leu Glu Ala Leu His His Gly Val Asn Val Ile
 65 70 75 80
 Leu Glu Lys Pro Leu Ala Asn Glu Leu Asp Gln Ala Gln Arg Leu Ile
 85 90 95
 Asp Tyr Leu Asp Glu Asn Pro Asp Gly Pro Lys Ile Ala Val Cys Tyr

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Gln Asn Arg Tyr Asn Val Ser	Ser Gln Glu Leu Arg	Arg Leu Leu Asp
115	120	125
Ser Gly Asp Leu Gly Ala Ile	Asn Gly Ala Tyr Ser	Ser Val Val Trp
130	135	140
Thr Arg Thr Pro Gly Tyr Tyr	Thr Gln Lys Pro Trp	Arg Gly Gln Gln
145	150	155
Ala His Ser Gly Gly Gly Leu	Leu Met Asn Gln Ala Ile	His Thr Leu
165	170	175
Asp Leu Leu Gln Trp Phe Leu	Gly Lys Ala Thr Glu Val	Lys Gly Thr
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Val Ser Thr Asp Lys Tyr Ala	Asp Val Ile Asp Val Glu	Asp Thr Ala
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 Met Lys Lys Lys Ile
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 Ala Val Val Thr Gly Ala Thr Gly Gly Met Gly Ile Glu Ile Val Lys
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 Asp Leu Ser Arg Asp His Ile Val Tyr Ala Leu Gly Arg Asn Pro Glu
 25 30 35
 cat ctg gca gct ctc gca gag atc gag gga gta gag cct atc gag tcc 259
 His Leu Ala Ala Leu Ala Glu Ile Glu Gly Val Glu Pro Ile Glu Ser
 40 45 50
 gat atc gtg aag gaa gtg ttg gaa gag gga ggc gtc gac aag cta aaa 307
 Asp Ile Val Lys Glu Val Leu Glu Glu Gly Gly Val Asp Lys Leu Lys
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 aac ctc gac cac gtg gat acg ctg gtg cac gcc gcg gcg gtg gcg cgt 355

Asn Leu Asp His Val Asp Thr Leu Val His Ala Ala Ala Val Ala Arg
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 gac acg acc atc gaa gcc ggc agt gtg gcc gaa tgg cac gca cac ctt 403
 Asp Thr Thr Ile Glu Ala Gly Ser Val Ala Glu Trp His Ala His Leu
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 Asp Leu Asn Val Ile Val Pro Ala Glu Leu Ser Arg Gln Leu Leu Pro
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 Gly Asn Gly Pro His Pro Gly Asn Thr Ile Tyr Ala Ala Ser Lys His
 135 140 145
 gcc ctc cgc gga ctc gcc gac gcc ttc cgc aaa gaa gaa gcc aac aac 595
 Ala Leu Arg Gly Leu Ala Asp Ala Phe Arg Lys Glu Glu Ala Asn Asn
 150 155 160 165
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 Gly Ile Arg Val Ser Thr Val Ser Pro Gly Pro Thr Asn Thr Pro Met
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 ctg caa ggc ctc atg gac tca caa ggc acc aac ttc cgc cca gag atc 691
 Leu Gln Gly Leu Met Asp Ser Gln Gly Thr Asn Phe Arg Pro Glu Ile
 185 190 195
 tac atc gaa cca aaa gaa atc gcc aac gca atc aga ttc gtg att gac 739
 Tyr Ile Glu Pro Lys Glu Ile Ala Asn Ala Ile Arg Phe Val Ile Asp
 200 205 210
 gct ggc gaa acc acc cag atc acc aac gtg gac gta cga cca cgt atc 787
 Ala Gly Glu Thr Thr Gln Ile Thr Asn Val Asp Val Arg Pro Arg Ile
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 Glu Leu Ala Asp Arg Lys Asp
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<211> 236

<212> PRT

<213> Corynebacterium glutamicum

<400> 314

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 Gly Arg Asn Pro Glu His Leu Ala Ala Leu Ala Glu Ile Glu Gly Val
 35 40 45
 Glu Pro Ile Glu Ser Asp Ile Val Lys Glu Val Leu Glu Glu Gly Gly
 50 55 60

Val Asp Lys Leu Lys Asn Leu Asp His Val Asp Thr Leu Val His Ala
 65 70 75 80
 Ala Ala Val Ala Arg Asp Thr Thr Ile Glu Ala Gly Ser Val Ala Glu
 85 90 95
 Trp His Ala His Leu Asp Leu Asn Val Ile Val Pro Ala Glu Leu Ser
 100 105 110
 Arg Gln Leu Leu Pro Ala Leu Arg Ala Ala Ser Gly Cys Val Ile Tyr
 115 120 125
 Ile Asn Ser Gly Ala Gly Asn Gly Pro His Pro Gly Asn Thr Ile Tyr
 130 135 140
 Ala Ala Ser Lys His Ala Leu Arg Gly Leu Ala Asp Ala Phe Arg Lys
 145 150 155 160
 Glu Glu Ala Asn Asn Gly Ile Arg Val Ser Thr Val Ser Pro Gly Pro
 165 170 175
 Thr Asn Thr Pro Met Leu Gln Gly Leu Met Asp Ser Gln Gly Thr Asn
 180 185 190
 Phe Arg Pro Glu Ile Tyr Ile Glu Pro Lys Glu Ile Ala Asn Ala Ile
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 210 215 220
 Val Arg Pro Arg Ile Glu Leu Ala Asp Arg Lys Asp
 225 230 235

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 <223> RXN02654

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 Met Ile Ser Leu Leu
 1 5
 aat gat cca cgt acg cta ttc ccg aaa gtc gat ccc cca aag caa agc 163
 Asn Asp Pro Arg Thr Leu Phe Pro Lys Val Asp Pro Pro Lys Gln Ser
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 cag ccg gaa cca ggc cta gat ata aaa ctt tcc ccc caa gcc gat att 211
 Gln Pro Glu Pro Gly Leu Asp Ile Lys Leu Ser Pro Gln Ala Asp Ile
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 ggt ctc tcc agc tat caa gga agt gga agg ctt aag ggc cgc aag gct 259

Gly	Leu	Ser	Ser	Tyr	Gln	Gly	Ser	Gly	Arg	Leu	Lys	Gly	Arg	Lys	Ala	
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ctt	att	act	ggt	ggc	gat	tct	ggg	att	gga	gct	gcc	gta	gca	atc	gct	307
Leu	Ile	Thr	Gly	Gly	Asp	Ser	Gly	Ile	Gly	Ala	Ala	Val	Ala	Ile	Ala	
	55						60				65					
tat	gct	cgc	gag	ggg	gca	gat	gtt	gcg	atc	gct	tac	ttg	ccc	gaa	gaa	355
Tyr	Ala	Arg	Glu	Gly	Ala	Asp	Val	Ala	Ile	Ala	Tyr	Leu	Pro	Glu	Glu	
	70				75				80					85		
caa	gcc	gat	gct	gac	aga	gtg	ctc	caa	gca	atc	gag	gaa	aca	ggt	caa	403
Gln	Ala	Asp	Ala	Asp	Arg	Val	Leu	Gln	Ala	Ile	Glu	Glu	Thr	Gly	Gln	
				90					95					100		
aaa	gct	ttt	tct	ttc	cct	ggt	gat	ctc	cgt	gat	cca	gaa	tac	tgt	cgc	451
Lys	Ala	Phe	Ser	Phe	Pro	Gly	Asp	Leu	Arg	Asp	Pro	Glu	Tyr	Cys	Arg	
			105				110						115			
tcg	ctg	gtc	caa	gag	acg	gtg	aac	gct	tta	ggt	ggc	cta	gac	atc	ttg	499
Ser	Leu	Val	Gln	Glu	Thr	Val	Asn	Ala	Leu	Gly	Gly	Leu	Asp	Ile	Leu	
		120					125					130				
gtc	aac	aac	gcg	tca	cgt	cag	gtg	tgg	gca	cct	ggt	ttg	acc	gaa	att	547
Val	Asn	Asn	Ala	Ser	Arg	Gln	Val	Trp	Ala	Pro	Gly	Leu	Thr	Glu	Ile	
	135					140					145					
acc	gac	gaa	aac	ttc	gac	cag	act	ttg	cag	gtt	aac	ctc	tat	ggt	agt	595
Thr	Asp	Glu	Asn	Phe	Asp	Gln	Thr	Leu	Gln	Val	Asn	Leu	Tyr	Gly	Ser	
	150				155				160						165	
ttt	cgg	gtt	acc	aaa	gca	gct	ata	cct	cat	ctg	aag	ccc	gga	tca	tcg	643
Phe	Arg	Val	Thr	Lys	Ala	Ala	Ile	Pro	His	Leu	Lys	Pro	Gly	Ser	Ser	
				170				175						180		
ata	atc	ttt	aca	tcg	tcc	att	cag	gcg	tac	caa	cct	tcg	gaa	acc	ctc	691
Ile	Ile	Phe	Thr	Ser	Ser	Ile	Gln	Ala	Tyr	Gln	Pro	Ser	Glu	Thr	Leu	
			185					190					195			
ttg	gat	tac	gcc	atg	act	aag	gcg	gca	ttg	aac	aat	ttg	tca	aag	ggc	739
Leu	Asp	Tyr	Ala	Met	Thr	Lys	Ala	Ala	Leu	Asn	Asn	Leu	Ser	Lys	Gly	
		200					205					210				
ttg	gca	agt	agt	ctg	ata	ggc	gat	ggc	att	cgg	gta	aat	tct	gta	gcc	787
Leu	Ala	Ser	Ser	Leu	Ile	Gly	Asp	Gly	Ile	Arg	Val	Asn	Ser	Val	Ala	
	215					220					225					
cca	ggt	cct	ttc	tgg	acg	ccg	ttg	caa	ccc	agc	cat	ggt	cag	cca	caa	835
Pro	Gly	Pro	Phe	Trp	Thr	Pro	Leu	Gln	Pro	Ser	His	Gly	Gln	Pro	Gln	
				235						240					245	
gag	aaa	ata	gaa	gga	ttt	ggc	cag	cac	gct	ccg	att	gga	aga	gcg	ggt	883
Glu	Lys	Ile	Glu	Gly	Phe	Gly	Gln	His	Ala	Pro	Ile	Gly	Arg	Ala	Gly	
				250				255						260		
cac	cct	gtt	gag	ttg	gca	ggt	gcg	tac	gtt	ttt	ctc	gct	tct	gac	gaa	931
His	Pro	Val	Glu	Leu	Ala	Gly	Ala	Tyr	Val	Phe	Leu	Ala	Ser	Asp	Glu	
			265					270					275			
gcc	agc	tat	gtg	gta	gga	gaa	acc	ctg	gga	gtc	aca	ggt	ggg	acg	ccc	979
Ala	Ser	Tyr	Val	Val	Gly	Glu	Thr	Leu	Gly	Val	Thr	Gly	Gly	Thr	Pro	

280 285 290

acc cca tagtcggtac aagcggaatc act 1008
 Thr Pro
 295

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 <212> PRT
 <213> Corynebacterium glutamicum

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 Pro Gln Ala Asp Ile Gly Leu Ser Ser Tyr Gln Gly Ser Gly Arg Leu
 35 40 45
 Lys Gly Arg Lys Ala Leu Ile Thr Gly Gly Asp Ser Gly Ile Gly Ala
 50 55 60
 Ala Val Ala Ile Ala Tyr Ala Arg Glu Gly Ala Asp Val Ala Ile Ala
 65 70 75 80
 Tyr Leu Pro Glu Glu Gln Ala Asp Ala Asp Arg Val Leu Gln Ala Ile
 85 90 95
 Glu Glu Thr Gly Gln Lys Ala Phe Ser Phe Pro Gly Asp Leu Arg Asp
 100 105 110
 Pro Glu Tyr Cys Arg Ser Leu Val Gln Glu Thr Val Asn Ala Leu Gly
 115 120 125
 Gly Leu Asp Ile Leu Val Asn Asn Ala Ser Arg Gln Val Trp Ala Pro
 130 135 140
 Gly Leu Thr Glu Ile Thr Asp Glu Asn Phe Asp Gln Thr Leu Gln Val
 145 150 155 160
 Asn Leu Tyr Gly Ser Phe Arg Val Thr Lys Ala Ala Ile Pro His Leu
 165 170 175
 Lys Pro Gly Ser Ser Ile Ile Phe Thr Ser Ser Ile Gln Ala Tyr Gln
 180 185 190
 Pro Ser Glu Thr Leu Leu Asp Tyr Ala Met Thr Lys Ala Ala Leu Asn
 195 200 205
 Asn Leu Ser Lys Gly Leu Ala Ser Ser Leu Ile Gly Asp Gly Ile Arg
 210 215 220
 Val Asn Ser Val Ala Pro Gly Pro Phe Trp Thr Pro Leu Gln Pro Ser
 225 230 235 240
 His Gly Gln Pro Gln Glu Lys Ile Glu Gly Phe Gly Gln His Ala Pro
 245 250 255

Ile Gly Arg Ala Gly His Pro Val Glu Leu Ala Gly Ala Tyr Val Phe
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Leu Ala Ser Asp Glu Ala Ser Tyr Val Val Gly Glu Thr Leu Gly Val
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Thr Gly Gly Thr Pro Thr Pro
 290 295

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 <223> FRXA02654

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gaggtacggt agttcgttcg aggacaacgt cgagaaaggc atg att tca ttg cta 115
 Met Ile Ser Leu Leu
 1 5

aat gat cca cgt acg cta ttc ccg aaa gtc gat ccc cca aag caa agc 163
 Asn Asp Pro Arg Thr Leu Phe Pro Lys Val Asp Pro Pro Lys Gln Ser
 10 15 20

cag ccg gaa cca ggc cta gat ata aaa ctt tcc ccc caa gcc gat att 211
 Gln Pro Glu Pro Gly Leu Asp Ile Lys Leu Ser Pro Gln Ala Asp Ile
 25 30 35

ggt ctc tcc agc tat caa gga agt gga agg ctt aag ggc cgc aag gct 259
 Gly Leu Ser Ser Tyr Gln Gly Ser Gly Arg Leu Lys Gly Arg Lys Ala
 40 45 50

ctt att act ggt ggc gat tct ggg att gga gct gcc gta gca atc gct 307
 Leu Ile Thr Gly Gly Asp Ser Gly Ile Gly Ala Ala Val Ala Ile Ala
 55 60 65

tat gct cgc gag ggg gca gat gtt gcg atc gct tac ttg ccc gaa gaa 355
 Tyr Ala Arg Glu Gly Ala Asp Val Ala Ile Ala Tyr Leu Pro Glu Glu
 70 75 80 85

caa gcc gat gct gac aga gtg ctc caa gca atc gag gaa aca ggt caa 403
 Gln Ala Asp Ala Asp Arg Val Leu Gln Ala Ile Glu Glu Thr Gly Gln
 90 95 100

aaa gct ttt tct ttc cct ggt gat ctc cgt gat cca gaa tac tgt cgc 451
 Lys Ala Phe Ser Phe Pro Gly Asp Leu Arg Asp Pro Glu Tyr Cys Arg
 105 110 115

tcg ctg gtc caa gag acg gtg aac gct tta ggt ggc cta gac atc ttg 499
 Ser Leu Val Gln Glu Thr Val Asn Ala Leu Gly Gly Leu Asp Ile Leu
 120 125 130

gtc aac aac gcg tca cgt cag gtg tgg gca cct ggt ttg acc gaa att 547
 Val Asn Asn Ala Ser Arg Gln Val Trp Ala Pro Gly Leu Thr Glu Ile

135	140	145	
acc gac gaa aac ttc gac cag act ttg cag gtt aac ctc tat ggt agt			595
Thr Asp Glu Asn Phe Asp Gln Thr Leu Gln Val Asn Leu Tyr Gly Ser			
150	155	160	165
ttt cgg gtt acc aaa gca gct ata cct cat ctg aag ccc gga tca tcg			643
Phe Arg Val Thr Lys Ala Ala Ile Pro His Leu Lys Pro Gly Ser Ser			
	170	175	180
ata atc ttt aca tcg tcc att cag gcg tac caa cct tcg gaa acc ctc			691
Ile Ile Phe Thr Ser Ser Ile Gln Ala Tyr Gln Pro Ser Glu Thr Leu			
	185	190	195
ttg gat tac gcc atg act aag gcg gca ttg aac aat ttg tca aag ggc			739
Leu Asp Tyr Ala Met Thr Lys Ala Ala Leu Asn Asn Leu Ser Lys Gly			
	200	205	210
ttg gca agt agt ctg ata ggc gat ggc att cgg gta aat tct gta gcc			787
Leu Ala Ser Ser Leu Ile Gly Asp Gly Ile Arg Val Asn Ser Val Ala			
	215	220	225
cca ggt cct ttc tgg acg ccg ttg caa ccc agc cat ggt cag cca caa			835
Pro Gly Pro Phe Trp Thr Pro Leu Gln Pro Ser His Gly Gln Pro Gln			
	230	235	240
gag aaa ata gaa gga ttt ggc cag cac gct ccg att gga aga gcg ggt			883
Glu Lys Ile Glu Gly Phe Gly Gln His Ala Pro Ile Gly Arg Ala Gly			
	250	255	260
cac cct gtt gag ttg gca ggt gcg tac gtt ttt ctc gct tct gac gaa			931
His Pro Val Glu Leu Ala Gly Ala Tyr Val Phe Leu Ala Ser Asp Glu			
	265	270	275
gcc agc tat gtg gta gga gaa acc ctg gga gtc aca ggt ggg acg ccc			979
Ala Ser Tyr Val Val Gly Glu Thr Leu Gly Val Thr Gly Gly Thr Pro			
	280	285	290
acc cca tagtcggtac aagcgggaatc act			1008
Thr Pro			
295			

<210> 318

<211> 295

<212> PRT

<213> Corynebacterium glutamicum

<400> 318

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			20					25					30		

Pro	Gln	Ala	Asp	Ile	Gly	Leu	Ser	Ser	Tyr	Gln	Gly	Ser	Gly	Arg	Leu
		35						40				45			

Lys	Gly	Arg	Lys	Ala	Leu	Ile	Thr	Gly	Gly	Asp	Ser	Gly	Ile	Gly	Ala
	50					55					60				

Ala Val Ala Ile Ala Tyr Ala Arg Glu Gly Ala Asp Val Ala Ile Ala
 65 70 75 80
 Tyr Leu Pro Glu Glu Gln Ala Asp Ala Asp Arg Val Leu Gln Ala Ile
 85 90 95
 Glu Glu Thr Gly Gln Lys Ala Phe Ser Phe Pro Gly Asp Leu Arg Asp
 100 105 110
 Pro Glu Tyr Cys Arg Ser Leu Val Gln Glu Thr Val Asn Ala Leu Gly
 115 120 125
 Gly Leu Asp Ile Leu Val Asn Asn Ala Ser Arg Gln Val Trp Ala Pro
 130 135 140
 Gly Leu Thr Glu Ile Thr Asp Glu Asn Phe Asp Gln Thr Leu Gln Val
 145 150 155 160
 Asn Leu Tyr Gly Ser Phe Arg Val Thr Lys Ala Ala Ile Pro His Leu
 165 170 175
 Lys Pro Gly Ser Ser Ile Ile Phe Thr Ser Ser Ile Gln Ala Tyr Gln
 180 185 190
 Pro Ser Glu Thr Leu Leu Asp Tyr Ala Met Thr Lys Ala Ala Leu Asn
 195 200 205
 Asn Leu Ser Lys Gly Leu Ala Ser Ser Leu Ile Gly Asp Gly Ile Arg
 210 215 220
 Val Asn Ser Val Ala Pro Gly Pro Phe Trp Thr Pro Leu Gln Pro Ser
 225 230 235 240
 His Gly Gln Pro Gln Glu Lys Ile Glu Gly Phe Gly Gln His Ala Pro
 245 250 255
 Ile Gly Arg Ala Gly His Pro Val Glu Leu Ala Gly Ala Tyr Val Phe
 260 265 270
 Leu Ala Ser Asp Glu Ala Ser Tyr Val Val Gly Glu Thr Leu Gly Val
 275 280 285
 Thr Gly Gly Thr Pro Thr Pro
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<210> 319
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 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(1582)
 <223> RXN01049

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 aagaatattc tttattagtc agacctttaa aggaaacctt atg gga tca att cca 115
 Met Gly Ser Ile Pro

	1	5	
aca atg tcc atc cct ttt gat gac tca cgt gga cct tat gtc ctt gct			163
Thr Met Ser Ile Pro Phe Asp Asp Ser Arg Gly Pro Tyr Val Leu Ala			
	10	20	
atg gat att ggt tcc act gca tca cga ggt gga ctt tat gat gct tcc			211
Met Asp Ile Gly Ser Thr Ala Ser Arg Gly Gly Leu Tyr Asp Ala Ser			
	25	35	
ggc tgc cca atc aaa ggc acc aag cag cgc gaa tcc cat gaa ttc acc			259
Gly Cys Pro Ile Lys Gly Thr Lys Gln Arg Glu Ser His Glu Phe Thr			
	40	50	
acc ggt gag ggc gtt tcc acc att gat gct gac cag gtg gtt tcg gag			307
Thr Gly Glu Gly Val Ser Thr Ile Asp Ala Asp Gln Val Val Ser Glu			
	55	65	
atc acc tca gtt att aat ggc att ttg aac gcg gct gat cat cac aac			355
Ile Thr Ser Val Ile Asn Gly Ile Leu Asn Ala Ala Asp His His Asn			
	70	85	
atc aaa gat cag atc gcc gct gtc gcg cta gat tct ttt gca tcc tca			403
Ile Lys Asp Gln Ile Ala Ala Val Ala Leu Asp Ser Phe Ala Ser Ser			
	90	100	
tta atc ttg gtc gat ggt gaa ggc aat gcg ctc acc ccg tgc att acc			451
Leu Ile Leu Val Asp Gly Glu Gly Asn Ala Leu Thr Pro Cys Ile Thr			
	105	115	
tac gcg gat tct cgt tct gca cag tat gtg gag cag ctg cgc gcg gaa			499
Tyr Ala Asp Ser Arg Ser Ala Gln Tyr Val Glu Gln Leu Arg Ala Glu			
	120	130	
atc gat gag aag gcc tac cac ggc cgc acc ggc gtc tgc ttg cac acc			547
Ile Asp Glu Lys Ala Tyr His Gly Arg Thr Gly Val Cys Leu His Thr			
	135	145	
tcc tac cac cca tcg cgc ttg ctg tgg ctg aaa act gag ttc gag aaa			595
Ser Tyr His Pro Ser Arg Leu Leu Trp Leu Lys Thr Glu Phe Glu Lys			
	150	165	
gag ttc aac aaa gcc aag tat gtg atg acc atc ggt gag tac gtc tac			643
Glu Phe Asn Lys Ala Lys Tyr Val Met Thr Ile Gly Glu Tyr Val Tyr			
	170	180	
ttc aaa ctt gca ggc atc acc gga atg gct act tcg att gcc gcg tgg			691
Phe Lys Leu Ala Gly Ile Thr Gly Met Ala Thr Ser Ile Ala Ala Trp			
	185	195	
agt ggc att ttg gac gcc cat acc ggc gaa ctt gat ctg act atc ttg			739
Ser Gly Ile Leu Asp Ala His Thr Gly Glu Leu Asp Leu Thr Ile Leu			
	200	210	
gag cac atc ggt gtt gat ccg gct ctg ttc ggt gag atc aga aac cct			787
Glu His Ile Gly Val Asp Pro Ala Leu Phe Gly Glu Ile Arg Asn Pro			
	215	225	
gat gaa cca gcc acc gat gcc aaa gtt gtc gac aaa aag tgg aag cac			835
Asp Glu Pro Ala Thr Asp Ala Lys Val Val Asp Lys Lys Trp Lys His			
	230	245	

ctg gaa gaa atc cct tgg ttc cat gcc att cca gac ggc tgg cct tcc	883
Leu Glu Glu Ile Pro Trp Phe His Ala Ile Pro Asp Gly Trp Pro Ser	
250 255 260	
aac att ggc cca ggc gcc gtg gat tct aaa acc gtc gca gtc gcc gcc	931
Asn Ile Gly Pro Gly Ala Val Asp Ser Lys Thr Val Ala Val Ala Ala	
265 270 275	
gct aca tcc ggc gcc atg cgc gtg atc ctt ccg agc gtt ccc gaa cag	979
Ala Thr Ser Gly Ala Met Arg Val Ile Leu Pro Ser Val Pro Glu Gln	
280 285 290	
atc ccc tct ggc ctg tgg tgt tac cgc gtt tcc cgc gac cag tgc atc	1027
Ile Pro Ser Gly Leu Trp Cys Tyr Arg Val Ser Arg Asp Gln Cys Ile	
295 300 305	
gtt ggt ggc gca ctc aac gac gtc gga cgc gcc gtc acc tgg ctg gaa	1075
Val Gly Gly Ala Leu Asn Asp Val Gly Arg Ala Val Thr Trp Leu Glu	
310 315 320 325	
cgc acc att atc aag cct gaa aac ctc gac gaa gtg ctg atc cgc gaa	1123
Arg Thr Ile Ile Lys Pro Glu Asn Leu Asp Glu Val Leu Ile Arg Glu	
330 335 340	
ccc ctc gaa ggc acc cca gct gtc ctg ccg ttc ttc tcc ggg gaa cgc	1171
Pro Leu Glu Gly Thr Pro Ala Val Leu Pro Phe Phe Ser Gly Glu Arg	
345 350 355	
tcc atc ggc tgg gca gcc tca gcg cag gcc acg atc acc aac att cag	1219
Ser Ile Gly Trp Ala Ala Ser Ala Gln Ala Thr Ile Thr Asn Ile Gln	
360 365 370	
gaa caa acc ggc cct gaa cac ttg tgg cgc ggc gtt ttc gaa gcc ctc	1267
Glu Gln Thr Gly Pro Glu His Leu Trp Arg Gly Val Phe Glu Ala Leu	
375 380 385	
gca ctc tcc tac cag cgc gtt tgg gaa cac atg ggg aaa gcc ggc gca	1315
Ala Leu Ser Tyr Gln Arg Val Trp Glu His Met Gly Lys Ala Gly Ala	
390 395 400 405	
gcc cct gaa cgg gtc atc gca tca gga cga gtc tcc acc gac cac cca	1363
Ala Pro Glu Arg Val Ile Ala Ser Gly Arg Val Ser Thr Asp His Pro	
410 415 420	
gaa ttc ctc gcg atg ctt tcc gac gcc ctc gac acc cca gtc atc cct	1411
Glu Phe Leu Ala Met Leu Ser Asp Ala Leu Asp Thr Pro Val Ile Pro	
425 430 435	
ctg gaa atg aag cgc gcc acc ctc cgc ggc acc gca ctt atc gtc ctt	1459
Leu Glu Met Lys Arg Ala Thr Leu Arg Gly Thr Ala Leu Ile Val Leu	
440 445 450	
gag cag ctc gaa cca ggc ggc acg cgc gcg acg cca cca ttc ggc acg	1507
Glu Gln Leu Glu Pro Gly Gly Thr Arg Ala Thr Pro Pro Phe Gly Thr	
455 460 465	
acg cat cag ccg cgc ttt gcg cac cat tac tcc aag gca aga gag ctt	1555
Thr His Gln Pro Arg Phe Ala His His Tyr Ser Lys Ala Arg Glu Leu	
470 475 480 485	

ttc gac gcc ctc tac ctc aag ttg gtc tagcttttcg cagtgggaacg 1602
 Phe Asp Ala Leu Tyr Leu Lys Leu Val
 490

cgc 1605

<210> 320

<211> 494

<212> PRT

<213> Corynebacterium glutamicum

<400> 320

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 Leu Tyr Asp Ala Ser Gly Cys Pro Ile Lys Gly Thr Lys Gln Arg Glu
 35 40 45
 Ser His Glu Phe Thr Thr Gly Glu Gly Val Ser Thr Ile Asp Ala Asp
 50 55 60
 Gln Val Val Ser Glu Ile Thr Ser Val Ile Asn Gly Ile Leu Asn Ala
 65 70 75 80
 Ala Asp His His Asn Ile Lys Asp Gln Ile Ala Ala Val Ala Leu Asp
 85 90 95
 Ser Phe Ala Ser Ser Leu Ile Leu Val Asp Gly Glu Gly Asn Ala Leu
 100 105 110
 Thr Pro Cys Ile Thr Tyr Ala Asp Ser Arg Ser Ala Gln Tyr Val Glu
 115 120 125
 Gln Leu Arg Ala Glu Ile Asp Glu Lys Ala Tyr His Gly Arg Thr Gly
 130 135 140
 Val Cys Leu His Thr Ser Tyr His Pro Ser Arg Leu Leu Trp Leu Lys
 145 150 155 160
 Thr Glu Phe Glu Lys Glu Phe Asn Lys Ala Lys Tyr Val Met Thr Ile
 165 170 175
 Gly Glu Tyr Val Tyr Phe Lys Leu Ala Gly Ile Thr Gly Met Ala Thr
 180 185 190
 Ser Ile Ala Ala Trp Ser Gly Ile Leu Asp Ala His Thr Gly Glu Leu
 195 200 205
 Asp Leu Thr Ile Leu Glu His Ile Gly Val Asp Pro Ala Leu Phe Gly
 210 215 220
 Glu Ile Arg Asn Pro Asp Glu Pro Ala Thr Asp Ala Lys Val Val Asp
 225 230 235 240
 Lys Lys Trp Lys His Leu Glu Glu Ile Pro Trp Phe His Ala Ile Pro
 245 250 255

Asp	Gly	Trp	Pro	Ser	Asn	Ile	Gly	Pro	Gly	Ala	Val	Asp	Ser	Lys	Thr
			260					265						270	
Val	Ala	Val	Ala	Ala	Ala	Thr	Ser	Gly	Ala	Met	Arg	Val	Ile	Leu	Pro
		275					280					285			
Ser	Val	Pro	Glu	Gln	Ile	Pro	Ser	Gly	Leu	Trp	Cys	Tyr	Arg	Val	Ser
	290					295					300				
Arg	Asp	Gln	Cys	Ile	Val	Gly	Gly	Ala	Leu	Asn	Asp	Val	Gly	Arg	Ala
305					310					315					320
Val	Thr	Trp	Leu	Glu	Arg	Thr	Ile	Ile	Lys	Pro	Glu	Asn	Leu	Asp	Glu
				325					330					335	
Val	Leu	Ile	Arg	Glu	Pro	Leu	Glu	Gly	Thr	Pro	Ala	Val	Leu	Pro	Phe
			340					345					350		
Phe	Ser	Gly	Glu	Arg	Ser	Ile	Gly	Trp	Ala	Ala	Ser	Ala	Gln	Ala	Thr
		355					360					365			
Ile	Thr	Asn	Ile	Gln	Glu	Gln	Thr	Gly	Pro	Glu	His	Leu	Trp	Arg	Gly
		370				375					380				
Val	Phe	Glu	Ala	Leu	Ala	Leu	Ser	Tyr	Gln	Arg	Val	Trp	Glu	His	Met
385					390					395					400
Gly	Lys	Ala	Gly	Ala	Ala	Pro	Glu	Arg	Val	Ile	Ala	Ser	Gly	Arg	Val
				405					410					415	
Ser	Thr	Asp	His	Pro	Glu	Phe	Leu	Ala	Met	Leu	Ser	Asp	Ala	Leu	Asp
			420					425					430		
Thr	Pro	Val	Ile	Pro	Leu	Glu	Met	Lys	Arg	Ala	Thr	Leu	Arg	Gly	Thr
		435					440					445			
Ala	Leu	Ile	Val	Leu	Glu	Gln	Leu	Glu	Pro	Gly	Gly	Thr	Arg	Ala	Thr
						455					460				
Pro	Pro	Phe	Gly	Thr	Thr	His	Gln	Pro	Arg	Phe	Ala	His	His	Tyr	Ser
465					470					475					480
Lys	Ala	Arg	Glu	Leu	Phe	Asp	Ala	Leu	Tyr	Leu	Lys	Leu	Val		
				485					490						

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<210> 321
<211> 1134
<212> DNA
<213> Corynebacterium glutamicum
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<220>
<221> CDS
<222> (101)..(1111)
<223> FRXA01049
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gcgtctgctt gcacacctcc taccacccat cgcgcttgct gtg gtg aaa act gag 115
Val Val.Lys Thr Glu

	1	5	
ttc gag aaa gag ttc aac aaa gcc aag tat gtg atg acc atc ggt gag			163
Phe Glu Lys Glu Phe Asn Lys Ala Lys Tyr Val Met Thr Ile Gly Glu			
	10	20	
tac gtc tac ttc aaa ctt gca ggc atc acc gga atg gct act tcg att			211
Tyr Val Tyr Phe Lys Leu Ala Gly Ile Thr Gly Met Ala Thr Ser Ile			
	25	35	
gcc gcg tgg agt ggc att ttg gac gcc cat acc ggc gaa ctt gat ctg			259
Ala Ala Trp Ser Gly Ile Leu Asp Ala His Thr Gly Glu Leu Asp Leu			
	40	50	
act atc ttg gag cac atc ggt gtt gat ccg gct ctg ttc ggt gag atc			307
Thr Ile Leu Glu His Ile Gly Val Asp Pro Ala Leu Phe Gly Glu Ile			
	55	65	
aga aac cct gat gaa cca gcc acc gat gcc aaa gtt gtc gac aaa aag			355
Arg Asn Pro Asp Glu Pro Ala Thr Asp Ala Lys Val Val Asp Lys Lys			
	70	85	
tgg aag cac ctg gaa gaa atc cct tgg ttc cat gcc att cca gac ggc			403
Trp Lys His Leu Glu Glu Ile Pro Trp Phe His Ala Ile Pro Asp Gly			
	90	100	
tgg cct tcc aac att ggc cca ggc gcc gtg gat tct aaa acc gtc gca			451
Trp Pro Ser Asn Ile Gly Pro Gly Ala Val Asp Ser Lys Thr Val Ala			
	105	115	
gtc gcc gcc gct aca tcc ggc gcc atg cgc gtg atc ctt ccg agc gtt			499
Val Ala Ala Ala Thr Ser Gly Ala Met Arg Val Ile Leu Pro Ser Val			
	120	130	
ccc gaa cag atc ccc tct ggc ctg tgg tgt tac cgc gtt tcc cgc gac			547
Pro Glu Gln Ile Pro Ser Gly Leu Trp Cys Tyr Arg Val Ser Arg Asp			
	135	145	
cag tgc atc gtt ggt ggc gca ctc aac gac gtc gga cgc gcc gtc acc			595
Gln Cys Ile Val Gly Gly Ala Leu Asn Asp Val Gly Arg Ala Val Thr			
	150	165	
tgg ctg gaa cgc acc att atc aag cct gaa aac ctc gac gaa gtg ctg			643
Trp Leu Glu Arg Thr Ile Ile Lys Pro Glu Asn Leu Asp Glu Val Leu			
	170	180	
atc cgc gaa ccc ctc gaa ggc acc cca gct gtc ctg ccg ttc ttc tcc			691
Ile Arg Glu Pro Leu Glu Gly Thr Pro Ala Val Leu Pro Phe Phe Ser			
	185	195	
ggg gaa cgc tcc atc ggc tgg gca gcc tca gcg cag gcc acg atc acc			739
Gly Glu Arg Ser Ile Gly Trp Ala Ala Ser Ala Gln Ala Thr Ile Thr			
	200	210	
aac att cag gaa caa acc ggc cct gaa cac ttg tgg cgc ggc gtt ttc			787
Asn Ile Gln Glu Gln Thr Gly Pro Glu His Leu Trp Arg Gly Val Phe			
	215	225	
gaa gcc ctc gca ctc tcc tac cag cgc gtt tgg gaa cac atg ggg aaa			835
Glu Ala Leu Ala Leu Ser Tyr Gln Arg Val Trp Glu His Met Gly Lys			
	230	245	

gcc ggc gca gcc cct gaa cgg gtc atc gca tca gga cga gtc tcc acc 883
 Ala Gly Ala Ala Pro Glu Arg Val Ile Ala Ser Gly Arg Val Ser Thr
 250 255 260

gac cac cca gaa ttc ctc gcg atg ctt tcc gac gcc ctc gac acc cca 931
 Asp His Pro Glu Phe Leu Ala Met Leu Ser Asp Ala Leu Asp Thr Pro
 265 270 275

gtc atc cct ctg gaa atg aag cgc gcc acc ctc cgc ggc acc gca ctt 979
 Val Ile Pro Leu Glu Met Lys Arg Ala Thr Leu Arg Gly Thr Ala Leu
 280 285 290

atc gtc ctt gag cag ctc gaa cca ggc ggc acg cgc gcg acg cca cca 1027
 Ile Val Leu Glu Gln Leu Glu Pro Gly Gly Thr Arg Ala Thr Pro Pro
 295 300 305

ttc ggc acg acg cat cag ccg cgc ttt gcg cac cat tac tcc aag gca 1075
 Phe Gly Thr Thr His Gln Pro Arg Phe Ala His His Tyr Ser Lys Ala
 310 315 320 325

aga gag ctt ttc gac gcc ctc tac ctc aag ttg gtc tagcttttcg 1121
 Arg Glu Leu Phe Asp Ala Leu Tyr Leu Lys Leu Val
 330 335

cagtggaacg cgc 1134

<210> 322
 <211> 337
 <212> PRT
 <213> *Corynebacterium glutamicum*

<400> 322
 Val Val Lys Thr Glu Phe Glu Lys Glu Phe Asn Lys Ala Lys Tyr Val
 1 5 10 15

Met Thr Ile Gly Glu Tyr Val Tyr Phe Lys Leu Ala Gly Ile Thr Gly
 20 25 30

Met Ala Thr Ser Ile Ala Ala Trp Ser Gly Ile Leu Asp Ala His Thr
 35 40 45

Gly Glu Leu Asp Leu Thr Ile Leu Glu His Ile Gly Val Asp Pro Ala
 50 55 60

Leu Phe Gly Glu Ile Arg Asn Pro Asp Glu Pro Ala Thr Asp Ala Lys
 65 70 75 80

Val Val Asp Lys Lys Trp Lys His Leu Glu Glu Ile Pro Trp Phe His
 85 90 95

Ala Ile Pro Asp Gly Trp Pro Ser Asn Ile Gly Pro Gly Ala Val Asp
 100 105 110

Ser Lys Thr Val Ala Val Ala Ala Thr Ser Gly Ala Met Arg Val
 115 120 125

Ile Leu Pro Ser Val Pro Glu Gln Ile Pro Ser Gly Leu Trp Cys Tyr
 130 135 140

Arg Val Ser Arg Asp Gln Cys Ile Val Gly Gly Ala Leu Asn Asp Val
 145 150 155 160
 Gly Arg Ala Val Thr Trp Leu Glu Arg Thr Ile Ile Lys Pro Glu Asn
 165 170 175
 Leu Asp Glu Val Leu Ile Arg Glu Pro Leu Glu Gly Thr Pro Ala Val
 180 185 190
 Leu Pro Phe Phe Ser Gly Glu Arg Ser Ile Gly Trp Ala Ala Ser Ala
 195 200 205
 Gln Ala Thr Ile Thr Asn Ile Gln Glu Gln Thr Gly Pro Glu His Leu
 210 215 220
 Trp Arg Gly Val Phe Glu Ala Leu Ala Leu Ser Tyr Gln Arg Val Trp
 225 230 235 240
 Glu His Met Gly Lys Ala Gly Ala Ala Pro Glu Arg Val Ile Ala Ser
 245 250 255
 Gly Arg Val Ser Thr Asp His Pro Glu Phe Leu Ala Met Leu Ser Asp
 260 265 270
 Ala Leu Asp Thr Pro Val Ile Pro Leu Glu Met Lys Arg Ala Thr Leu
 275 280 285
 Arg Gly Thr Ala Leu Ile Val Leu Glu Gln Leu Glu Pro Gly Gly Thr
 290 295 300
 Arg Ala Thr Pro Pro Phe Gly Thr Thr His Gln Pro Arg Phe Ala His
 305 310 315 320
 His Tyr Ser Lys Ala Arg Glu Leu Phe Asp Ala Leu Tyr Leu Lys Leu
 325 330 335

Val

<210> 323
 <211> 597
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(574)
 <223> FRXA01050

<400> 323
 aagcacagca attgagcaat actcccatgc atgttttcgc gtgatcacgc tatatcctta 60
 aagaatattc tttattagtc agacctttaa aggaaacctt atg gga tca att cca 115
 Met Gly Ser Ile Pro
 1 5
 aca atg tcc atc cct ttt gat gac tca cgt gga cct tat gtc ctt gct 163
 Thr Met Ser Ile Pro Phe Asp Asp Ser Arg Gly Pro Tyr Val Leu Ala
 10 15 20

atg gat att ggt tcc act gca tca cga ggt gga ctt tat gat gct tcc 211
 Met Asp Ile Gly Ser Thr Ala Ser Arg Gly Gly Leu Tyr Asp Ala Ser
 25 30 35

 ggc tgc cca atc aaa ggc acc aag cag cgc gaa tcc cat gaa ttc acc 259
 Gly Cys Pro Ile Lys Gly Thr Lys Gln Arg Glu Ser His Glu Phe Thr
 40 45 50

 acc ggt gag ggc gtt tcc acc att gat gct gac cag gtg gtt tcg gag 307
 Thr Gly Glu Gly Val Ser Thr Ile Asp Ala Asp Gln Val Val Ser Glu
 55 60 65

 atc acc tca gtt att aat ggc att ttg aac gcg gct gat cat cac aac 355
 Ile Thr Ser Val Ile Asn Gly Ile Leu Asn Ala Ala Asp His His Asn
 70 75 80 85

 atc aaa gat cag atc gcc gct gtc gcg cta gat tct ttt gca tcc tca 403
 Ile Lys Asp Gln Ile Ala Ala Val Ala Leu Asp Ser Phe Ala Ser Ser
 90 95 100

 tta atc ttg gtc gat ggt gaa ggc aat gcg ctc acc ccg tgc att acc 451
 Leu Ile Leu Val Asp Gly Glu Gly Asn Ala Leu Thr Pro Cys Ile Thr
 105 110 115

 tac gcg gat tct cgt tct gca cag tat gtg gag cag ctg cgc gcg gaa 499
 Tyr Ala Asp Ser Arg Ser Ala Gln Tyr Val Glu Gln Leu Arg Ala Glu
 120 125 130

 atc gat gag aag gcc tac cac ggc cgc acc ggc gtc tgc ttg cac acc 547
 Ile Asp Glu Lys Ala Tyr His Gly Arg Thr Gly Val Cys Leu His Thr
 135 140 145

 tcc tac cac cca tcg cgc ttg ctg tgg tgaaaaactga gttcgagaaa 594
 Ser Tyr His Pro Ser Arg Leu Leu Trp
 150 155

 gag 597

<210> 324

<211> 158

<212> PRT

<213> Corynebacterium glutamicum

<400> 324

Met Gly Ser Ile Pro Thr Met Ser Ile Pro Phe Asp Asp Ser Arg Gly
 1 5 10 15

 Pro Tyr Val Leu Ala Met Asp Ile Gly Ser Thr Ala Ser Arg Gly Gly
 20 25 30

 Leu Tyr Asp Ala Ser Gly Cys Pro Ile Lys Gly Thr Lys Gln Arg Glu
 35 40 45

 Ser His Glu Phe Thr Thr Gly Glu Gly Val Ser Thr Ile Asp Ala Asp
 50 55 60

 Gln Val Val Ser Glu Ile Thr Ser Val Ile Asn Gly Ile Leu Asn Ala
 65 70 75 80

 Ala Asp His His Asn Ile Lys Asp Gln Ile Ala Ala Val Ala Leu Asp

85	90	95
Ser Phe Ala Ser Ser Leu Ile Leu Val Asp Gly Glu Gly Asn Ala Leu		
100	105	110
Thr Pro Cys Ile Thr Tyr Ala Asp Ser Arg Ser Ala Gln Tyr Val Glu		
115	120	125
Gln Leu Arg Ala Glu Ile Asp Glu Lys Ala Tyr His Gly Arg Thr Gly		
130	135	140
Val Cys Leu His Thr Ser Tyr His Pro Ser Arg Leu Leu Trp		
145	150	155
 <210> 325		
<211> 1065		
<212> DNA		
<213> Corynebacterium glutamicum		
 <220>		
<221> CDS		
<222> (101)..(1042)		
<223> RXA00202		
 <400> 325		
ctggcagcag attgtcatcg gttgtgtcat cgcgcttgcg gtgggcttcg atgtcatccg 60		
aaacaaaacc tctaagtaat tcttgaaagg aaattttcac atg tac gct cgt aaa 115		
	Met Tyr Ala Arg Lys	1 5
ctt att gct ctg tcc gct tct gtc gtt ttg gct ttc agc ttg tct gct 163		
Leu Ile Ala Leu Ser Ala Ser Val Val Leu Ala Phe Ser Leu Ser Ala	10	15 20
tgc aac cgt gaa tct tct ggc acc agc gca gac ggc ggt tct gcg gat 211		
Cys Asn Arg Glu Ser Ser Gly Thr Ser Ala Asp Gly Gly Ser Ala Asp	25	30 35
ggg tcg atc acc ttg gct ctg tct acc cag acc aac ccg ttc ttt gtg 259		
Gly Ser Ile Thr Leu Ala Leu Ser Thr Gln Thr Asn Pro Phe Phe Val	40	45 50
cag ctt cgt gat ggt gcc cag gaa aag gct gat gaa ttg ggc gtg acc 307		
Gln Leu Arg Asp Gly Ala Gln Glu Lys Ala Asp Glu Leu Gly Val Thr	55	60 65
ctc aat gtt cag gat gct tcc gat gac gct gca acg cag gcc aac cag 355		
Leu Asn Val Gln Asp Ala Ser Asp Asp Ala Ala Thr Gln Ala Asn Gln	70	75 80 85
ctc aac aac gct gtc acc acc ggt gct ggc gtg gtg att gtc aac cca 403		
Leu Asn Asn Ala Val Thr Thr Gly Ala Gly Val Val Ile Val Asn Pro	90	95 100
act gat tct gat gct gtg gtg ccg tcg gtg gaa gct ctc aac cag gct 451		
Thr Asp Ser Asp Ala Val Val Pro Ser Val Glu Ala Leu Asn Gln Ala	105	110 115
gac att cct gtt gtg gct gtc gac cgt tcc tcc aat ggt ggc gag gtg 499		


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Asp Ile Pro Val Val Ala Val Asp Arg Ser Ser Asn Gly Gly Glu Val
    120                      125                      130

gcg tcc ttc gtg gca tct gac aac gtt gct ggc ggc gcg cag gct gct 547
Ala Ser Phe Val Ala Ser Asp Asn Val Ala Gly Gly Ala Gln Ala Ala
    135                      140                      145

gca gcc ctg gca gag gcg atc ggt ggc gaa ggt gaa atc ctc atg ctg 595
Ala Ala Leu Ala Glu Ala Ile Gly Gly Glu Gly Glu Ile Leu Met Leu
    150                      155                      160                      165

caa ggc att gcg gga tcc tct gca tca cgt gat cgt gga cag gga ttt 643
Gln Gly Ile Ala Gly Ser Ser Ala Ser Arg Asp Arg Gly Gln Gly Phe
    170                      175                      180

gaa gag gag atc gct aag cat gag ggc att tcc att gtg gct aag cag 691
Glu Glu Glu Ile Ala Lys His Glu Gly Ile Ser Ile Val Ala Lys Gln
    185                      190                      195

acc gcc aac ttt gac cgc ggt gag ggc ctg gac gtg gca act aac ctg 739
Thr Ala Asn Phe Asp Arg Gly Glu Gly Leu Asp Val Ala Thr Asn Leu
    200                      205                      210

ctg cag gca cac ccc aat gtg aag gcg atc ttc gcg gaa aac gat gag 787
Leu Gln Ala His Pro Asn Val Lys Ala Ile Phe Ala Glu Asn Asp Glu
    215                      220                      225

atg gcg ttg ggc gca atc gaa gcc ctg ggt gct cgt gct ggt gaa gat 835
Met Ala Leu Gly Ala Ile Glu Ala Leu Gly Ala Arg Ala Gly Glu Asp
    230                      235                      240                      245

gtc atc gtt gtc ggt ttc gat ggc acc aat gat ggt ctg gca gcg gtt 883
Val Ile Val Val Gly Phe Asp Gly Thr Asn Asp Gly Leu Ala Ala Val
    250                      255                      260

gaa gat gga cgc atg ttg gcc acc gtt gct cag cag cca gaa gag ctg 931
Glu Asp Gly Arg Met Leu Ala Thr Val Ala Gln Gln Pro Glu Glu Leu
    265                      270                      275

gga gca aag gct gtg gaa gaa gca gct aag ctc ctg cgc ggt gag gac 979
Gly Ala Lys Ala Val Glu Glu Ala Ala Lys Leu Leu Arg Gly Glu Asp
    280                      285                      290

gct gaa aca gag gta cca gtt gag gtt gtc act gtg aag ctc gac aac 1027
Ala Glu Thr Glu Val Pro Val Glu Val Val Thr Val Lys Leu Asp Asn
    295                      300                      305

gtc gcg gac ttc aag tagtcggcga tgaaaaagtc cgt 1065
Val Ala Asp Phe Lys
310

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<210> 326

<211> 314

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 326

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Met Tyr Ala Arg Lys Leu Ile Ala Leu Ser Ala Ser Val Val Leu Ala
  1                      5                      10                      15

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Phe Ser Leu Ser Ala Cys Asn Arg Glu Ser Ser Gly Thr Ser Ala Asp
 20 25 30
 Gly Gly Ser Ala Asp Gly Ser Ile Thr Leu Ala Leu Ser Thr Gln Thr
 35 40 45
 Asn Pro Phe Phe Val Gln Leu Arg Asp Gly Ala Gln Glu Lys Ala Asp
 50 55 60
 Glu Leu Gly Val Thr Leu Asn Val Gln Asp Ala Ser Asp Asp Ala Ala
 65 70 75 80
 Thr Gln Ala Asn Gln Leu Asn Asn Ala Val Thr Thr Gly Ala Gly Val
 85 90 95
 Val Ile Val Asn Pro Thr Asp Ser Asp Ala Val Val Pro Ser Val Glu
 100 105 110
 Ala Leu Asn Gln Ala Asp Ile Pro Val Val Ala Val Asp Arg Ser Ser
 115 120 125
 Asn Gly Gly Glu Val Ala Ser Phe Val Ala Ser Asp Asn Val Ala Gly
 130 135 140
 Gly Ala Gln Ala Ala Ala Leu Ala Glu Ala Ile Gly Gly Glu Gly
 145 150 155 160
 Glu Ile Leu Met Leu Gln Gly Ile Ala Gly Ser Ser Ala Ser Arg Asp
 165 170 175
 Arg Gly Gln Gly Phe Glu Glu Glu Ile Ala Lys His Glu Gly Ile Ser
 180 185 190
 Ile Val Ala Lys Gln Thr Ala Asn Phe Asp Arg Gly Glu Gly Leu Asp
 195 200 205
 Val Ala Thr Asn Leu Leu Gln Ala His Pro Asn Val Lys Ala Ile Phe
 210 215 220
 Ala Glu Asn Asp Glu Met Ala Leu Gly Ala Ile Glu Ala Leu Gly Ala
 225 230 235 240
 Arg Ala Gly Glu Asp Val Ile Val Val Gly Phe Asp Gly Thr Asn Asp
 245 250 255
 Gly Leu Ala Ala Val Glu Asp Gly Arg Met Leu Ala Thr Val Ala Gln
 260 265 270
 Gln Pro Glu Glu Leu Gly Ala Lys Ala Val Glu Glu Ala Ala Lys Leu
 275 280 285
 Leu Arg Gly Glu Asp Ala Glu Thr Glu Val Pro Val Glu Val Val Thr
 290 295 300
 Val Lys Leu Asp Asn Val Ala Asp Phe Lys
 305 310

<210> 327

<211> 1077

<212> DNA

<213> *Corynebacterium glutamicum*

<220>

<221> CDS

<222> (101)..(1054)

<223> RXN00872

<400> 327

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gaaatgtatt gctttgtcag gacaatgtgt tattgtcatg acatgcatc gtgagggtcg 60
ccacattcca tcaaaaatga gtgaagggtt gcatcgccac atg act aac ttg acg 115
                                     Met Thr Asn Leu Thr
                                     1 5
agc act cac gaa gtc cta gct atc ggc cgc ttg ggc gta gat att tac 163
Ser Thr His Glu Val Leu Ala Ile Gly Arg Leu Gly Val Asp Ile Tyr
                                     10 15 20
cca ctt caa agt gga gta gga ctg gcc gat gtt caa tct ttc ggc aag 211
Pro Leu Gln Ser Gly Val Gly Leu Ala Asp Val Gln Ser Phe Gly Lys
                                     25 30 35
tac ctc ggc gga agc gca gca aac gtt tct gtt gca gcc gcc cgc cat 259
Tyr Leu Gly Gly Ser Ala Ala Asn Val Ser Val Ala Ala Ala Arg His
                                     40 45 50
gga cac aat tcc gca ctg ctg tcc cgt gtg gga aat gat cct ttc ggc 307
Gly His Asn Ser Ala Leu Leu Ser Arg Val Gly Asn Asp Pro Phe Gly
                                     55 60 65
gag tac ctg ctt gct gag ctg gag cgt ttg ggc gtg gac aac cag tac 355
Glu Tyr Leu Leu Ala Glu Leu Glu Arg Leu Gly Val Asp Asn Gln Tyr
                                     70 75 80 85
gtt gcc acc gat cag act ttt aag acc cca gtg acc ttc tgt gaa att 403
Val Ala Thr Asp Gln Thr Phe Lys Thr Pro Val Thr Phe Cys Glu Ile
                                     90 95 100
ttc cca ccg gat gat ttc cca ctg tac ttc tac cgc gaa cca aag gct 451
Phe Pro Pro Asp Phe Pro Leu Tyr Phe Tyr Arg Glu Pro Lys Ala
                                     105 110 115
ccg gat ctc aat att gaa tcc gca gac gtc agc ctg gac gat gtg cgc 499
Pro Asp Leu Asn Ile Glu Ser Ala Asp Val Ser Leu Asp Asp Val Arg
                                     120 125 130
gaa gcc gat att ttg tgg ttc aca ctc act ggt ttc agt gaa gag cca 547
Glu Ala Asp Ile Leu Trp Phe Thr Leu Thr Gly Phe Ser Glu Glu Pro
                                     135 140 145
agc cgc ggc aca cac cgc gag atc ttg act act cgt gcg aac cgt cgc 595
Ser Arg Gly Thr His Arg Glu Ile Leu Thr Thr Arg Ala Asn Arg Arg
                                     150 155 160 165
cac acc atc ttt gat ctg gac tac cga cca atg ttc tgg gaa tcc cca 643
His Thr Ile Phe Asp Leu Asp Tyr Arg Pro Met Phe Trp Glu Ser Pro
                                     170 175 180
gaa gag gcc acc aag cag gcg gaa tgg gcg ttg cag cat tcc acg gtg 691
Glu Glu Ala Thr Lys Gln Ala Glu Trp Ala Leu Gln His Ser Thr Val
                                     185 190 195

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gcg gtt ggc aac aag gaa gaa tgc gaa atc gca gtg ggc gag acc gag 739
 Ala Val Gly Asn Lys Glu Glu Cys Glu Ile Ala Val Gly Glu Thr Glu
 200 205 210

cca gag cgc gcg ggc cga gca ctg ttg gaa cgc ggt gtg gag ttg gcc 787
 Pro Glu Arg Ala Gly Arg Ala Leu Leu Glu Arg Gly Val Glu Leu Ala
 215 220 225

atc gtc aag cag gga cct aag ggt gtc atg gcg atg acc aag gac gaa 835
 Ile Val Lys Gln Gly Pro Lys Gly Val Met Ala Met Thr Lys Asp Glu
 230 235 240 245

acc gta gaa gtt cct ccg ttc ttc gtc gat gtc atc aac ggt ctt ggt 883
 Thr Val Glu Val Pro Pro Phe Phe Val Asp Val Ile Asn Gly Leu Gly
 250 255 260

gcc ggc gat gca ttc ggc ggc gcg ctg tgc cac ggt ctg ctc tct gaa 931
 Ala Gly Asp Ala Phe Gly Gly Ala Leu Cys His Gly Leu Leu Ser Glu
 265 270 275

tgg ccg ttg gaa aag gtt ctc cgt ttt gcc aac acc gcg ggt gcg ctt 979
 Trp Pro Leu Glu Lys Val Leu Arg Phe Ala Asn Thr Ala Gly Ala Leu
 280 285 290

gtg gcg tcc cgt ctt gaa tgc tcc acc gca atg cct act acc gat gag 1027
 Val Ala Ser Arg Leu Glu Cys Ser Thr Ala Met Pro Thr Thr Asp Glu
 295 300 305

gtg gaa gcc tcc ctc aac cag aaa gtc tgatatgact cctccgatta 1074
 Val Glu Ala Ser Leu Asn Gln Lys Val
 310 315

tct 1077

<210> 328

<211> 318

<212> PRT

<213> Corynebacterium glutamicum

<400> 328

Met Thr Asn Leu Thr Ser Thr His Glu Val Leu Ala Ile Gly Arg Leu
 1 5 10 15

Gly Val Asp Ile Tyr Pro Leu Gln Ser Gly Val Gly Leu Ala Asp Val
 20 25 30

Gln Ser Phe Gly Lys Tyr Leu Gly Gly Ser Ala Ala Asn Val Ser Val
 35 40 45

Ala Ala Ala Arg His Gly His Asn Ser Ala Leu Leu Ser Arg Val Gly
 50 55 60

Asn Asp Pro Phe Gly Glu Tyr Leu Leu Ala Glu Leu Glu Arg Leu Gly
 65 70 75 80

Val Asp Asn Gln Tyr Val Ala Thr Asp Gln Thr Phe Lys Thr Pro Val
 85 90 95

Thr Phe Cys Glu Ile Phe Pro Pro Asp Asp Phe Pro Leu Tyr Phe Tyr

100 105 110
 Arg Glu Pro Lys Ala Pro Asp Leu Asn Ile Glu Ser Ala Asp Val Ser
 115 120 125
 Leu Asp Asp Val Arg Glu Ala Asp Ile Leu Trp Phe Thr Leu Thr Gly
 130 135 140
 Phe Ser Glu Glu Pro Ser Arg Gly Thr His Arg Glu Ile Leu Thr Thr
 145 150 155 160
 Arg Ala Asn Arg Arg His Thr Ile Phe Asp Leu Asp Tyr Arg Pro Met
 165 170 175
 Phe Trp Glu Ser Pro Glu Glu Ala Thr Lys Gln Ala Glu Trp Ala Leu
 180 185 190
 Gln His Ser Thr Val Ala Val Gly Asn Lys Glu Glu Cys Glu Ile Ala
 195 200 205
 Val Gly Glu Thr Glu Pro Glu Arg Ala Gly Arg Ala Leu Leu Glu Arg
 210 215 220
 Gly Val Glu Leu Ala Ile Val Lys Gln Gly Pro Lys Gly Val Met Ala
 225 230 235 240
 Met Thr Lys Asp Glu Thr Val Glu Val Pro Pro Phe Phe Val Asp Val
 245 250 255
 Ile Asn Gly Leu Gly Ala Gly Asp Ala Phe Gly Gly Ala Leu Cys His
 260 265 270
 Gly Leu Leu Ser Glu Trp Pro Leu Glu Lys Val Leu Arg Phe Ala Asn
 275 280 285
 Thr Ala Gly Ala Leu Val Ala Ser Arg Leu Glu Cys Ser Thr Ala Met
 290 295 300
 Pro Thr Thr Asp Glu Val Glu Ala Ser Leu Asn Gln Lys Val
 305 310 315

 <210> 329
 <211> 622
 <212> DNA
 <213> Corynebacterium glutamicum

 <220>
 <221> CDS
 <222> (101)..(622)
 <223> FRXA00872

 <400> 329
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 ccacattcca tcaaaaatga gtgaagggtt gcatcgccac atg act aac ttg acg 115
 Met Thr Asn Leu Thr
 1 5

 agc act cac gaa gtc cta gct atc ggc cgc ttg ggc gta gat att tac 163
 Ser Thr His Glu Val Leu Ala Ile Gly Arg Leu Gly Val Asp Ile Tyr

	10	15	20	
cca ctt caa agt gga gta gga ctg gcc gat gtt caa tct ttc ggc aag				211
Pro Leu Gln Ser Gly Val Gly Leu Ala Asp Val Gln Ser Phe Gly Lys				
	25	30	35	
tac ctc ggc gga agc gca gca aac gtt tct gtt gca gcc gcc cgc cat				259
Tyr Leu Gly Gly Ser Ala Ala Asn Val Ser Val Ala Ala Ala Arg His				
	40	45	50	
gga cac aat tcc gca ctg ctg tcc cgt gtg gga aat gat cct ttc ggc				307
Gly His Asn Ser Ala Leu Leu Ser Arg Val Gly Asn Asp Pro Phe Gly				
	55	60	65	
gag tac ctg ctt gct gag ctg gag cgt ttg ggc gtg gac aac cag tac				355
Glu Tyr Leu Leu Ala Glu Leu Glu Arg Leu Gly Val Asp Asn Gln Tyr				
	70	75	80	85
gtt gcc acc gat cag act ttt aag acc cca gtg acc ttc tgt gaa att				403
Val Ala Thr Asp Gln Thr Phe Lys Thr Pro Val Thr Phe Cys Glu Ile				
	90	95	100	
ttc cca ccg gat gat ttc cca ctg tac ttc tac cgc gaa cca aag gct				451
Phe Pro Pro Asp Asp Phe Pro Leu Tyr Phe Tyr Arg Glu Pro Lys Ala				
	105	110	115	
ccg gat ctc aat att gaa tcc gca gac gtc agc ctg gac gat gtg cgc				499
Pro Asp Leu Asn Ile Glu Ser Ala Asp Val Ser Leu Asp Asp Val Arg				
	120	125	130	
gaa gcc gat att ttg tgg ttc aca ctc act ggt ttc agt gaa gag cca				547
Glu Ala Asp Ile Leu Trp Phe Thr Leu Thr Gly Phe Ser Glu Glu Pro				
	135	140	145	
agc cgc ggc aca cac cgc gag atc ttg act act cgt gcg aac cgt cgc				595
Ser Arg Gly Thr His Arg Glu Ile Leu Thr Thr Arg Ala Asn Arg Arg				
	150	155	160	165
cac acc atc ttt gat ctg gac tac cga				622
His Thr Ile Phe Asp Leu Asp Tyr Arg				
	170			

<210> 330

<211> 174

<212> PRT

<213> Corynebacterium glutamicum

<400> 330

Met Thr Asn Leu Thr Ser Thr His Glu Val Leu Ala Ile Gly Arg Leu				
1	5	10	15	
Gly Val Asp Ile Tyr Pro Leu Gln Ser Gly Val Gly Leu Ala Asp Val				
20	25	30		
Gln Ser Phe Gly Lys Tyr Leu Gly Gly Ser Ala Ala Asn Val Ser Val				
35	40	45		
Ala Ala Ala Arg His Gly His Asn Ser Ala Leu Leu Ser Arg Val Gly				
50	55	60		

Asn Asp Pro Phe Gly Glu Tyr Leu Leu Ala Glu Leu Glu Arg Leu Gly
 65 70 75 80
 Val Asp Asn Gln Tyr Val Ala Thr Asp Gln Thr Phe Lys Thr Pro Val
 85 90 95
 Thr Phe Cys Glu Ile Phe Pro Pro Asp Asp Phe Pro Leu Tyr Phe Tyr
 100 105 110
 Arg Glu Pro Lys Ala Pro Asp Leu Asn Ile Glu Ser Ala Asp Val Ser
 115 120 125
 Leu Asp Asp Val Arg Glu Ala Asp Ile Leu Trp Phe Thr Leu Thr Gly
 130 135 140
 Phe Ser Glu Glu Pro Ser Arg Gly Thr His Arg Glu Ile Leu Thr Thr
 145 150 155 160
 Arg Ala Asn Arg Arg His Thr Ile Phe Asp Leu Asp Tyr Arg
 165 170

<210> 331
 <211> 1767
 <212> DNA
 <213> *Corynebacterium glutamicum*

<220>
 <221> CDS
 <222> (101)..(1744)
 <223> RXN00799

<400> 331
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 ctgactacga tggttaagaaa taaggaaaga gattaccatt atg tct caa gag cgg 115
 Met Ser Gln Glu Arg
 1 5
 cct caa atc ggc tcc cgc ctc tct cgt gtc att gaa caa gac ggc cta 163
 Pro Gln Ile Gly Ser Arg Leu Ser Arg Val Ile Glu Gln Asp Gly Leu
 10 15 20
 caa ttc cgc gat ctc gac ggc gac ggc gta ctt gca cct tat gaa gat 211
 Gln Phe Arg Asp Leu Asp Gly Asp Gly Val Leu Ala Pro Tyr Glu Asp
 25 30 35
 tgg cgt cta acc cca gca gag cgt gcc gct gac ctg gtg aaa cgt atg 259
 Trp Arg Leu Thr Pro Ala Glu Arg Ala Ala Asp Leu Val Lys Arg Met
 40 45 50
 aat gtg gaa gaa aaa gcg ggc ctg atg atc atc ggt tcg cac tac ccc 307
 Asn Val Glu Glu Lys Ala Gly Leu Met Ile Ile Gly Ser His Tyr Pro
 55 60 65
 gga tac tcg cct ttg gcg ccg gag agt gaa ggc aaa gac gcg gaa aag 355
 Gly Tyr Ser Pro Leu Ala Pro Glu Ser Glu Gly Lys Asp Ala Glu Lys
 70 75 80 85
 tgc gag cct ttg ctg aac cct gtc gat atg tgg cgt gag gat aac ccg 403
 Cys Glu Pro Leu Leu Asn Pro Val Asp Met Trp Arg Glu Asp Asn Pro

90										95					100					
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 Tyr Asn Arg Thr Phe Ile Gln Asp Leu Leu Arg Asp Ala Met Gly His
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 Arg Gly Tyr Val Asn Ser Asp Ser Gly Val Ile Asp Ala Met Met Trp
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 Pro Tyr Val Ser Glu Asp Glu Ala Glu Lys Ile Ile Gly Ala Pro Glu
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 Arg Asn Asn Pro Ile Arg Ala Ala Thr Gly Ser Cys Ser Lys Pro Glu
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Gly Ser His Tyr Pro Gly Tyr Ser Pro Leu Ala Pro Glu Ser Glu Gly
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Ala Thr Ser Ser Thr Glu Asn Ala Ile Asn Leu Arg Asn Gln Arg Tyr
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Asn Ala Val Gln Glu Val Ala Glu Arg Ser Arg Leu Gly Ile Pro Val
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Ala Phe Ala Ser Asn Pro Arg Asn His Val Ala Leu Val Ala Gln Phe
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Gly Val Asn Glu Ser Ala Gly Val Phe Ser Glu Trp Pro Gly Glu Leu
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Gly Leu Ala Ala Leu Arg Asp Ala Glu Leu Met Glu Thr Phe Gly Thr
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Tyr Met Ala Asp Leu Ala Ser Glu Pro Arg Trp Ser Arg Phe Asn Gly
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Thr Phe Gly Glu Asp Pro Glu Leu Ile Ser Asp Tyr Ile Ala Ala Val
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Val Arg Gly Leu Gln Gly Pro Glu Leu Ser Lys Asn Ser Val Ser Thr
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Thr Ile Lys His Phe Pro Gly Gly Gly Val Arg Leu Asp Gly His Asp
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Pro His Phe His Trp Gly Gln Thr Asn Glu Tyr Pro Thr Glu Asp Ala
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Leu Gly Lys Tyr His Leu Pro Pro Phe Gln Ala Ala Ile Asp Ala Gly
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 Asp Ala Met Gly His Arg Gly Tyr Val Asn Ser Asp Ser Gly Val Ile
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 Asp Ala Met Met Trp Gly Val Glu Glu Leu Ser Glu Pro Glu Arg Phe
 385 390 395 400
 Ala Ala Ala Val Arg Ala Gly Thr Asp Ile Phe Ser Asp Met Ala Asn
 405 410 415
 Pro Arg Arg Leu Leu Glu Ala Val Ala Glu Gly His Leu Asp Glu Ser
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 Glu Leu Asn Gln Pro Val Gln Arg Leu Leu Glu Glu Ile Phe Gln Leu
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 Gly Leu Phe Glu Asn Pro Tyr Val Ser Glu Asp Glu Ala Glu Lys Ile
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 Ser Val Thr Leu Leu Arg Asn Asn Pro Ile Arg Ala Ala Thr Gly Ser
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 Cys Ser Lys Pro Glu Asp Leu Pro Ile Gly Tyr Trp Pro Tyr Gln Asp
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Asp Trp Arg Leu Thr Pro Ala Glu Arg Ala Ala Asp Leu Val Lys Arg	
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Met Asn Val Glu Glu Lys Ala Gly Leu Met Ile Ile Gly Ser His Tyr	
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Pro Gly Tyr Ser Pro Leu Ala Pro Glu Ser Glu Gly Lys Asp Ala Glu	
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Lys Cys Glu Pro Leu Leu Asn Pro Val Asp Met Trp Arg Glu Asp Asn	
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Thr Glu Asn Ala Ile Asn Leu Arg Asn Gln Arg Tyr Leu Ile Val Arg	
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Asn Pro Arg Asn His Val Ala Leu Val Ala Gln Phe Gly Val Asn Glu	
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Ser Ala Gly Val Phe Ser Glu Trp Pro Gly Glu Leu Gly Leu Ala Ala	
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Leu Arg Asp Ala Glu Leu Met Glu Thr Phe Gly Thr Glu Ala Ala Lys	
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Asp Pro Glu Leu Ile Ser Asp Tyr Ile Ala Ala Val Val Arg Gly Leu	
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Gln Gly Pro Glu Leu Ser Lys Asn Ser Val Ser Thr Thr Ile Lys His	
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Trp	Gly	Gln	Thr	Asn	Glu	Tyr	Pro	Thr	Glu	Asp	Ala	Leu	Gly	Lys	Tyr		
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Pro	Val	Gln	Arg	Leu	Leu	Glu	Glu	Ile	Phe	Gln	Leu	Gly	Leu	Phe	Glu		
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Asn	Pro	Tyr	Val	Ser	Glu	Asp	Glu	Ala	Glu	Lys	Ile	Ile	Gly	Ala	Pro		
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 Lys Cys Glu Pro Leu Leu Asn Pro Val Asp Met Trp Arg Glu Asp Asn
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 Thr Glu Asn Ala Ile Asn Leu Arg Asn Gln Arg Tyr Leu Ile Val Arg
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 Glu Val Ala Glu Arg Ser Arg Leu Gly Ile Pro Val Ala Phe Ala Ser
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 Ser Ala Gly Val Phe Ser Glu Trp Pro Gly Glu Leu Gly Leu Ala Ala
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 Gln Gly Pro Glu Leu Ser Lys Asn Ser Val Ser Thr Thr Ile Lys His

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Gln	Gln	Leu	Trp	Gln 325	Asn	Pro	Thr	Thr	Gln 330	Phe	Glu	Glu	Val	Ala 335	Phe	
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gat	cac	ctt	tat	acc	ctg	acc	act	aaa	gct	cct	gat	gga	act	ctt	gat	403
Asp	His	Leu	Tyr	Thr	Leu	Thr	Thr	Lys	Ala	Pro	Asp	Gly	Thr	Leu	Asp	
				90					95					100		

caa	aaa	atc	atc	gga	tcc	atc	att	gac	tac	gtg	ttc	gct	ccc	gag	gac	451
Gln	Lys	Ile	Ile	Gly	Ser	Ile	Ile	Asp	Tyr	Val	Phe	Ala	Pro	Glu	Asp	
			105					110					115			

cca	gca	cgg	gcc	gtt	gca	acc	ctc	gcg	cag	gac	tcc	atc	cgc	att	gtt	499
Pro	Ala	Arg	Ala	Val	Ala	Thr	Leu	Ala	Gln	Asp	Ser	Ile	Arg	Ile	Val	
		120					125					130				

tcc	ctc	acg	gtg	act	gaa	ggc	gga	tac	aac	atc	gat	ccg	gcg	aca	gaa	547
Ser	Leu	Thr	Val	Thr	Glu	Gly	Gly	Tyr	Asn	Ile	Asp	Pro	Ala	Thr	Glu	
	135					140					145					

gat	ttc	gac	cac	acc	aac	cct	cga	atc	gtt	gct	gac	cgc	gaa	gcc	ctg	595
Asp	Phe	Asp	His	Thr	Asn	Pro	Arg	Ile	Val	Ala	Asp	Arg	Glu	Ala	Leu	
	150				155					160					165	

cag	gcg	ggc	gat	act	tcc	act	ttg	cag	acc	ttc	ttt	ggg	ttg	atc	act	643
Gln	Ala	Gly	Asp	Thr	Ser	Thr	Leu	Gln	Thr	Phe	Phe	Gly	Leu	Ile	Thr	
				170					175					180		

gcc	gca	ttg	att	tcc	cga	aaa	gaa	tca	gga	tct	acg	cca	ttt	acc	atc	691
Ala	Ala	Leu	Ile	Ser	Arg	Lys	Glu	Ser	Gly	Ser	Thr	Pro	Phe	Thr	Ile	
		185						190					195			

atg agc tgc gat aac atc caa ggc aac ggc gat ctg gct aag cgt ttc	739
Met Ser Cys Asp Asn Ile Gln Gly Asn Gly Asp Leu Ala Lys Arg Phe	
200 205 210	
ttc ctc gcc ttc gca cat tcc gtg tct tct gag ctc ggc gaa tgg gtg	787
Phe Leu Ala Phe Ala His Ser Val Ser Ser Glu Leu Gly Glu Trp Val	
215 220 225	
gaa aac aac gtg gcc ttc ccc aac tcc atg gtg gac cgc atc acc cct	835
Glu Asn Asn Val Ala Phe Pro Asn Ser Met Val Asp Arg Ile Thr Pro	
230 235 240 245	
gaa acc acc gac ggc gac cgc gat gac atc aag gaa atc ggc tac atc	883
Glu Thr Thr Asp Gly Asp Arg Asp Ile Lys Glu Ile Gly Tyr Ile	
250 255 260	
gat gcg tgg cca gtg gtt tct gaa gat ttc acc caa tgg gtc ctc gag	931
Asp Ala Trp Pro Val Val Ser Glu Asp Phe Thr Gln Trp Val Leu Glu	
265 270 275	
gat gcc ttc acc cag ggc cgc ccc gcg tac gag gag gtt ggc gtg cag	979
Asp Ala Phe Thr Gln Gly Arg Pro Ala Tyr Glu Glu Val Gly Val Gln	
280 285 290	
gtc gtc tcc gac gtg gag cct tat gaa tta atg aag ctg cgc ctg ctc	1027
Val Val Ser Asp Val Glu Pro Tyr Glu Leu Met Lys Leu Arg Leu Leu	
295 300 305	
aac gcc tcc cac cag gga ctt tgc tac ttc ggc cac ttg gct ggc cac	1075
Asn Ala Ser His Gln Gly Leu Cys Tyr Phe Gly His Leu Ala Gly His	
310 315 320 325	
cac atg gtc cac gac gtc atg gcg gat acc cgc ttc cag gat ttc ctc	1123
His Met Val His Asp Val Met Ala Asp Thr Arg Phe Gln Asp Phe Leu	
330 335 340	
ctg gct tac atg gag cgc gaa gcc acc cct acc ctc aag gaa ctt cca	1171
Leu Ala Tyr Met Glu Arg Glu Ala Thr Pro Thr Leu Lys Glu Leu Pro	
345 350 355	
ggt gtc gat cta gat gct tat cga cgc caa ctc atc gcg cga ttc ggc	1219
Gly Val Asp Leu Asp Ala Tyr Arg Arg Gln Leu Ile Ala Arg Phe Gly	
360 365 370	
aac gcc gca gtc aaa gac acc gta ccg cgc ctg tgt gcg gaa tcc tcc	1267
Asn Ala Ala Val Lys Asp Thr Val Pro Arg Leu Cys Ala Glu Ser Ser	
375 380 385	
gac cgc att cca aag tgg ctg ttg cca gtc gta cgc gaa aac ctc gca	1315
Asp Arg Ile Pro Lys Trp Leu Leu Pro Val Val Arg Glu Asn Leu Ala	
390 395 400 405	
gca ggc cgc gac gtc aca ctt tct gca gcc atc gtc gca tcc tgg gcg	1363
Ala Gly Arg Asp Val Thr Leu Ser Ala Ala Ile Val Ala Ser Trp Ala	
410 415 420	
cgc tac gca gaa ggc acc gac gag cag ggc aac cca ata aag att gtt	1411
Arg Tyr Ala Glu Gly Thr Asp Glu Gln Gly Asn Pro Ile Lys Ile Val	
425 430 435	
gac cgt ttg agt gag cgc gtc caa gaa aac gca tca gga aat cgc acc	1459

Asp Arg Leu Ser Glu Arg Val Gln Glu Asn Ala Ser Gly Asn Arg Thr
 440 445 450
 gat att ttg tca ttc atc cgc gac cgt gga atc ttc gga gac ttg gtc 1507
 Asp Ile Leu Ser Phe Ile Arg Asp Arg Gly Ile Phe Gly Asp Leu Val
 455 460 465
 gat gct gaa cca ttc acc aag gca tac tcc gag aca ctg tcc tcc ctt 1555
 Asp Ala Glu Pro Phe Thr Lys Ala Tyr Ser Glu Thr Leu Ser Ser Leu
 470 475 480 485
 cat gac cgt ggc gcg gaa gca acc atc gat gca ctt ctt acg cag gta 1603
 His Asp Arg Gly Ala Glu Ala Thr Ile Asp Ala Leu Leu Thr Gln Val
 490 495 500
 act gtc taaatccggtt gcgcgctagg gtt 1632
 Thr Val

<210> 336
 <211> 503
 <212> PRT
 <213> Corynebacterium glutamicum

<400> 336
 Met Asn Thr Pro Leu Gln Leu Asn Thr Glu Asn Leu Gln Glu Ile Ala
 1 5 10 15
 Ser Thr Ser Gly Val Gln Ile Pro Ala Phe Asn Arg Ala Asp Val Ala
 20 25 30
 Pro Gly Ile Val His Phe Gly Val Gly Gly Phe His Arg Ala His Gln
 35 40 45
 Ala Met Tyr Leu Asn Glu Leu Met Asn Glu Gly Lys Ala Leu Asp Trp
 50 55 60
 Gly Ile Ile Gly Met Gly Val Met Pro Ser Asp Val Arg Met Arg Asp
 65 70 75 80
 Ala Leu Ala Ser Gln Asp His Leu Tyr Thr Leu Thr Thr Lys Ala Pro
 85 90 95
 Asp Gly Thr Leu Asp Gln Lys Ile Ile Gly Ser Ile Ile Asp Tyr Val
 100 105 110
 Phe Ala Pro Glu Asp Pro Ala Arg Ala Val Ala Thr Leu Ala Gln Asp
 115 120 125
 Ser Ile Arg Ile Val Ser Leu Thr Val Thr Glu Gly Gly Tyr Asn Ile
 130 135 140
 Asp Pro Ala Thr Glu Asp Phe Asp His Thr Asn Pro Arg Ile Val Ala
 145 150 155 160
 Asp Arg Glu Ala Leu Gln Ala Gly Asp Thr Ser Thr Leu Gln Thr Phe
 165 170 175
 Phe Gly Leu Ile Thr Ala Ala Leu Ile Ser Arg Lys Glu Ser Gly Ser
 180 185 190

Thr Pro Phe Thr Ile Met Ser Cys Asp Asn Ile Gln Gly Asn Gly Asp
 195 200 205
 Leu Ala Lys Arg Phe Phe Leu Ala Phe Ala His Ser Val Ser Ser Glu
 210 215 220
 Leu Gly Glu Trp Val Glu Asn Asn Val Ala Phe Pro Asn Ser Met Val
 225 230 235 240
 Asp Arg Ile Thr Pro Glu Thr Thr Asp Gly Asp Arg Asp Asp Ile Lys
 245 250 255
 Glu Ile Gly Tyr Ile Asp Ala Trp Pro Val Val Ser Glu Asp Phe Thr
 260 265 270
 Gln Trp Val Leu Glu Asp Ala Phe Thr Gln Gly Arg Pro Ala Tyr Glu
 275 280 285
 Glu Val Gly Val Gln Val Val Ser Asp Val Glu Pro Tyr Glu Leu Met
 290 295 300
 Lys Leu Arg Leu Leu Asn Ala Ser His Gln Gly Leu Cys Tyr Phe Gly
 305 310 315 320
 His Leu Ala Gly His His Met Val His Asp Val Met Ala Asp Thr Arg
 325 330 335
 Phe Gln Asp Phe Leu Leu Ala Tyr Met Glu Arg Glu Ala Thr Pro Thr
 340 345 350
 Leu Lys Glu Leu Pro Gly Val Asp Leu Asp Ala Tyr Arg Arg Gln Leu
 355 360 365
 Ile Ala Arg Phe Gly Asn Ala Ala Val Lys Asp Thr Val Pro Arg Leu
 370 375 380
 Cys Ala Glu Ser Ser Asp Arg Ile Pro Lys Trp Leu Leu Pro Val Val
 385 390 395 400
 Arg Glu Asn Leu Ala Ala Gly Arg Asp Val Thr Leu Ser Ala Ala Ile
 405 410 415
 Val Ala Ser Trp Ala Arg Tyr Ala Glu Gly Thr Asp Glu Gln Gly Asn
 420 425 430
 Pro Ile Lys Ile Val Asp Arg Leu Ser Glu Arg Val Gln Glu Asn Ala
 435 440 445
 Ser Gly Asn Arg Thr Asp Ile Leu Ser Phe Ile Arg Asp Arg Gly Ile
 450 455 460
 Phe Gly Asp Leu Val Asp Ala Glu Pro Phe Thr Lys Ala Tyr Ser Glu
 465 470 475 480
 Thr Leu Ser Ser Leu His Asp Arg Gly Ala Glu Ala Thr Ile Asp Ala
 485 490 495
 Leu Leu Thr Gln Val Thr Val
 500

gaa tca ctt tcc acc acg cag gaa cga atg cgc ggt att agt cat gcg 691
 Glu Ser Leu Ser Thr Thr Gln Glu Arg Met Arg Gly Ile Ser His Ala
 185 190 195

gcg tcg ata tat ggg gct gag gtg acg ttc cat ttt ggc cac tat tct 739
 Ala Ser Ile Tyr Gly Ala Glu Val Thr Phe His Phe Gly His Tyr Ser
 200 205 210

gtc gaa tct ggc gaa gag atg gct cag gtg gtg ttt aac aac ggc ctt 787
 Val Glu Ser Gly Glu Glu Met Ala Gln Val Val Phe Asn Asn Gly Leu
 215 220 225

ccc gat gca ttg att gtg gcg tct cct cgg ctg atg gct ggg gtg atg 835
 Pro Asp Ala Leu Ile Val Ala Ser Pro Arg Leu Met Ala Gly Val Met
 230 235 240 245

cgt gct ttt act cgc ctg aat gtc cgc gtt ccc cac gat gtg gtg att 883
 Arg Ala Phe Thr Arg Leu Asn Val Arg Val Pro His Asp Val Val Ile
 250 255 260

ggt ggt tat gac gat cct gag tgg tac agc ttt gtc ggc gcg ggg att 931
 Gly Gly Tyr Asp Asp Pro Glu Trp Tyr Ser Phe Val Gly Ala Gly Ile
 265 270 275

acc acg ttt gtt cca ccg cat gag gag atg ggg aaa gag gcc gtg cgc 979
 Thr Thr Phe Val Pro Pro His Glu Glu Met Gly Lys Glu Ala Val Arg
 280 285 290

ttg ttg gta gat ctg att gaa aat ccc gaa ctt ccc acc ggc gat gtg 1027
 Leu Leu Val Asp Leu Ile Glu Asn Pro Glu Leu Pro Thr Gly Asp Val
 295 300 305

gtt ttg cag ggg cag gtg atc ctt cgg ggg tcg agc aca cat tcc ggg 1075
 Val Leu Gln Gly Gln Val Ile Leu Arg Gly Ser Ser Thr His Ser Gly
 310 315 320 325

tagaattgcc caaatgtcat caa 1098

<210> 338

<211> 325

<212> PRT

<213> Corynebacterium glutamicum

<400> 338

Met Ser Ala Lys Ser Ser Leu Lys Glu Val Ala Glu Leu Ala Gly Val
 1 5 10 15

Gly Tyr Ala Thr Ala Ser Arg Ala Leu Ser Gly Lys Gly Tyr Val Ser
 20 25 30

Pro Gln Thr Arg Glu Lys Val Gln Ala Ala Ala Lys Glu Leu Asn Tyr
 35 40 45

Val Pro Asn Gln Leu Ala Lys Ala Leu Arg Glu His Arg Ser Ala Leu
 50 55 60

Val Gly Val Ile Val Pro Asp Leu Ser Asn Glu Tyr Tyr Ser Glu Ser
 65 70 75 80

Leu Gln Thr Ile Gln Gln Asp Leu Lys Ala Ala Gly Tyr Gln Met Leu
 85 90 95
 Val Ala Glu Ala Asn Ser Val Gln Ala Gln Asp Val Val Met Glu Ser
 100 105 110
 Leu Ile Ser Ile Gln Ala Ala Gly Ile Ile His Val Pro Val Val Gly
 115 120 125
 Ser Ile Ala Pro Glu Gly Ile Pro Met Val Gln Leu Thr Arg Gly Glu
 130 135 140
 Leu Gly Pro Gly Phe Pro Arg Val Leu Cys Asp Asp Glu Ala Gly Phe
 145 150 155 160
 Phe Gln Leu Thr Glu Ser Val Leu Gly Gly Ser Gly Met Asn Ile Ala
 165 170 175
 Ala Leu Val Gly Glu Glu Ser Leu Ser Thr Thr Gln Glu Arg Met Arg
 180 185 190
 Gly Ile Ser His Ala Ala Ser Ile Tyr Gly Ala Glu Val Thr Phe His
 195 200 205
 Phe Gly His Tyr Ser Val Glu Ser Gly Glu Glu Met Ala Gln Val Val
 210 215 220
 Phe Asn Asn Gly Leu Pro Asp Ala Leu Ile Val Ala Ser Pro Arg Leu
 225 230 235 240
 Met Ala Gly Val Met Arg Ala Phe Thr Arg Leu Asn Val Arg Val Pro
 245 250 255
 His Asp Val Val Ile Gly Gly Tyr Asp Asp Pro Glu Trp Tyr Ser Phe
 260 265 270
 Val Gly Ala Gly Ile Thr Thr Phe Val Pro Pro His Glu Glu Met Gly
 275 280 285
 Lys Glu Ala Val Arg Leu Leu Val Asp Leu Ile Glu Asn Pro Glu Leu
 290 295 300
 Pro Thr Gly Asp Val Val Leu Gln Gly Gln Val Ile Leu Arg Gly Ser
 305 310 315 320
 Ser Thr His Ser Gly
 325

<210> 339

<211> 1246

<212> DNA

<213> *Corynebacterium glutamicum*

<220>

<221> CDS

<222> (101)..(1246)

<223> RXN00316

<400> 339

agcgcacgat cgatgcctgc gagtccgcag gggccaact tggcgtgctc ttccagcgcc 60

gcttctgccc	cgcggtcaa	aaaatgaaaa	aggagccgtc	atg	ggc	caa	tgc	acg	115
				Met	Gly	Gln	Cys	Thr	
				1				5	
gta	gcg	ctt	tac	cga	gag	cat	tcc	tat	163
Val	Ala	Leu	Tyr	Arg	Glu	His	Ser	Tyr	
				10				15	
									20
gga	acc	tgg	gca	gcc	gat	ggc	ggg	gga	211
Gly	Thr	Trp	Ala	Ala	Asp	Gly	Gly	Gly	
				25				30	
									35
cac	tac	atc	gat	ctt	ttg	tac	tgg	ctg	259
His	Tyr	Ile	Asp	Leu	Leu	Tyr	Trp	Leu	
				40				45	
									50
ttc	ggc	tac	acc	aac	tcc	ttc	aaa	cac	307
Phe	Gly	Tyr	Thr	Asn	Ser	Phe	Lys	His	
				55				60	
									65
gac	agc	gcc	gtt	gcc	act	gtg	cgt	ttt	355
Asp	Ser	Ala	Val	Ala	Thr	Val	Arg	Phe	
				75				80	
									85
att	tca	gcc	acc	acc	gcc	gca	gag	cca	403
Ile	Ser	Ala	Thr	Thr	Ala	Ala	Glu	Pro	
				90				95	
									100
gtg	atg	gga	aca	aag	ggg	gcc	acc	atg	451
Val	Met	Gly	Thr	Lys	Gly	Ala	Thr	Met	
				105				110	
									115
ggg	acc	gac	ggc	agg	ctc	att	gtt	cgc	499
Gly	Thr	Asp	Gly	Arg	Leu	Ile	Val	Arg	
				120				125	
									130
aac	cac	ccc	att	cca	ccc	cgc	gga	tct	547
Asn	His	Pro	Ile	Pro	Pro	Arg	Gly	Ser	
				135				140	
									145
cat	cat	caa	cgg	tgc	ttt	gat	ccc	gta	595
His	His	Gln	Arg	Cys	Phe	Asp	Pro	Val	
				155				160	
									165
ctt	tat	cga	tgc	gct	caa	cga	agg	ccg	643
Leu	Tyr	Arg	Cys	Ala	Gln	Arg	Arg	Pro	
				170				175	
									180
cga	tgc	cac	cag	agc	tct	gaa	agt	tct	691
Arg	Cys	His	Gln	Ser	Ser	Glu	Ser	Ser	
				185				190	
									195
agc	cac	cca	cca	gcc	ggg	ctc	ttt	gat	739
Ser	His	Pro	Pro	Ala	Gly	Leu	Phe	Asp	
				200				205	
									210
tca	cgc	caa	atc	ggg	ctt	gca	cct	tta	787
Ser	Arg	Gln	Ile	Gly	Leu	Ala	Pro	Leu	
				215				220	
									225

gat caa cta gtg cgc ctc gca gct gcc act ggt ttc tcc ttt gtc ggt 835
 Asp Gln Leu Val Arg Leu Ala Ala Ala Thr Gly Phe Ser Phe Val Gly
 230 235 240 245

ctg cgc gtc atc gca gta acc ccc aac gaa cgt gta tat gac ctt tcc 883
 Leu Arg Val Ile Ala Val Thr Pro Asn Glu Arg Val Tyr Asp Leu Ser
 250 255 260

cca gga tcc cca ctg ctg gct gca acc caa caa gcg ttg aaa gaa acc 931
 Pro Gly Ser Pro Leu Leu Ala Ala Thr Gln Gln Ala Leu Lys Glu Thr
 265 270 275

gcc ctg tat gtg ctc gac act gaa ttc cta cag gta aac gca gac acc 979
 Ala Leu Tyr Val Leu Asp Thr Glu Phe Leu Gln Val Asn Ala Asp Thr
 280 285 290

acc cgc gag gcc tgg ctt ccc gca cta gaa gcc gcc gga gca ctg gga 1027
 Thr Arg Glu Ala Trp Leu Pro Ala Leu Glu Ala Ala Gly Ala Leu Gly
 295 300 305

gct aaa acc ttc acc atc gcc gcc ggt gat gac aac att gcg ccc ctg 1075
 Ala Lys Thr Phe Thr Ile Ala Ala Gly Asp Asp Asn Ile Ala Pro Leu
 310 315 320 325

acc gac acg atc ggt gcc atg gtt gac gat gcc cgt gat ttc gga gtc 1123
 Thr Asp Thr Ile Gly Ala Met Val Asp Asp Ala Arg Asp Phe Gly Val
 330 335 340

acc cca gcc cta gag cca atc tct tac cgc agc gtg cat tcc att ccg 1171
 Thr Pro Ala Leu Glu Pro Ile Ser Tyr Arg Ser Val His Ser Ile Pro
 345 350 355

cag gca gca gca atc gcc aga gac tcc ggc gga aaa gtc gtg gcg gac 1219
 Gln Ala Ala Ala Ile Ala Arg Asp Ser Gly Gly Lys Val Val Ala Asp
 360 365 370

acc ttg cac atg gcc agg ttc gga gcc 1246
 Thr Leu His Met Ala Arg Phe Gly Ala
 375 380

<210> 340

<211> 382

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 340

Met Gly Gln Cys Thr Val Ala Leu Tyr Arg Glu His Ser Tyr Tyr Thr
 1 5 10 15

Ala Thr Pro Trp Arg Gly Thr Trp Ala Ala Asp Gly Gly Gly Val Leu
 20 25 30

Met Thr Gln Ala Ile His Tyr Ile Asp Leu Leu Tyr Trp Leu Leu Gly
 35 40 45

Glu Pro Val Glu Val Phe Gly Tyr Thr Asn Ser Phe Lys His Gly Asp
 50 55 60

Asn Ile Glu Val Glu Asp Ser Ala Val Ala Thr Val Arg Phe Glu Ser
 65 70 75 80

Gly Ala Leu Ala Thr Ile Ser Ala Thr Thr Ala Ala Glu Pro Ala Leu
 85 90 95
 Gly Ala Gln Val Gln Val Met Gly Thr Lys Gly Ala Thr Met Thr Ile
 100 105 110
 Leu Glu Phe Pro Glu Gly Thr Asp Gly Arg Leu Ile Val Arg Ser Glu
 115 120 125
 Asn Asp Thr Arg Arg Asn His Pro Ile Pro Pro Arg Gly Ser Leu Ser
 130 135 140
 Gln Cys Arg Ser Phe His His Gln Arg Cys Phe Asp Pro Val Ser His
 145 150 155 160
 Arg Pro Asp Arg Arg Leu Tyr Arg Cys Ala Gln Arg Arg Pro Pro Thr
 165 170 175
 Thr Asp His Arg Pro Arg Cys His Gln Ser Ser Glu Ser Ser Pro Trp
 180 185 190
 Cys Leu Arg Ile Ser Ser His Pro Pro Ala Gly Leu Phe Asp Leu Thr
 195 200 205
 Glu Ala Phe Lys Thr Ser Arg Gln Ile Gly Leu Ala Pro Leu Ser Ser
 210 215 220
 Leu Ser Thr Pro Pro Asp Gln Leu Val Arg Leu Ala Ala Ala Thr Gly
 225 230 235 240
 Phe Ser Phe Val Gly Leu Arg Val Ile Ala Val Thr Pro Asn Glu Arg
 245 250 255
 Val Tyr Asp Leu Ser Pro Gly Ser Pro Leu Leu Ala Ala Thr Gln Gln
 260 265 270
 Ala Leu Lys Glu Thr Ala Leu Tyr Val Leu Asp Thr Glu Phe Leu Gln
 275 280 285
 Val Asn Ala Asp Thr Thr Arg Glu Ala Trp Leu Pro Ala Leu Glu Ala
 290 295 300
 Ala Gly Ala Leu Gly Ala Lys Thr Phe Thr Ile Ala Ala Gly Asp Asp
 305 310 315 320
 Asn Ile Ala Pro Leu Thr Asp Thr Ile Gly Ala Met Val Asp Asp Ala
 325 330 335
 Arg Asp Phe Gly Val Thr Pro Ala Leu Glu Pro Ile Ser Tyr Arg Ser
 340 345 350
 Val His Ser Ile Pro Gln Ala Ala Ala Ile Ala Arg Asp Ser Gly Gly
 355 360 365
 Lys Val Val Ala Asp Thr Leu His Met Ala Arg Phe Gly Ala
 370 375 380

<210> 341

<211> 412

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(412)

<223> FRXA00309

<400> 341

agcgcatgat cgatgcctgc gagtccgcag ggggtccaact tggcgtgctc ttccagcgcc 60

gcttctggcc cgcggtctcaa aaaatgaaaa aggagccgctc atg ggc caa tgc acg 115
 Met Gly Gln Cys Thr
 1 5

gta gcg ctt tac cga gag cat tcc tat tac aca gca acc cca tgg cga 163
 Val Ala Leu Tyr Arg Glu His Ser Tyr Tyr Thr Ala Thr Pro Trp Arg
 10 15 20

gga acc tgg gca gcc gat ggc ggt gga gtg ctc atg act caa gcc atc 211
 Gly Thr Trp Ala Ala Asp Gly Gly Gly Val Leu Met Thr Gln Ala Ile
 25 30 35

cac tac atc gat ctt ttg tac tgg ctg ttg ggc gaa ccc gtg gaa gtt 259
 His Tyr Ile Asp Leu Leu Tyr Trp Leu Leu Gly Glu Pro Val Glu Val
 40 45 50

ttc ggc tac acc aac tcc ttc aaa cac ggc gac aac atc gaa gtc gaa 307
 Phe Gly Tyr Thr Asn Ser Phe Lys His Gly Asp Asn Ile Glu Val Glu
 55 60 65

gac agc gcc gtt gcc act gtg cgt ttt gaa tcg ggc gcg ttg gcc aca 355
 Asp Ser Ala Val Ala Thr Val Arg Phe Glu Ser Gly Ala Leu Ala Thr
 70 75 80 85

att tca gcc acc acc gcc gca gag cca gca ctc ggc gca caa gtg cag 403
 Ile Ser Ala Thr Thr Ala Ala Glu Pro Ala Leu Gly Ala Gln Val Gln
 90 95 100

gtg atg gga 412
 Val Met Gly

<210> 342

<211> 104

<212> PRT

<213> Corynebacterium glutamicum

<400> 342

Met Gly Gln Cys Thr Val Ala Leu Tyr Arg Glu His Ser Tyr Tyr Thr
 1 5 10 15

Ala Thr Pro Trp Arg Gly Thr Trp Ala Ala Asp Gly Gly Gly Val Leu
 20 25 30

Met Thr Gln Ala Ile His Tyr Ile Asp Leu Leu Tyr Trp Leu Leu Gly
 35 40 45

Glu Pro Val Glu Val Phe Gly Tyr Thr Asn Ser Phe Lys His Gly Asp
 50 55 60

Asn Ile Glu Val Glu Asp Ser Ala Val Ala Thr Val Arg Phe Glu Ser
 65 70 75 80

Gly Ala Leu Ala Thr Ile Ser Ala Thr Thr Ala Ala Glu Pro Ala Leu
 85 90 95

Gly Ala Gln Val Gln Val Met Gly
 100

<210> 343

<211> 558

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(535)

<223> RXN00310

<400> 343

ttgcgggatt catcatcggc gcaatcgcac tgtctgccgc agttattttg accaccaagg 60

aaaccgcctt caccaagctt gaagatctag ggaagaaata atg tct gac aag atc 115
 Met Ser Asp Lys Ile
 1 5

tgg aaa gtc ggc atc atc ggt tgc ggt gca atc agc cga aac cat atc 163
 Trp Lys Val Gly Ile Ile Gly Cys Gly Ala Ile Ser Arg Asn His Ile
 10 15 20

gaa gca gtt cag gca atc ccc ggc gca gaa gtc agc gca gtc tgt gat 211
 Glu Ala Val Gln Ala Ile Pro Gly Ala Glu Val Ser Ala Val Cys Asp
 25 30 35

gtg gat ggt gcg aaa gca tcg gaa acc gca gcg aaa tat gga att tct 259
 Val Asp Gly Ala Lys Ala Ser Glu Thr Ala Ala Lys Tyr Gly Ile Ser
 40 45 50

ccc agt ttc acg tct gtc gat gag atc ctc gcc tcc ggg gtg gac att 307
 Pro Ser Phe Thr Ser Val Asp Glu Ile Leu Ala Ser Gly Val Asp Ile
 55 60 65

gtc gca gtc tgc acc cca cat cca acc cac gaa aca gtg gtc ctc gcc 355
 Val Ala Val Cys Thr Pro His Pro Thr His Glu Thr Val Val Leu Ala
 70 75 80 85

gct gct gcc gcc gga gtg cac gtg ctt tgt gag aag cca atc gcc atc 403
 Ala Ala Ala Ala Gly Val His Val Leu Cys Glu Lys Pro Ile Ala Ile
 90 95 100

gaa ctc gat tcc gca cag cgc atg atc gat gcc tgc gag tcc gca ggg 451
 Glu Leu Asp Ser Ala Gln Arg Met Ile Asp Ala Cys Glu Ser Ala Gly
 105 110 115

gtc caa ctt ggc gtg ctc ttc cag cgc cgc ttc tgg ccc gcg gct caa 499
 Val Gln Leu Gly Val Leu Phe Gln Arg Arg Phe Trp Pro Ala Ala Gln
 120 125 130

aaa atg aaa aag gag ccg tca tgg gcc aat gca cgg tagcgcttta 545

Lys Met Lys Lys Glu Pro Ser Trp Ala Asn Ala Arg
 135 140 145

ccgagagcat tcc

558

<210> 344

<211> 145

<212> PRT

<213> Corynebacterium glutamicum

<400> 344

Met Ser Asp Lys Ile Trp Lys Val Gly Ile Ile Gly Cys Gly Ala Ile
 1 5 10 15

Ser Arg Asn His Ile Glu Ala Val Gln Ala Ile Pro Gly Ala Glu Val
 20 25 30

Ser Ala Val Cys Asp Val Asp Gly Ala Lys Ala Ser Glu Thr Ala Ala
 35 40 45

Lys Tyr Gly Ile Ser Pro Ser Phe Thr Ser Val Asp Glu Ile Leu Ala
 50 55 60

Ser Gly Val Asp Ile Val Ala Val Cys Thr Pro His Pro Thr His Glu
 65 70 75 80

Thr Val Val Leu Ala Ala Ala Ala Gly Val His Val Leu Cys Glu
 85 90 95

Lys Pro Ile Ala Ile Glu Leu Asp Ser Ala Gln Arg Met Ile Asp Ala
 100 105 110

Cys Glu Ser Ala Gly Val Gln Leu Gly Val Leu Phe Gln Arg Arg Phe
 115 120 125

Trp Pro Ala Ala Gln Lys Met Lys Lys Glu Pro Ser Trp Ala Asn Ala
 130 135 140

Arg
 145

<210> 345

<211> 558

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(535)

<223> FRXA00310

<400> 345

ttgcgggatt catcatcggc gcaatcgac tgtctgccgc agttattttg accaccaagg 60

aaaccgcctt caccaagctt gaagatctag ggaagaaata atg tct gac aag atc 115
 Met Ser Asp Lys Ile
 1 5

tgg aaa gtc ggc atc atc ggt tgc ggt gca atc agc cga aac cat atc 163

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Trp Lys Val Gly Ile Ile Gly Cys Gly Ala Ile Ser Arg Asn His Ile
      10              15              20

gaa gca gtt cag gca atc ccc ggc gca gaa gtc agc gca gtc tgt gat 211
Glu Ala Val Gln Ala Ile Pro Gly Ala Glu Val Ser Ala Val Cys Asp
      25              30              35

gtg gat ggt gcg aaa gca tcg gaa acc gca gcg aaa tat gga att tct 259
Val Asp Gly Ala Lys Ala Ser Glu Thr Ala Ala Lys Tyr Gly Ile Ser
      40              45              50

ccc agt ttc acg tct gtc gat gag atc ctc gcc tcc ggg gtg gac att 307
Pro Ser Phe Thr Ser Val Asp Glu Ile Leu Ala Ser Gly Val Asp Ile
      55              60              65

gtc gca gtc tgc acc cca cat cca acc cac gaa aca gtg gtc ctc gcc 355
Val Ala Val Cys Thr Pro His Pro Thr His Glu Thr Val Val Leu Ala
      70              75              80              85

gct gct gcc gcc gga gtg cac gtg ctt tgt gag aag cca atc gcc atc 403
Ala Ala Ala Ala Gly Val His Val Leu Cys Glu Lys Pro Ile Ala Ile
      90              95              100

gaa ctc gat tcc gca cag cgc atg atc gat gcc tgc gag tcc gca ggg 451
Glu Leu Asp Ser Ala Gln Arg Met Ile Asp Ala Cys Glu Ser Ala Gly
      105              110              115

gtc caa ctt ggc gtg ctc ttc cag cgc cgc ttc tgg ccc gcg gct caa 499
Val Gln Leu Gly Val Leu Phe Gln Arg Arg Phe Trp Pro Ala Ala Gln
      120              125              130

aaa atg aaa aag gag ccg tca tgg gcc aat gca cgg tagcgcttta 545
Lys Met Lys Lys Glu Pro Ser Trp Ala Asn Ala Arg
      135              140              145

ccgagagcat tcc 558

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<210> 346

<211> 145

<212> PRT

<213> Corynebacterium glutamicum

<400> 346

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Met Ser Asp Lys Ile Trp Lys Val Gly Ile Ile Gly Cys Gly Ala Ile
  1              5              10              15

Ser Arg Asn His Ile Glu Ala Val Gln Ala Ile Pro Gly Ala Glu Val
      20              25              30

Ser Ala Val Cys Asp Val Asp Gly Ala Lys Ala Ser Glu Thr Ala Ala
      35              40              45

Lys Tyr Gly Ile Ser Pro Ser Phe Thr Ser Val Asp Glu Ile Leu Ala
      50              55              60

Ser Gly Val Asp Ile Val Ala Val Cys Thr Pro His Pro Thr His Glu
      65              70              75              80

Thr Val Val Leu Ala Ala Ala Ala Ala Gly Val His Val Leu Cys Glu
      85              90              95

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[illegible]

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<210> 347
<211> 1342
<212> DNA
<213> Corynebacterium glutamicum
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<220>  
<221> CDS  
<222> (101)..(1342)  
<223> RXA00041
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<400> 347																
atgaagcagc	agcatccaag	ctggaaaacg	ctgatcacta	ccgtctcatg	gagcaattaa	60										
agctgcgcta	gaaacaaaaa	ggaaagtagt	gtgtggggct	atg	cac	aca	gaa	ctt	115							
				Met	His	Thr	Glu	Leu								
				1				5								
tcc agt	ttg	cgc	cct	gcg	tac	cat	gtg	act	cct	ccg	cag	ggc	agg	ctc	163	
Ser	Ser	Leu	Arg	Pro	Ala	Tyr	His	Val	Thr	Pro	Pro	Gln	Gly	Arg	Leu	
			10					15						20		
aat gat	ccc	aac	gga	atg	tac	gtc	gat	ggc	gat	acc	ctc	cac	gtc	tac	211	
Asn	Asp	Pro	Asn	Gly	Met	Tyr	Val	Asp	Gly	Asp	Thr	Leu	His	Val	Tyr	
			25					30					35			
tac cag	cac	gat	cca	ggg	ttc	ccc	ttc	gca	cca	aag	cgc	acc	ggc	tgg	259	
Tyr	Gln	His	Asp	Pro	Gly	Phe	Pro	Phe	Ala	Pro	Lys	Arg	Thr	Gly	Trp	
			40				45					50				
gct cac	acc	acc	acg	ccg	ttg	acc	gga	ccg	cag	cga	ttg	cag	tgg	acg	307	
Ala	His	Thr	Thr	Thr	Pro	Leu	Thr	Gly	Pro	Gln	Arg	Leu	Gln	Trp	Thr	
	55					60				65						
cac ctg	ccc	gac	gct	ctt	tac	ccg	gat	gca	tcc	tat	gac	ctg	gat	gga	355	
His	Leu	Pro	Asp	Ala	Leu	Tyr	Pro	Asp	Ala	Ser	Tyr	Asp	Leu	Asp	Gly	
	70				75				80					85		
tgc tat	tcc	ggg	gga	gcc	gta	ttt	act	gac	ggc	aca	ctt	aaa	ctt	ttc	403	
Cys	Tyr	Ser	Gly	Gly	Ala	Val	Phe	Thr	Asp	Gly	Thr	Leu	Lys	Leu	Phe	
			90						95				100			
tac acc	ggc	aac	cta	aaa	att	gac	ggc	aag	cgc	cgc	gcc	acc	caa	aac	451	
Tyr	Thr	Gly	Asn	Leu	Lys	Ile	Asp	Gly	Lys	Arg	Arg	Ala	Thr	Gln	Asn	
			105					110				115				
ctc gtc	gaa	gtc	gag	gac	cca	act	ggg	ctg	atg	ggc	ggc	att	cat	cgc	499	
Leu	Val	Glu	Val	Glu	Asp	Pro	Thr	Gly	Leu	Met	Gly	Gly	Ile	His	Arg	

120	125	130	
cgt tcg cct aaa aat ccg ctt atc gac gga ccc gcc agc ggt ttc aca			547
Arg Ser Pro Lys Asn Pro Leu Ile Asp Gly Pro Ala Ser Gly Phe Thr			
135	140	145	
ccc cat tac cgc gat ccc atg atc agc cct gat ggt gat ggt tgg aaa			595
Pro His Tyr Arg Asp Pro Met Ile Ser Pro Asp Gly Asp Gly Trp Lys			
150	155	160	165
atg gtt ctt ggg gcc caa cgc gaa aac ctc acc ggt gca gcg gtt cta			643
Met Val Leu Gly Ala Gln Arg Glu Asn Leu Thr Gly Ala Ala Val Leu			
	170	175	180
tac cgc tcg aca gat ctt gaa aac tgg gaa ttc tcc ggt gaa atc acc			691
Tyr Arg Ser Thr Asp Leu Glu Asn Trp Glu Phe Ser Gly Glu Ile Thr			
	185	190	195
ttt gac ctc agt gat gca caa cct ggt tct gct cct gat ctc gtt ccc			739
Phe Asp Leu Ser Asp Ala Gln Pro Gly Ser Ala Pro Asp Leu Val Pro			
	200	205	210
ggt ggc tac atg tgg gaa tgc ccc aac ctt ttt acg ctt cgc gat gaa			787
Gly Gly Tyr Met Trp Glu Cys Pro Asn Leu Phe Thr Leu Arg Asp Glu			
	215	220	225
gaa act ggc gaa gat ctc gac gtg ctg att ttc tgt cca caa gga ttg			835
Glu Thr Gly Glu Asp Leu Asp Val Leu Ile Phe Cys Pro Gln Gly Leu			
	230	235	240
gac cga atc cac gat gag gtt act cac tac gca agc tct gac cag tgc			883
Asp Arg Ile His Asp Glu Val Thr His Tyr Ala Ser Ser Asp Gln Cys			
	250	255	260
gga tat gtc gtc ggc aag ctt gaa gga acg acc ttc cgc gtc ttg cga			931
Gly Tyr Val Val Gly Lys Leu Glu Gly Thr Thr Phe Arg Val Leu Arg			
	265	270	275
gga ttc agc gag ctg gat ttc ggc cat gaa ttc tac gca ccg cag gtt			979
Gly Phe Ser Glu Leu Asp Phe Gly His Glu Phe Tyr Ala Pro Gln Val			
	280	285	290
gca gta aac ggt tct gat gcc tgg ctc gtg ggc tgg atg ggg ctg ccc			1027
Ala Val Asn Gly Ser Asp Ala Trp Leu Val Gly Trp Met Gly Leu Pro			
	295	300	305
gcg cag gat gat cac cca aca gtt gca cgg gaa gga tgg gtg cac tgc			1075
Ala Gln Asp Asp His Pro Thr Val Ala Arg Glu Gly Trp Val His Cys			
	310	315	320
ctg act gtg ccc cgc aag ctt cat ttg cgc aac cac gcg atc tat caa			1123
Leu Thr Val Pro Arg Lys Leu His Leu Arg Asn His Ala Ile Tyr Gln			
	330	335	340
gag ctt ctt ctc cca gag ggg gag tca ggg gta atc aga tct gta tta			1171
Glu Leu Leu Leu Pro Glu Gly Glu Ser Gly Val Ile Arg Ser Val Leu			
	345	350	355
ggt tct gaa cct gtc cga gta gac atc cga ggc aat att tcc ctc gag			1219
Gly Ser Glu Pro Val Arg Val Asp Ile Arg Gly Asn Ile Ser Leu Glu			
	360	365	370

tgg gat ggt gtc cgt ttg tct gtg gat cgt ggt ggt gat cgt cgc gta 1267
 Trp Asp Gly Val Arg Leu Ser Val Asp Arg Gly Gly Asp Arg Arg Val
 375 380 385

 gct gag gta aaa cct ggc gaa tta gtg atc gcg gac gat aat aca gcc 1315
 Ala Glu Val Lys Pro Gly Glu Leu Val Ile Ala Asp Asp Asn Thr Ala
 390 395 400 405

 att gag ata act gca ggt gat gga cag 1342
 Ile Glu Ile Thr Ala Gly Asp Gly Gln
 410

<210> 348

<211> 414

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 348

Met His Thr Glu Leu Ser Ser Leu Arg Pro Ala Tyr His Val Thr Pro
 1 5 10 15

 Pro Gln Gly Arg Leu Asn Asp Pro Asn Gly Met Tyr Val Asp Gly Asp
 20 25 30

 Thr Leu His Val Tyr Tyr Gln His Asp Pro Gly Phe Pro Phe Ala Pro
 35 40 45

 Lys Arg Thr Gly Trp Ala His Thr Thr Thr Pro Leu Thr Gly Pro Gln
 50 55 60

 Arg Leu Gln Trp Thr His Leu Pro Asp Ala Leu Tyr Pro Asp Ala Ser
 65 70 75 80

 Tyr Asp Leu Asp Gly Cys Tyr Ser Gly Gly Ala Val Phe Thr Asp Gly
 85 90 95

 Thr Leu Lys Leu Phe Tyr Thr Gly Asn Leu Lys Ile Asp Gly Lys Arg
 100 105 110

 Arg Ala Thr Gln Asn Leu Val Glu Val Glu Asp Pro Thr Gly Leu Met
 115 120 125

 Gly Gly Ile His Arg Arg Ser Pro Lys Asn Pro Leu Ile Asp Gly Pro
 130 135 140

 Ala Ser Gly Phe Thr Pro His Tyr Arg Asp Pro Met Ile Ser Pro Asp
 145 150 155 160

 Gly Asp Gly Trp Lys Met Val Leu Gly Ala Gln Arg Glu Asn Leu Thr
 165 170 175

 Gly Ala Ala Val Leu Tyr Arg Ser Thr Asp Leu Glu Asn Trp Glu Phe
 180 185 190

 Ser Gly Glu Ile Thr Phe Asp Leu Ser Asp Ala Gln Pro Gly Ser Ala
 195 200 205

 Pro Asp Leu Val Pro Gly Gly Tyr Met Trp Glu Cys Pro Asn Leu Phe
 210 215 220

Thr Leu Arg Asp Glu Glu Thr Gly Glu Asp Leu Asp Val Leu Ile Phe
 225 230 235 240
 Cys Pro Gln Gly Leu Asp Arg Ile His Asp Glu Val Thr His Tyr Ala
 245 250 255
 Ser Ser Asp Gln Cys Gly Tyr Val Val Gly Lys Leu Glu Gly Thr Thr
 260 265 270
 Phe Arg Val Leu Arg Gly Phe Ser Glu Leu Asp Phe Gly His Glu Phe
 275 280 285
 Tyr Ala Pro Gln Val Ala Val Asn Gly Ser Asp Ala Trp Leu Val Gly
 290 295 300
 Trp Met Gly Leu Pro Ala Gln Asp Asp His Pro Thr Val Ala Arg Glu
 305 310 315 320
 Gly Trp Val His Cys Leu Thr Val Pro Arg Lys Leu His Leu Arg Asn
 325 330 335
 His Ala Ile Tyr Gln Glu Leu Leu Leu Pro Glu Gly Glu Ser Gly Val
 340 345 350
 Ile Arg Ser Val Leu Gly Ser Glu Pro Val Arg Val Asp Ile Arg Gly
 355 360 365
 Asn Ile Ser Leu Glu Trp Asp Gly Val Arg Leu Ser Val Asp Arg Gly
 370 375 380
 Gly Asp Arg Arg Val Ala Glu Val Lys Pro Gly Glu Leu Val Ile Ala
 385 390 395 400
 Asp Asp Asn Thr Ala Ile Glu Ile Thr Ala Gly Asp Gly Gln
 405 410

<210> 349

<211> 720

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (1)..(720)

<223> RXA02026

<400> 349

cca ttt cat ata caa cca gaa aca ggt tta tta aat gat ccc aac gga 48
 Pro Phe His Ile Gln Pro Glu Thr Gly Leu Leu Asn Asp Pro Asn Gly
 1 5 10 15
 ctt att ttt tat aaa ggg aag tat tat gtt tca cat caa tgg ttc cca 96
 Leu Ile Phe Tyr Lys Gly Lys Tyr Tyr Val Ser His Gln Trp Phe Pro
 20 25 30
 tta ggc gca gta cat ggc tta aag tat tgg tat aac tac acg agt gat 144
 Leu Gly Ala Val His Gly Leu Lys Tyr Trp Tyr Asn Tyr Thr Ser Asp
 35 40 45

gac tta ata aac ttt aaa cct gaa ggg cca ata tta aat cca gat act 192
 Asp Leu Ile Asn Phe Lys Pro Glu Gly Pro Ile Leu Asn Pro Asp Thr
 50 55 60

aaa tat gac agc cat ggt gtt tat agc ggt agc gct ttt gaa tat aac 240
 Lys Tyr Asp Ser His Gly Val Tyr Ser Gly Ser Ala Phe Glu Tyr Asn
 65 70 75 80

ggg cat tta tat tat atg tac aca gga aat cat cga gat aat cat tgg 288
 Gly His Leu Tyr Tyr Met Tyr Thr Gly Asn His Arg Asp Asn His Trp
 85 90 95

caa cga cat gcg agt cag atg atc gca cga ttg aaa gaa gac ggt tca 336
 Gln Arg His Ala Ser Gln Met Ile Ala Arg Leu Lys Glu Asp Gly Ser
 100 105 110

gtt gaa aag ttt cca aag cca gta att agc cag caa cca gaa gga tat 384
 Val Glu Lys Phe Pro Lys Pro Val Ile Ser Gln Gln Pro Glu Gly Tyr
 115 120 125

aca agt cat ttt aga gat cct aaa gtt ttt aaa tat ggt gag aaa tat 432
 Thr Ser His Phe Arg Asp Pro Lys Val Phe Lys Tyr Gly Glu Lys Tyr
 130 135 140

tat gca atc att ggc gca caa aat aat gat cag caa ggt cga tta tta 480
 Tyr Ala Ile Ile Gly Ala Gln Asn Asn Asp Gln Gln Gly Arg Leu Leu
 145 150 155 160

ctt tat aat act gaa gat ata att aat tgg cat tat tta ggt gaa ata 528
 Leu Tyr Asn Thr Glu Asp Ile Ile Asn Trp His Tyr Leu Gly Glu Ile
 165 170 175

aat aca gag tta gat gat ttt gga tat atg tgg gaa tgc cca gat tac 576
 Asn Thr Glu Leu Asp Asp Phe Gly Tyr Met Trp Glu Cys Pro Asp Tyr
 180 185 190

ttt aat tta gat aat caa gat gtc ata ctt att tgt cca caa ggt att 624
 Phe Asn Leu Asp Asn Gln Asp Val Ile Leu Ile Cys Pro Gln Gly Ile
 195 200 205

gaa cca aaa ggc aat cag ttc aaa aat att tat caa agt ggt tat ata 672
 Glu Pro Lys Gly Asn Gln Phe Lys Asn Ile Tyr Gln Ser Gly Tyr Ile
 210 215 220

ctt gga aag ttt gat att gaa aag tta aca tat gaa cat gaa aat ttt 720
 Leu Gly Lys Phe Asp Ile Glu Lys Leu Thr Tyr Glu His Glu Asn Phe
 225 230 235 240

<210> 350

<211> 240

<212> PRT

<213> Corynebacterium glutamicum

<400> 350

Pro Phe His Ile Gln Pro Glu Thr Gly Leu Leu Asn Asp Pro Asn Gly
 1 5 10 15

Leu Ile Phe Tyr Lys Gly Lys Tyr Tyr Val Ser His Gln Trp Phe Pro
 20 25 30

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<210> 351
<211> 1617
<212> DNA
<213> Corynebacterium glutamicum
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<220>  
<221> CDS  
<222> (101)..(1594)  
<223> RXA02061
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<400> 351
taacctgcct tcacctggga ttatccaccc atgtgtgatg aaatcgetac cctgaatcaa 60

agacactggc gtaattgagt gaaggcagga caataaagag atg acg aac gtt tcc 115
Met Thr Asn Val Ser
1 5

492

Gly Tyr His Arg	Pro Glu Leu His Ile Thr Ala Glu Ser Gly Val Leu	
	10 15 20	
ttt gca cct gca ggc gtt ctg ttg gat gac gac acg tgg cat ttc ttc	211	
Phe Ala Pro Ala Gly Val Leu Leu Asp Asp Thr Trp His Phe Phe		
	25 30 35	
cac cag tac cgt ccc tca cca gat cac ggc ccc agg tgg gcg cac caa	259	
His Gln Tyr Arg Pro Ser Pro Asp His Gly Pro Arg Trp Ala His Gln		
	40 45 50	
ttc gca gag cgc act cca ttt gtg tgg gat atc tgc gat gac gtg cta	307	
Phe Ala Glu Arg Thr Pro Phe Val Trp Asp Ile Cys Asp Asp Val Leu		
	55 60 65	
gcc cct gaa ggc gat gaa acc cag gtt cgc gct ggc tca gtg gtg tcc	355	
Ala Pro Glu Gly Asp Glu Thr Gln Val Arg Ala Gly Ser Val Val Ser		
	70 75 80 85	
aac aac ggt ggc gtt gat ctg tac ttc acc tcg gtt gtt ggc ccc act	403	
Asn Asn Gly Gly Val Asp Leu Tyr Phe Thr Ser Val Val Gly Pro Thr		
	90 95 100	
tcc act atc cag ttg gca cac atc aac aac atc cgt ggc acc acc gaa	451	
Ser Thr Ile Gln Leu Ala His Ile Asn Asn Ile Arg Gly Thr Thr Glu		
	105 110 115	
ctg atc aat gag gac gag ctg ggg ctc gat cca gat gtc tcc cga atc	499	
Leu Ile Asn Glu Asp Glu Leu Gly Leu Asp Pro Asp Val Ser Arg Ile		
	120 125 130	
ggc gaa gtg gtt ggc aac act gat ggt tat gta aag ttc cgc tca ccg	547	
Gly Glu Val Val Gly Asn Thr Asp Gly Tyr Val Lys Phe Arg Ser Pro		
	135 140 145	
tgc gtt atc cca ggt tgg gaa gac caa gga aac cgc gat gaa ggc cac	595	
Cys Val Ile Pro Gly Trp Glu Asp Gln Gly Asn Arg Asp Glu Gly His		
	150 155 160 165	
tca gga tgg ttg atg ctc gca gtt act ggc cca gtt gaa gcc cca aca	643	
Ser Gly Trp Leu Met Leu Ala Val Thr Gly Pro Val Glu Ala Pro Thr		
	170 175 180	
gta gtg gtc ctc gac tcg cca gat gga aga gaa tgg tcc att aca ggt	691	
Val Val Val Leu Asp Ser Pro Asp Gly Arg Glu Trp Ser Ile Thr Gly		
	185 190 195	
ccc ctg tct ctc aac ggc ctc tct gga tta gag tca gac gaa gtt cta	739	
Pro Leu Ser Leu Asn Gly Leu Ser Gly Leu Glu Ser Asp Glu Val Leu		
	200 205 210	
gtt gct cct cgc atg att cgt ctg cgc gat gaa gtg gat cat gaa atc	787	
Val Ala Pro Arg Met Ile Arg Leu Arg Asp Glu Val Asp His Glu Ile		
	215 220 225	
tac gat gtc ctc att gtc acc att gaa caa gac ggg att gac att tcg	835	
Tyr Asp Val Leu Ile Val Thr Ile Glu Gln Asp Gly Ile Asp Ile Ser		
	230 235 240 245	
gga tac ctg gta ggc cag ctc aac ggc tca gaa ttc gat gtg aag act	883	
Gly Tyr Leu Val Gly Gln Leu Asn Gly Ser Glu Phe Asp Val Lys Thr		

250						255						260						
cca	ttt	acc	cgc	atc	gat	ttt	ggc	cat	gat	ttc	tct	cgc	ccc	cgc	aac	931		
Pro	Phe	Thr	Arg	Ile	Asp	Phe	Gly	His	Asp	Phe	Ser	Arg	Pro	Arg	Asn			
265						270						275						
acc	aac	tac	gcc	gaa	acc	acc	atc	ggc	tac	gac	ttc	gcc	cac	atc	ttt	979		
Thr	Asn	Tyr	Ala	Glu	Thr	Thr	Ile	Gly	Tyr	Asp	Phe	Ala	His	Ile	Phe			
280						285						290						
ggt	ctc	atg	aat	ggc	gta	ggt	cgt	ttg	gac	tcc	ccc	act	gag	cat	ctc	1027		
Gly	Leu	Met	Asn	Gly	Val	Gly	Arg	Leu	Asp	Ser	Pro	Thr	Glu	His	Leu			
295						300						305						
agt	tgg	aag	gaa	gaa	ggc	tgg	gca	aac	gct	att	tct	ttc	cca	cgt	att	1075		
Ser	Trp	Lys	Glu	Glu	Gly	Trp	Ala	Asn	Ala	Ile	Ser	Phe	Pro	Arg	Ile			
310						315						320						325
gtc	acg	ctc	cag	gac	ggt	acg	gtc	ttc	cag	acc	cct	cca	gaa	gga	ttg	1123		
Val	Thr	Leu	Gln	Asp	Gly	Thr	Val	Phe	Gln	Thr	Pro	Pro	Glu	Gly	Leu			
330						335						340						
ctt	gat	gcc	att	cat	gaa	tcc	gag	gca	gcg	gca	ggt	tgg	acc	gga	ctg	1171		
Leu	Asp	Ala	Ile	His	Glu	Ser	Glu	Ala	Ala	Ala	Gly	Trp	Thr	Gly	Leu			
345						350						355						
tgc	gaa	atc	cca	tca	aac	agc	gca	gtt	gaa	gtg	gcg	ttg	aag	gac	caa	1219		
Cys	Glu	Ile	Pro	Ser	Asn	Ser	Ala	Val	Glu	Val	Ala	Leu	Lys	Asp	Gln			
360						365						370						
gaa	ggt	gaa	atc	gct	gca	aca	atc	act	cac	cgc	cac	aat	cag	cta	gtc	1267		
Glu	Gly	Glu	Ile	Ala	Ala	Thr	Ile	Thr	His	Arg	His	Asn	Gln	Leu	Val			
375						380						385						
gtt	gat	cgg	tcc	atg	aac	ccc	aac	cac	gcg	ggt	gat	cca	cac	gcg	att	1315		
Val	Asp	Arg	Ser	Met	Asn	Pro	Asn	His	Ala	Gly	Asp	Pro	His	Ala	Ile			
390						395						400						405
gca	cca	ttg	act	gat	gat	gaa	aca	gat	tca	ctg	ttc	att	gtc	gtt	gac	1363		
Ala	Pro	Leu	Thr	Asp	Asp	Glu	Thr	Asp	Ser	Leu	Phe	Ile	Val	Val	Asp			
410						415						420						
ggc	tct	aca	gta	gaa	gtt	ttt	gct	gat	ggc	ggt	tat	gta	tca	atg	gca	1411		
Gly	Ser	Thr	Val	Glu	Val	Phe	Ala	Asp	Gly	Gly	Tyr	Val	Ser	Met	Ala			
425						430						435						
agc	cgt	gtg	tat	ttc	aac	aac	gga	cca	ttc	agc	gaa	ttt	gag	gtc	acc	1459		
Ser	Arg	Val	Tyr	Phe	Asn	Asn	Gly	Pro	Phe	Ser	Glu	Phe	Glu	Val	Thr			
440						445						450						
acc	acc	ggt	gac	gca	agc	att	att	cgc	cag	gaa	agt	cac	ttc	cct	gtt	1507		
Thr	Thr	Gly	Asp	Ala	Ser	Ile	Ile	Arg	Gln	Glu	Ser	His	Phe	Pro	Val			
455						460						465						
gat	ttc	agt	tcg	gtg	tcc	cta	gat	ata	gat	gat	ctc	act	gcg	ctc	atg	1555		
Asp	Phe	Ser	Ser	Val	Ser	Leu	Asp	Ile	Asp	Asp	Leu	Thr	Ala	Leu	Met			
470						475						480						485
cag	ttc	gat	gaa															

atgcgttcca gcc

1617

<210> 352

<211> 498

<212> PRT

<213> Corynebacterium glutamicum

<400> 352

Met Thr Asn Val Ser Gly Tyr His Arg Pro Glu Leu His Ile Thr Ala
 1 5 10 15

Glu Ser Gly Val Leu Phe Ala Pro Ala Gly Val Leu Leu Asp Asp Asp
 20 25 30

Thr Trp His Phe Phe His Gln Tyr Arg Pro Ser Pro Asp His Gly Pro
 35 40 45

Arg Trp Ala His Gln Phe Ala Glu Arg Thr Pro Phe Val Trp Asp Ile
 50 55 60

Cys Asp Asp Val Leu Ala Pro Glu Gly Asp Glu Thr Gln Val Arg Ala
 65 70 75 80

Gly Ser Val Val Ser Asn Asn Gly Gly Val Asp Leu Tyr Phe Thr Ser
 85 90 95

Val Val Gly Pro Thr Ser Thr Ile Gln Leu Ala His Ile Asn Asn Ile
 100 105 110

Arg Gly Thr Thr Glu Leu Ile Asn Glu Asp Glu Leu Gly Leu Asp Pro
 115 120 125

Asp Val Ser Arg Ile Gly Glu Val Val Gly Asn Thr Asp Gly Tyr Val
 130 135 140

Lys Phe Arg Ser Pro Cys Val Ile Pro Gly Trp Glu Asp Gln Gly Asn
 145 150 155 160

Arg Asp Glu Gly His Ser Gly Trp Leu Met Leu Ala Val Thr Gly Pro
 165 170 175

Val Glu Ala Pro Thr Val Val Val Leu Asp Ser Pro Asp Gly Arg Glu
 180 185 190

Trp Ser Ile Thr Gly Pro Leu Ser Leu Asn Gly Leu Ser Gly Leu Glu
 195 200 205

Ser Asp Glu Val Leu Val Ala Pro Arg Met Ile Arg Leu Arg Asp Glu
 210 215 220

Val Asp His Glu Ile Tyr Asp Val Leu Ile Val Thr Ile Glu Gln Asp
 225 230 235 240

Gly Ile Asp Ile Ser Gly Tyr Leu Val Gly Gln Leu Asn Gly Ser Glu
 245 250 255

Phe Asp Val Lys Thr Pro Phe Thr Arg Ile Asp Phe Gly His Asp Phe
 260 265 270

Ser Arg Pro Arg Asn Thr Asn Tyr Ala Glu Thr Thr Ile Gly Tyr Asp
 275 280 285
 Phe Ala His Ile Phe Gly Leu Met Asn Gly Val Gly Arg Leu Asp Ser
 290 295 300
 Pro Thr Glu His Leu Ser Trp Lys Glu Glu Gly Trp Ala Asn Ala Ile
 305 310 315 320
 Ser Phe Pro Arg Ile Val Thr Leu Gln Asp Gly Thr Val Phe Gln Thr
 325 330 335
 Pro Pro Glu Gly Leu Leu Asp Ala Ile His Glu Ser Glu Ala Ala Ala
 340 345 350
 Gly Trp Thr Gly Leu Cys Glu Ile Pro Ser Asn Ser Ala Val Glu Val
 355 360 365
 Ala Leu Lys Asp Gln Glu Gly Glu Ile Ala Ala Thr Ile Thr His Arg
 370 375 380
 His Asn Gln Leu Val Val Asp Arg Ser Met Asn Pro Asn His Ala Gly
 385 390 395 400
 Asp Pro His Ala Ile Ala Pro Leu Thr Asp Asp Glu Thr Asp Ser Leu
 405 410 415
 Phe Ile Val Val Asp Gly Ser Thr Val Glu Val Phe Ala Asp Gly Gly
 420 425 430
 Tyr Val Ser Met Ala Ser Arg Val Tyr Phe Asn Asn Gly Pro Phe Ser
 435 440 445
 Glu Phe Glu Val Thr Thr Thr Gly Asp Ala Ser Ile Ile Arg Gln Glu
 450 455 460
 Ser His Phe Pro Val Asp Phe Ser Ser Val Ser Leu Asp Ile Asp Asp
 465 470 475 480
 Leu Thr Ala Leu Met Gln Phe Asp Glu Asn Glu Pro His Glu Gly Pro
 485 490 495

Val Arg

<210> 353
 <211> 1305
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(1282)
 <223> RXN01369

<400> 353
 ctgcgacgga cctagcaaag gggcgctgac acaagcactg cgtttgctgg tgcgcggaca 60
 gtcagccacg acctattcca ttgaagaaaa ggacttgtaa atg gag cta ttg gaa 115
 Met Glu Leu Leu Glu

	1	5	
ggc tca ctg cgc acc tac cca tgg ggt tca aga aca ctg atc gct gat			163
Gly Ser Leu Arg Thr Tyr Pro Trp Gly Ser Arg Thr Leu Ile Ala Asp	10	20	
ctc aaa ggc gaa gaa tca cca tcg tct cgc cca gag gcc gaa gtc tgg			211
Leu Lys Gly Glu Glu Ser Pro Ser Ser Arg Pro Glu Ala Glu Val Trp	25	35	
ttc ggt gcc cac cca gga tca cca tca acc atc ggt gga aac gca ctc			259
Phe Gly Ala His Pro Gly Ser Pro Ser Thr Ile Gly Gly Asn Ala Leu	40	50	
aac gaa gtc atc gca gcg aac ccc gaa gaa gca ttg ggc acg cgt gtt			307
Asn Glu Val Ile Ala Ala Asn Pro Glu Glu Ala Leu Gly Thr Arg Val	55	65	
gcc gaa gcg ttt gaa aat gag ctt cca ttc ctc ctc aaa atc ctc gca			355
Ala Glu Ala Phe Glu Asn Glu Leu Pro Phe Leu Leu Lys Ile Leu Ala	70	85	
gcg gga gca ccc cta tca ctg cag gcc cac cca tcg ctg gaa cag gcc			403
Ala Gly Ala Pro Leu Ser Leu Gln Ala His Pro Ser Leu Glu Gln Ala	90	100	
cgt gaa gga ttc gcc cgc gaa aac tca gca gga att gac ctc ggc gca			451
Arg Glu Gly Phe Ala Arg Glu Asn Ser Ala Gly Ile Asp Leu Gly Ala	105	115	
ccg aac cgc aac tac cgc gac cca aac cac aag cca gag ctg atc gtt			499
Pro Asn Arg Asn Tyr Arg Asp Pro Asn His Lys Pro Glu Leu Ile Val	120	130	
gct ctc acg gaa ttc atc gcg atg gca ggc ttc cgc cca ctg cgg aac			547
Ala Leu Thr Glu Phe Ile Ala Met Ala Gly Phe Arg Pro Leu Arg Asn	135	145	
acc ctc acc att ttc gac gcc ctc gcc tgc gaa ccc ctc gac cgc tac			595
Thr Leu Thr Ile Phe Asp Ala Leu Ala Cys Glu Pro Leu Asp Arg Tyr	150	165	
cgc agc atg ctc acc gtc gac aac gag gaa gaa tcc ctc cgc gca ctg			643
Arg Ser Met Leu Thr Val Asp Asn Glu Glu Glu Ser Leu Arg Ala Leu	170	180	
ttt acc acc tgg atc acc atc ccc atc ggt aaa cga cac gaa ctc atc			691
Phe Thr Thr Trp Ile Thr Ile Pro Ile Gly Lys Arg His Glu Leu Ile	185	195	
gat gcc ctc atc agc aac gcc cac acc tac ctt gag gca agc gat cgt			739
Asp Ala Leu Ile Ser Asn Ala His Thr Tyr Leu Glu Ala Ser Asp Arg	200	210	
gac gag gac atc gca ttc gtg ctc tca cac atc atc gag ctc aac gaa			787
Asp Glu Asp Ile Ala Phe Val Leu Ser His Ile Ile Glu Leu Asn Glu	215	225	
cag tac ccc ggc gat gtc ggc gtt ctg ggt gct ctg ctg ttg aac ttc			835
Gln Tyr Pro Gly Asp Val Gly Val Leu Gly Ala Leu Leu Leu Asn Phe	230	245	

tac aaa ctt gcc cca ggc gaa gcc ctc tac ctc gac gcc gca aac ctt 883
 Tyr Lys Leu Ala Pro Gly Glu Ala Leu Tyr Leu Asp Ala Ala Asn Leu
 250 255 260

 cac gca tac atc agc ggc ctc ggc gta gag atc atg gcg aac tcc gac 931
 His Ala Tyr Ile Ser Gly Leu Gly Val Glu Ile Met Ala Asn Ser Asp
 265 270 275

 aac gtg ctc cgc ggt gga ctg aca tcc aaa tac gtc gac gtc ccg gag 979
 Asn Val Leu Arg Gly Gly Leu Thr Ser Lys Tyr Val Asp Val Pro Glu
 280 285 290

 ctt gtg cgc gtg ttg gat ttc aac tct ttg gaa aac gct cgc gtg gac 1027
 Leu Val Arg Val Leu Asp Phe Asn Ser Leu Glu Asn Ala Arg Val Asp
 295 300 305

 gtt gaa gaa gac ggt gca acg acc cac tac cca gtt cca atc aac gaa 1075
 Val Glu Glu Asp Gly Ala Thr Thr His Tyr Pro Val Pro Ile Asn Glu
 310 315 320 325

 ttc caa ctc gat cgc gtt gca gtt cag ggc gaa gca gaa gcc aac cac 1123
 Phe Gln Leu Asp Arg Val Ala Val Gln Gly Glu Ala Glu Ala Asn His
 330 335 340

 gat ggt ccc atg att gtt ctg tgc acc tcc gga act gtt tcc ttg gaa 1171
 Asp Gly Pro Met Ile Val Leu Cys Thr Ser Gly Thr Val Ser Leu Glu
 345 350 355

 gca ggg gag aag acc ctc gaa gta gca gca ggt cac gcc gca tgg gtt 1219
 Ala Gly Glu Lys Thr Leu Glu Val Ala Ala Gly His Ala Ala Trp Val
 360 365 370

 cca gca aac gac cca acc att gcg atg cgt tct gag gac gca gaa gta 1267
 Pro Ala Asn Asp Pro Thr Ile Ala Met Arg Ser Glu Asp Ala Glu Val
 375 380 385

 ttc ctc gct agg gtt tagatctttt tagattaaaa tca 1305
 Phe Leu Ala Arg Val
 390

<210> 354

<211> 394

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 354

Met Glu Leu Leu Glu Gly Ser Leu Arg Thr Tyr Pro Trp Gly Ser Arg
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 Thr Leu Ile Ala Asp Leu Lys Gly Glu Glu Ser Pro Ser Ser Arg Pro
 20 25 30

 Glu Ala Glu Val Trp Phe Gly Ala His Pro Gly Ser Pro Ser Thr Ile
 35 40 45

 Gly Gly Asn Ala Leu Asn Glu Val Ile Ala Ala Asn Pro Glu Glu Ala
 50 55 60

 Leu Gly Thr Arg Val Ala Glu Ala Phe Glu Asn Glu Leu Pro Phe Leu

65		70		75		80
Leu Lys Ile Leu	Ala Ala Gly Ala Pro Leu Ser Leu Gln Ala His Pro					
	85		90			95
Ser Leu Glu Gln Ala Arg Glu Gly Phe Ala Arg Glu Asn Ser Ala Gly						
	100		105			110
Ile Asp Leu Gly Ala Pro Asn Arg Asn Tyr Arg Asp Pro Asn His Lys						
	115		120			125
Pro Glu Leu Ile Val Ala Leu Thr Glu Phe Ile Ala Met Ala Gly Phe						
	130		135			140
Arg Pro Leu Arg Asn Thr Leu Thr Ile Phe Asp Ala Leu Ala Cys Glu						
	145		150			155
Pro Leu Asp Arg Tyr Arg Ser Met Leu Thr Val Asp Asn Glu Glu Glu						
			165			170
Ser Leu Arg Ala Leu Phe Thr Thr Trp Ile Thr Ile Pro Ile Gly Lys						
	180		185			190
Arg His Glu Leu Ile Asp Ala Leu Ile Ser Asn Ala His Thr Tyr Leu						
	195		200			205
Glu Ala Ser Asp Arg Asp Glu Asp Ile Ala Phe Val Leu Ser His Ile						
	210		215			220
Ile Glu Leu Asn Glu Gln Tyr Pro Gly Asp Val Gly Val Leu Gly Ala						
	225		230			235
Leu Leu Leu Asn Phe Tyr Lys Leu Ala Pro Gly Glu Ala Leu Tyr Leu						
			245			250
Asp Ala Ala Asn Leu His Ala Tyr Ile Ser Gly Leu Gly Val Glu Ile						
	260		265			270
Met Ala Asn Ser Asp Asn Val Leu Arg Gly Gly Leu Thr Ser Lys Tyr						
	275		280			285
Val Asp Val Pro Glu Leu Val Arg Val Leu Asp Phe Asn Ser Leu Glu						
	290		295			300
Asn Ala Arg Val Asp Val Glu Glu Asp Gly Ala Thr Thr His Tyr Pro						
	305		310			315
Val Pro Ile Asn Glu Phe Gln Leu Asp Arg Val Ala Val Gln Gly Glu						
			325			330
Ala Glu Ala Asn His Asp Gly Pro Met Ile Val Leu Cys Thr Ser Gly						
	340		345			350
Thr Val Ser Leu Glu Ala Gly Glu Lys Thr Leu Glu Val Ala Ala Gly						
	355		360			365
His Ala Ala Trp Val Pro Ala Asn Asp Pro Thr Ile Ala Met Arg Ser						
	370		375			380
Glu Asp Ala Glu Val Phe Leu Ala Arg Val						
	385		390			

<210> 355
 <211> 524
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (1)..(501)
 <223> FRXA01369

<400> 355
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 Asn Glu Gln Cys Leu Gly Asp Val Gly Val Leu Gly Ala Leu Leu Leu
 1 \ 5 10 15
 aac ttc tac aaa ctt gcc cca ggc gaa gcc ctc tac ctc gac gcc gca 96
 Asn Phe Tyr Lys Leu Ala Pro Gly Glu Ala Leu Tyr Leu Asp Ala Ala
 20 25 30
 aac ctt cac gca tac atc agc ggc ctc ggc gta gag atc atg gcg aac 144
 Asn Leu His Ala Tyr Ile Ser Gly Leu Gly Val Glu Ile Met Ala Asn
 35 40 45
 tcc gac aac gtg ctc cgc ggt gga ctg aca tcc aaa tac gtc gac gtc 192
 Ser Asp Asn Val Leu Arg Gly Gly Leu Thr Ser Lys Tyr Val Asp Val
 50 55 60
 ccg gag ctt gtg cgc gtg ttg gat ttc aac tct ttg gaa aac gct cgc 240
 Pro Glu Leu Val Arg Val Leu Asp Phe Asn Ser Leu Glu Asn Ala Arg
 65 70 75 80
 gtg gac gtt gaa gaa gac ggt gca acg acc cac tac cca gtt cca atc 288
 Val Asp Val Glu Glu Asp Gly Ala Thr Thr His Tyr Pro Val Pro Ile
 85 90 95
 aac gaa ttc caa ctc gat cgc gtt gca gtt cag ggc gaa gca gaa gcc 336
 Asn Glu Phe Gln Leu Asp Arg Val Ala Val Gln Gly Glu Ala Glu Ala
 100 105 110
 aac cac gat ggt ccc atg att gtt ctg tgc acc tcc gga act gtt tcc 384
 Asn His Asp Gly Pro Met Ile Val Leu Cys Thr Ser Gly Thr Val Ser
 115 120 125
 ttg gaa gca ggg gag aag acc ctc gaa gta gca gca ggt cac gcc gca 432
 Leu Glu Ala Gly Glu Lys Thr Leu Glu Val Ala Ala Gly His Ala Ala
 130 135 140
 tgg gtt cca gca aac gac cca acc att gcg atg cgt tct gag gac gca 480
 Trp Val Pro Ala Asn Asp Pro Thr Ile Ala Met Arg Ser Glu Asp Ala
 145 150 155 160
 gaa gta ttc ctc gct agg gtt tagatctttt tagattaaaa tca 524
 Glu Val Phe Leu Ala Arg Val
 165

<210> 356
 <211> 167
 <212> PRT

<213> Corynebacterium glutamicum

<400> 356

Asn Glu Gln Cys Leu Gly Asp Val Gly Val Leu Gly Ala Leu Leu Leu
 1 5 10 15

Asn Phe Tyr Lys Leu Ala Pro Gly Glu Ala Leu Tyr Leu Asp Ala Ala
 20 25 30

Asn Leu His Ala Tyr Ile Ser Gly Leu Gly Val Glu Ile Met Ala Asn
 35 40 45

Ser Asp Asn Val Leu Arg Gly Gly Leu Thr Ser Lys Tyr Val Asp Val
 50 55 60

Pro Glu Leu Val Arg Val Leu Asp Phe Asn Ser Leu Glu Asn Ala Arg
 65 70 75 80

Val Asp Val Glu Glu Asp Gly Ala Thr Thr His Tyr Pro Val Pro Ile
 85 90 95

Asn Glu Phe Gln Leu Asp Arg Val Ala Val Gln Gly Glu Ala Glu Ala
 100 105 110

Asn His Asp Gly Pro Met Ile Val Leu Cys Thr Ser Gly Thr Val Ser
 115 120 125

Leu Glu Ala Gly Glu Lys Thr Leu Glu Val Ala Ala Gly His Ala Ala
 130 135 140

Trp Val Pro Ala Asn Asp Pro Thr Ile Ala Met Arg Ser Glu Asp Ala
 145 150 155 160

Glu Val Phe Leu Ala Arg Val
 165

<210> 357

<211> 808

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(808)

<223> FRXA01373

<400> 357

ctgcgacgga cctagcaaag gggcgctgac acaagcactg cgtttgctgg tgcgcggaca 60

gtcagccacg acctattcca ttgaagaaaa ggacttgtaa atg gag cta ttg gaa 115
 Met Glu Leu Leu Glu
 1 5

ggc tca ctg cgc acc tac cca tgg ggt tca aga aca ctg atc gct gat 163
 Gly Ser Leu Arg Thr Tyr Pro Trp Gly Ser Arg Thr Leu Ile Ala Asp
 10 15 20

ctc aaa ggc gaa gaa tca cca tcg tct cgc cca gag gcc gaa gtc tgg 211
 Leu Lys Gly Glu Glu Ser Pro Ser Ser Arg Pro Glu Ala Glu Val Trp
 25 30 35

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ttc ggt gcc cac cca gga tca cca tca acc atc ggt gga aac gca ctc 259
Phe Gly Ala His Pro Gly Ser Pro Ser Thr Ile Gly Gly Asn Ala Leu
      40                      45                      50

aac gaa gtc atc gca gcg aac ccc gaa gaa gca ttg ggc acg cgt gtt 307
Asn Glu Val Ile Ala Ala Asn Pro Glu Glu Ala Leu Gly Thr Arg Val
      55                      60                      65

gcc gaa gcg ttt gaa aat gag ctt cca ttc ctc ctc aaa atc ctc gca 355
Ala Glu Ala Phe Glu Asn Glu Leu Pro Phe Leu Leu Lys Ile Leu Ala
      70                      75                      80                      85

gcg gga gca ccc cta tca ctg cag gcc cac cca tcg ctg gaa cag gcc 403
Ala Gly Ala Pro Leu Ser Leu Gln Ala His Pro Ser Leu Glu Gln Ala
      90                      95                      100

cgt gaa gga ttc gcc cgc gaa aac tca gca gga att gac ctc ggc gca 451
Arg Glu Gly Phe Ala Arg Glu Asn Ser Ala Gly Ile Asp Leu Gly Ala
      105                      110                      115

ccg aac cgc aac tac cgc gac cca aac cac aag cca gag ctg atc gtt 499
Pro Asn Arg Asn Tyr Arg Asp Pro Asn His Lys Pro Glu Leu Ile Val
      120                      125                      130

gct ctc acg gaa ttc atc gcg atg gca ggc ttc cgc cca ctg cgg aac 547
Ala Leu Thr Glu Phe Ile Ala Met Ala Gly Phe Arg Pro Leu Arg Asn
      135                      140                      145

acc ctc acc att ttc gac gcc ctc gcc tgc gaa ccc ctc gac cgc tac 595
Thr Leu Thr Ile Phe Asp Ala Leu Ala Cys Glu Pro Leu Asp Arg Tyr
      150                      155                      160                      165

cgc agc atg ctc acc gtc gac aac gag gaa gaa tcc ctc cgc gca ctg 643
Arg Ser Met Leu Thr Val Asp Asn Glu Glu Glu Ser Leu Arg Ala Leu
      170                      175                      180

ttt acc acc tgg atc acc atc ccc atc ggt aaa cga cac gaa ctc atc 691
Phe Thr Thr Trp Ile Thr Ile Pro Ile Gly Lys Arg His Glu Leu Ile
      185                      190                      195

gat gcc ctc atc agc aac gcc cac acc tac ctt gag gca agc gat cgt 739
Asp Ala Leu Ile Ser Asn Ala His Thr Tyr Leu Glu Ala Ser Asp Arg
      200                      205                      210

gac gag gac atc gca ttc gtg ctc tca cac atc atc gag ctc aac gaa 787
Asp Glu Asp Ile Ala Phe Val Leu Ser His Ile Ile Glu Leu Asn Glu
      215                      220                      225

cag tac ccc ggc gat gtc ggc 808
Gln Tyr Pro Gly Asp Val Gly
      230                      235

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<210> 358

<211> 236

<212> PRT

<213> Corynebacterium glutamicum

<400> 358

Met Glu Leu Leu Glu Gly Ser Leu Arg Thr Tyr Pro Trp Gly Ser Arg

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<400> 359
gat gcg tgg tcg gat cct atg gct acg tgg cgt cat gcg att acc act 48
Asp Ala Trp Ser Asp Pro Met Ala Thr Trp Arg His Ala Ile Thr Thr
  1             5             10             15
aag att gag gcc ggc cag ggt tcg gat gag ttg tat aac gac ttt gag 96

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Lys	Ile	Glu	Ala	Gly	Gln	Gly	Ser	Asp	Glu	Leu	Tyr	Asn	Asp	Phe	Glu		
			20					25					30				
cac	ggg	gct	cag	ctg	ttt	gag	cgt	gct	gcg	gag	aat	ttg	tct	aaa	gag	144	
His	Gly	Ala	Gln	Leu	Phe	Glu	Arg	Ala	Ala	Glu	Asn	Leu	Ser	Lys	Glu		
			35				40					45					
gat	agg	act	gcg	ctt	ttc	gac	gtc	gcc	tcc	tct	ctg	cgg	cgc	ggc	ggc	192	
Asp	Arg	Thr	Ala	Leu	Phe	Asp	Val	Ala	Ser	Ser	Leu	Arg	Arg	Gly	Gly		
			50				55				60						
gat	gta	cgc	gca	cgt	ctc	gcc	cca	gcg	ctc	acc	gcg	agt	gtc	act	cat	240	
Asp	Val	Arg	Ala	Arg	Leu	Ala	Pro	Ala	Leu	Thr	Ala	Ser	Val	Thr	His		
			65			70				75					80		
ctt	tta	gaa	ctt	aac	ccg	ttg	cgt	gag	ttg	gtc	acg	atg	ggt	gaa	aac	288	
Leu	Leu	Glu	Leu	Asn	Pro	Leu	Arg	Glu	Leu	Val	Thr	Met	Gly	Glu	Asn		
				85					90					95			
ctg	cag	gtt	cgt	gtc	gag	cgt	cgt	gcc	gct	ttg	gtc	aac	tct	tgg	tat	336	
Leu	Gln	Val	Arg	Val	Glu	Arg	Arg	Ala	Ala	Leu	Val	Asn	Ser	Trp	Tyr		
			100					105					110				
gag	ctt	ttc	cct	cgt	tcc	aca	ggg	ggg	tgg	gat	gag	tcc	ggc	acc	ccc	384	
Glu	Leu	Phe	Pro	Arg	Ser	Thr	Gly	Gly	Trp	Asp	Glu	Ser	Gly	Thr	Pro		
			115				120					125					
gtt	cat	ggc	act	ttc	gct	acc	act	gct	cag	gcg	ttg	gag	cgt	gtc	gcg	432	
Val	His	Gly	Thr	Phe	Ala	Thr	Thr	Ala	Gln	Ala	Leu	Glu	Arg	Val	Ala		
			130			135					140						
aag	atg	ggc	ttc	gat	act	gtt	tac	ttc	ccg	ccg	atc	cat	ccg	att	ggc	480	
Lys	Met	Gly	Phe	Asp	Thr	Val	Tyr	Phe	Pro	Pro	Ile	His	Pro	Ile	Gly		
					150					155					160		
gag	gtc	aac	cgc	aag	ggc	cgc	aat	aat	acg	ctg	acc	ccg	gaa	cct	cat	528	
Glu	Val	Asn	Arg	Lys	Gly	Arg	Asn	Asn	Thr	Leu	Thr	Pro	Glu	Pro	His		
				165					170					175			
gat	gtg	ggt	tcg	ccg	tgg	gct	att	ggg	tct	aaa	gat	ggt	ggg	cat	gat	576	
Asp	Val	Gly	Ser	Pro	Trp	Ala	Ile	Gly	Ser	Lys	Asp	Gly	Gly	His	Asp		
			180					185					190				
gca	acg	cat	ccg	cgg	ttg	ggc	acc	att	gaa	gat	ttc	cag	gcg	ttg	ttg	624	
Ala	Thr	His	Pro	Arg	Leu	Gly	Thr	Ile	Glu	Asp	Phe	Gln	Ala	Leu	Leu		
			195				200					205					
gct	cgc	gca	cgg	gaa	ctc	aat	ttg	gaa	gtt	gca	ctc	gat	cta	gct	ctg	672	
Ala	Arg	Ala	Arg	Glu	Leu	Asn	Leu	Glu	Val	Ala	Leu	Asp	Leu	Ala	Leu		
			210			215					220						
cag	gct	gcc	cct	gat	cat	cca	tgg	gcg	cag	gaa	cac	cgc	gag	ttt	ttc	720	
Gln	Ala	Ala	Pro	Asp	His	Pro	Trp	Ala	Gln	Glu	His	Arg	Glu	Phe	Phe		
			225			230				235				240			
acg	gtg	ttg	gct	gat	ggc	acc	att	gcg	tat	gca	gaa	aac	cca	ccg	aag	768	
Thr	Val	Leu	Ala	Asp	Gly	Thr	Ile	Ala	Tyr	Ala	Glu	Asn	Pro	Pro	Lys		
				245				250					255				
aag	tac	cag	gat	att	tat	ccc	atc	aac	ttt	gat	aat	gat	gct	ccg	aag	816	
Lys	Tyr	Gln	Asp	Ile	Tyr	Pro	Ile	Asn	Phe	Asp	Asn	Asp	Ala	Pro	Lys		

260	265	270	
atc tac gaa gag gtc tat cgt gtg gtg aag ttc tgg gtg gat ttg ggt Ile Tyr Glu Glu Val Tyr Arg Val Val Lys Phe Trp Val Asp Leu Gly 275 280 285			864
gtg acc aca ttc cgc gtg gat aac ccg cac act aag ccc gct aat ttc Val Thr Thr Phe Arg Val Asp Asn Pro His Thr Lys Pro Ala Asn Phe 290 295 300			912
tgg cag tgg ctt att tct gcc atc cat aaa tca aac cct gag gtc att Trp Gln Trp Leu Ile Ser Ala Ile His Lys Ser Asn Pro Glu Val Ile 305 310 315 320			960
ttc cta gcg gag gcg tct act cgc ccg gca cgt ctg tat ttc ttg tcc Phe Leu Ala Glu Ala Ser Thr Arg Pro Ala Arg Leu Tyr Phe Leu Ser 325 330 335			1008
aag att ggt ttc tcc cag tct tac acc tac ttc acc tgg aag gtc acc Lys Ile Gly Phe Ser Gln Ser Tyr Thr Tyr Phe Thr Trp Lys Val Thr 340 345 350			1056
aac gag gag ctc acc gag ttc gct act gag atc gcc ccc atg gcg gat Asn Glu Glu Leu Thr Glu Phe Ala Thr Glu Ile Ala Pro Met Ala Asp 355 360 365			1104
att tct cgt ccg aac ctg ttt gtg aac act ccc gac att ttg cat gcg Ile Ser Arg Pro Asn Leu Phe Val Asn Thr Pro Asp Ile Leu His Ala 370 375 380			1152
tct ctg cag cat ggt gga cgc gcc atg ttc gct atc cgc gcc gca ttg Ser Leu Gln His Gly Gly Arg Ala Met Phe Ala Ile Arg Ala Ala Leu 385 390 395 400			1200
gcc gcc acg atg tct cct gtg tgg ggc gta tat tcc gga tat gag ctc Ala Ala Thr Met Ser Pro Val Trp Gly Val Tyr Ser Gly Tyr Glu Leu 405 410 415			1248
ttt gag cac gag gcc gtc aag cct ggt tgc gaa gag tac ttg gat tct Phe Glu His Glu Ala Val Lys Pro Gly Ser Glu Glu Tyr Leu Asp Ser 420 425 430			1296
gag aag tac gag ctg cgt ccc cgc gat ttc gag ggt gct ctg gaa cgt Glu Lys Tyr Glu Leu Arg Pro Arg Asp Phe Glu Gly Ala Leu Glu Arg 435 440 445			1344
ggc gat tct ctc gag gat tac atc gct ctg ctc aac cag atc cgt cgc Gly Asp Ser Leu Glu Asp Tyr Ile Ala Leu Leu Asn Gln Ile Arg Arg 450 455 460			1392
gcg aac cct gcc ttg cag caa cta cgc aac atc cac ttc cac gaa gcg Ala Asn Pro Ala Leu Gln Gln Leu Arg Asn Ile His Phe His Glu Ala 465 470 475 480			1440
gac aat gat cag atc atc gcc tac tcc aag gtt gat gct ttg acc gga Asp Asn Asp Gln Ile Ile Ala Tyr Ser Lys Val Asp Ala Leu Thr Gly 485 490 495			1488
aat acc gtg ttg att gtg gtc aac ttg gat cca cgt agt gct cgt gag Asn Thr Val Leu Ile Val Val Asn Leu Asp Pro Arg Ser Ala Arg Glu 500 505 510			1536

gct act gtt cgc ctt gat ctt gga gcg ctt ggc tta gaa gcg ggt gca 1584
 Ala Thr Val Arg Leu Asp Leu Gly Ala Leu Gly Leu Glu Ala Gly Ala
 515 520 525

cag ttt gag gtg cgc gat gcg atc acc ggc tcc cgt tac ctg tgg tca 1632
 Gln Phe Glu Val Arg Asp Ala Ile Thr Gly Ser Arg Tyr Leu Trp Ser
 530 535 540

gag acg aac ttt gtc cgc ctc gag ccc cta cgc gat gtc gcc cac atc 1680
 Glu Thr Asn Phe Val Arg Leu Glu Pro Leu Arg Asp Val Ala His Ile
 545 550 555 560

ttt gtt ctt cct gaa ctt cca gcg tct cgc cgt gag cgt ctc gcg tgg 1728
 Phe Val Leu Pro Glu Leu Pro Ala Ser Arg Arg Glu Arg Leu Ala Trp
 565 570 575

cgc gaa atc aag acc tac cgc gcg taatttccca tctctgtacc ttc 1775
 Arg Glu Ile Lys Thr Tyr Arg Ala
 580

<210> 360

<211> 584

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 360

Asp Ala Trp Ser Asp Pro Met Ala Thr Trp Arg His Ala Ile Thr Thr
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Lys Ile Glu Ala Gly Gln Gly Ser Asp Glu Leu Tyr Asn Asp Phe Glu
 20 25 30

His Gly Ala Gln Leu Phe Glu Arg Ala Ala Glu Asn Leu Ser Lys Glu
 35 40 45

Asp Arg Thr Ala Leu Phe Asp Val Ala Ser Ser Leu Arg Arg Gly Gly
 50 55 60

Asp Val Arg Ala Arg Leu Ala Pro Ala Leu Thr Ala Ser Val Thr His
 65 70 75 80

Leu Leu Glu Leu Asn Pro Leu Arg Glu Leu Val Thr Met Gly Glu Asn
 85 90 95

Leu Gln Val Arg Val Glu Arg Arg Ala Ala Leu Val Asn Ser Trp Tyr
 100 105 110

Glu Leu Phe Pro Arg Ser Thr Gly Gly Trp Asp Glu Ser Gly Thr Pro
 115 120 125

Val His Gly Thr Phe Ala Thr Thr Ala Gln Ala Leu Glu Arg Val Ala
 130 135 140

Lys Met Gly Phe Asp Thr Val Tyr Phe Pro Pro Ile His Pro Ile Gly
 145 150 155 160

Glu Val Asn Arg Lys Gly Arg Asn Asn Thr Leu Thr Pro Glu Pro His
 165 170 175

Asp Val Gly Ser Pro Trp Ala Ile Gly Ser Lys Asp Gly Gly His Asp
 180 185 190
 Ala Thr His Pro Arg Leu Gly Thr Ile Glu Asp Phe Gln Ala Leu Leu
 195 200 205
 Ala Arg Ala Arg Glu Leu Asn Leu Glu Val Ala Leu Asp Leu Ala Leu
 210 215 220
 Gln Ala Ala Pro Asp His Pro Trp Ala Gln Glu His Arg Glu Phe Phe
 225 230 235 240
 Thr Val Leu Ala Asp Gly Thr Ile Ala Tyr Ala Glu Asn Pro Pro Lys
 245 250 255
 Lys Tyr Gln Asp Ile Tyr Pro Ile Asn Phe Asp Asn Asp Ala Pro Lys
 260 265 270
 Ile Tyr Glu Glu Val Tyr Arg Val Val Lys Phe Trp Val Asp Leu Gly
 275 280 285
 Val Thr Thr Phe Arg Val Asp Asn Pro His Thr Lys Pro Ala Asn Phe
 290 295 300
 Trp Gln Trp Leu Ile Ser Ala Ile His Lys Ser Asn Pro Glu Val Ile
 305 310 315 320
 Phe Leu Ala Glu Ala Ser Thr Arg Pro Ala Arg Leu Tyr Phe Leu Ser
 325 330 335
 Lys Ile Gly Phe Ser Gln Ser Tyr Thr Tyr Phe Thr Trp Lys Val Thr
 340 345 350
 Asn Glu Glu Leu Thr Glu Phe Ala Thr Glu Ile Ala Pro Met Ala Asp
 355 360 365
 Ile Ser Arg Pro Asn Leu Phe Val Asn Thr Pro Asp Ile Leu His Ala
 370 375 380
 Ser Leu Gln His Gly Gly Arg Ala Met Phe Ala Ile Arg Ala Ala Leu
 385 390 395 400
 Ala Ala Thr Met Ser Pro Val Trp Gly Val Tyr Ser Gly Tyr Glu Leu
 405 410 415
 Phe Glu His Glu Ala Val Lys Pro Gly Ser Glu Glu Tyr Leu Asp Ser
 420 425 430
 Glu Lys Tyr Glu Leu Arg Pro Arg Asp Phe Glu Gly Ala Leu Glu Arg
 435 440 445
 Gly Asp Ser Leu Glu Asp Tyr Ile Ala Leu Leu Asn Gln Ile Arg Arg
 450 455 460
 Ala Asn Pro Ala Leu Gln Gln Leu Arg Asn Ile His Phe His Glu Ala
 465 470 475 480
 Asp Asn Asp Gln Ile Ile Ala Tyr Ser Lys Val Asp Ala Leu Thr Gly
 485 490 495
 Asn Thr Val Leu Ile Val Val Asn Leu Asp Pro Arg Ser Ala Arg Glu

500 505 510

Ala Thr Val Arg Leu Asp Leu Gly Ala Leu Gly Leu Glu Ala Gly Ala
515 520 525

Gln Phe Glu Val Arg Asp Ala Ile Thr Gly Ser Arg Tyr Leu Trp Ser
530 535 540

Glu Thr Asn Phe Val Arg Leu Glu Pro Leu Arg Asp Val Ala His Ile
545 550 555 560

Phe Val Leu Pro Glu Leu Pro Ala Ser Arg Arg Glu Arg Leu Ala Trp
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Arg Glu Ile Lys Thr Tyr Arg Ala
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<210> 361
<211> 2316
<212> DNA
<213> Corynebacterium glutamicum

<220>
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<223> RXA02612

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taatttccca tctctgtacc ttctatcaag gattatcatc atg acc gtt gac ccc 115
Met Thr Val Asp Pro
1 5

gcg agc cac atc acc atc cct gaa gca gat ctg gcc cgc ctg cgc cac 163
Ala Ser His Ile Thr Ile Pro Glu Ala Asp Leu Ala Arg Leu Arg His
10 15 20

tgc aac cat cac gat cct cat gga ttt tat ggt tgg cat gag acc gaa 211
Cys Asn His His Asp Pro His Gly Phe Tyr Gly Trp His Glu Thr Glu
25 30 35

gct ggt tcg gtt atc cgc acg cgc cag gtc ggc gcg acg cag gtt aat 259
Ala Gly Ser Val Ile Arg Thr Arg Gln Val Gly Ala Thr Gln Val Asn
40 45 50

ttg ctt atc gac gac acc tcc cac gtc atg acc cct atc ggc gac gac 307
Leu Leu Ile Asp Asp Thr Ser His Val Met Thr Pro Ile Gly Asp Asp
55 60 65

att ttc gca att gac tta ggt cac cgc gag cgc gct gac tat cgc ttg 355
Ile Phe Ala Ile Asp Leu Gly His Arg Glu Arg Ala Asp Tyr Arg Leu
70 75 80 85

gaa gtc acc tgg cct gat caa gaa ccg cag gtc aag gct gat cca tac 403
Glu Val Thr Trp Pro Asp Gln Glu Pro Gln Val Lys Ala Asp Pro Tyr
90 95 100

tac ttc ctc ccc acc gta ggc gag atg gat att tac ctc ttc tct gag 451
Tyr Phe Leu Pro Thr Val Gly Glu Met Asp Ile Tyr Leu Phe Ser Glu

105	110	115	
gga cgc cat gag cgt ttg tgg gag att ctc ggt gcc aac atc aag acc Gly Arg His Glu Arg Leu Trp Glu Ile Leu Gly Ala Asn Ile Lys Thr 120 125 130			499
tac caa act gcg ctc gga aca gtt cgt ggc acc gca ttt act gtg tgg Tyr Gln Thr Ala Leu Gly Thr Val Arg Gly Thr Ala Phe Thr Val Trp 135 140 145			547
gct cca aac gca att ggc tgc gca gtg gtc ggt ggc ttc aac ggt tgg Ala Pro Asn Ala Ile Gly Cys Ala Val Val Gly Gly Phe Asn Gly Trp 150 155 160 165			595
aat gca tcc cag cat ccg atg cgt tct atg ggt ggt tcg ggt ctg tgg Asn Ala Ser Gln His Pro Met Arg Ser Met Gly Gly Ser Gly Leu Trp 170 175 180			643
gag ctg ttc atc cca ggc ata gag gaa ggc gaa gtg tac aaa ttc gcc Glu Leu Phe Ile Pro Gly Ile Glu Glu Gly Glu Val Tyr Lys Phe Ala 185 190 195			691
gtc caa acc agg gaa ggc caa cgt cgt gat aag gcc gat ccg atg gct Val Gln Thr Arg Glu Gly Gln Arg Arg Asp Lys Ala Asp Pro Met Ala 200 205 210			739
cgt cgc gca gaa ctg gcg ccg gca acc gga tct att gtc gct tcc tct Arg Arg Ala Glu Leu Ala Pro Ala Thr Gly Ser Ile Val Ala Ser Ser 215 220 225			787
gag tac cag tgg cag gat tcc gag tgg ctg cgc gag cgt tcc caa act Glu Tyr Gln Trp Gln Asp Ser Glu Trp Leu Arg Glu Arg Ser Gln Thr 230 235 240 245			835
gat ctc gca tcc aag cca atg agt gtc tac gag gtc cac ctc ggt tct Asp Leu Ala Ser Lys Pro Met Ser Val Tyr Glu Val His Leu Gly Ser 250 255 260			883
tgg cgc tgg ggt aag aac tat gag gat ttg gct act gag ctg gtt gat Trp Arg Trp Gly Lys Asn Tyr Glu Asp Leu Ala Thr Glu Leu Val Asp 265 270 275			931
tac gtc gca gat ctt ggc tac acc cac gtg gaa ttc ctc cct gtc gca Tyr Val Ala Asp Leu Gly Tyr Thr His Val Glu Phe Leu Pro Val Ala 280 285 290			979
gag cac ccc ttc ggt ggt tcc tgg ggt tac cag gtc acc ggc tac tac Glu His Pro Phe Gly Gly Ser Trp Gly Tyr Gln Val Thr Gly Tyr Tyr 295 300 305			1027
gca ccg acc tct cgt tgg ggt act cca gat cag ttc cgt gcg cta gtc Ala Pro Thr Ser Arg Trp Gly Thr Pro Asp Gln Phe Arg Ala Leu Val 310 315 320 325			1075
gac gct ttc cac gcc cgc ggt att ggc gtg atc atg gac tgg gtt cct Asp Ala Phe His Ala Arg Gly Ile Gly Val Ile Met Asp Trp Val Pro 330 335 340			1123
gcc cac ttc cct aag gat gat tgg gct ctt gcc cgc ttt gat ggc gaa Ala His Phe Pro Lys Asp Asp Trp Ala Leu Ala Arg Phe Asp Gly Glu 345 350 355			1171

gcc ctc tat gaa cac cct gac tgg agg cgc ggc gaa caa aag gat tgg	1219
Ala Leu Tyr Glu His Pro Asp Trp Arg Arg Gly Glu Gln Lys Asp Trp	
360 365 370	
ggc acc ctg gtc ttt gac ttc ggt cgc aac gaa gtc cgc aac ttc ctc	1267
Gly Thr Leu Val Phe Asp Phe Gly Arg Asn Glu Val Arg Asn Phe Leu	
375 380 385	
gtc gct aat gcg ttg tac tgg att gaa gaa ttc cac atc gat ggt ctg	1315
Val Ala Asn Ala Leu Tyr Trp Ile Glu Glu Phe His Ile Asp Gly Leu	
390 395 400 405	
cgc gtc gac gcc gtg gcc tcc atg ctg tac ctc gat tac tcc cgt gag	1363
Arg Val Asp Ala Val Ala Ser Met Leu Tyr Leu Asp Tyr Ser Arg Glu	
410 415 420	
cac ggc gaa tgg gaa cca aac atc tac ggt ggt cgc gag aac ctc gag	1411
His Gly Glu Trp Glu Pro Asn Ile Tyr Gly Gly Arg Glu Asn Leu Glu	
425 430 435	
gca gtg cag ttc ctg cag gaa atg aac gcc acg gtg ctg cga ctg cac	1459
Ala Val Gln Phe Leu Gln Glu Met Asn Ala Thr Val Leu Arg Leu His	
440 445 450	
cct ggt gcg ctc acc atc gct gag gaa tca act tca tgg cct ggc gtg	1507
Pro Gly Ala Leu Thr Ile Ala Glu Glu Ser Thr Ser Trp Pro Gly Val	
455 460 465	
acc gca cca acg tgg gac ggc ggc ttg gga ttc tcc ctc aag tgg aac	1555
Thr Ala Pro Thr Trp Asp Gly Gly Leu Gly Phe Ser Leu Lys Trp Asn	
470 475 480 485	
atg ggc tgg atg cac gac acc tta gag tac ttc tcc aaa aac cct gtg	1603
Met Gly Trp Met His Asp Thr Leu Glu Tyr Phe Ser Lys Asn Pro Val	
490 495 500	
cac cgc gca ttc cac cac agt gag ctc act ttc tcc ttg gtg tac gca	1651
His Arg Ala Phe His His Ser Glu Leu Thr Phe Ser Leu Val Tyr Ala	
505 510 515	
ttc tct gag cgt ttt gta ctt ccg atc tct cac gat gaa gtc gtc cac	1699
Phe Ser Glu Arg Phe Val Leu Pro Ile Ser His Asp Glu Val Val His	
520 525 530	
ggc aag ggt tcc ctg tgg gac cgt atg cct ggc gat acg tgg aac aag	1747
Gly Lys Gly Ser Leu Trp Asp Arg Met Pro Gly Asp Thr Trp Asn Lys	
535 540 545	
gcc gct ggt ctt cgc acc ttc ctt gcg tac atg tgg tca cac cca ggc	1795
Ala Ala Gly Leu Arg Thr Phe Leu Ala Tyr Met Trp Ser His Pro Gly	
550 555 560 565	
aag aag ctg ctt ttc atg ggt cag gag ttt ggt cag cgt gaa gag tgg	1843
Lys Lys Leu Leu Phe Met Gly Gln Glu Phe Gly Gln Arg Glu Glu Trp	
570 575 580	
gct gaa ggc cag gga ctg cca tgg gat att gtc gac ggc tgg caa ggc	1891
Ala Glu Gly Gln Gly Leu Pro Trp Asp Ile Val Asp Gly Trp Gln Gly	
585 590 595	

gag tac cac gaa gcc atc cgc act ctg acc cgc tcc ctc aac ggt gtc 1939
 Glu Tyr His Glu Ala Ile Arg Thr Leu Thr Arg Ser Leu Asn Gly Val
 600 605 610
 tac tca gac tcc cct gcg ctg cac act cag gat ttc acc gga gaa ggc 1987
 Tyr Ser Asp Ser Pro Ala Leu His Thr Gln Asp Phe Thr Gly Glu Gly
 615 620 625
 ttc aca tgg aat aag ggc gac gac gcc acc aac aac att ttg gcg ttc 2035
 Phe Thr Trp Asn Lys Gly Asp Asp Ala Thr Asn Asn Ile Leu Ala Phe
 630 635 640 645
 act cgt ttc ggc agc gac ggc tcc cag atg ctg tgt gta ttc aac ctg 2083
 Thr Arg Phe Gly Ser Asp Gly Ser Gln Met Leu Cys Val Phe Asn Leu
 650 655 660
 tct gga acc tcc cag cct gag tac cag ctc ggt gtt gca gcg ggt ggc 2131
 Ser Gly Thr Ser Gln Pro Glu Tyr Gln Leu Gly Val Ala Ala Gly Gly
 665 670 675
 gaa tgg aag ctc gtt ctc aac act gat gat gct gaa ttc ctc ggt gca 2179
 Glu Trp Lys Leu Val Leu Asn Thr Asp Asp Ala Glu Phe Leu Gly Ala
 680 685 690
 gaa aac gat atc gct act tcc gtt caa gca gca gcg aca cca cgc gat 2227
 Glu Asn Asp Ile Ala Thr Ser Val Gln Ala Ala Thr Pro Arg Asp
 695 700 705
 aat ttc gcc tac tca ctc tca ctg cat gtc cca gcg atg agt gct cag 2275
 Asn Phe Ala Tyr Ser Leu Ser Leu His Val Pro Ala Met Ser Ala Gln
 710 715 720 725
 ttc tac tca ctg cag aag taggacacag gaaaatgcat cct 2316
 Phe Tyr Ser Leu Gln Lys
 730

<210> 362

<211> 731

<212> PRT

<213> Corynebacterium glutamicum

<400> 362

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 Ala Arg Leu Arg His Cys Asn His His Asp Pro His Gly Phe Tyr Gly
 20 25 30
 Trp His Glu Thr Glu Ala Gly Ser Val Ile Arg Thr Arg Gln Val Gly
 35 40 45
 Ala Thr Gln Val Asn Leu Leu Ile Asp Asp Thr Ser His Val Met Thr
 50 55 60
 Pro Ile Gly Asp Asp Ile Phe Ala Ile Asp Leu Gly His Arg Glu Arg
 65 70 75 80
 Ala Asp Tyr Arg Leu Glu Val Thr Trp Pro Asp Gln Glu Pro Gln Val
 85 90 95

Lys Ala Asp Pro Tyr Tyr Phe Leu Pro Thr Val Gly Glu Met Asp Ile
 100 105 110
 Tyr Leu Phe Ser Glu Gly Arg His Glu Arg Leu Trp Glu Ile Leu Gly
 115 120 125
 Ala Asn Ile Lys Thr Tyr Gln Thr Ala Leu Gly Thr Val Arg Gly Thr
 130 135 140
 Ala Phe Thr Val Trp Ala Pro Asn Ala Ile Gly Cys Ala Val Val Gly
 145 150 155 160
 Gly Phe Asn Gly Trp Asn Ala Ser Gln His Pro Met Arg Ser Met Gly
 165 170 175
 Gly Ser Gly Leu Trp Glu Leu Phe Ile Pro Gly Ile Glu Glu Gly Glu
 180 185 190
 Val Tyr Lys Phe Ala Val Gln Thr Arg Glu Gly Gln Arg Arg Asp Lys
 195 200 205
 Ala Asp Pro Met Ala Arg Arg Ala Glu Leu Ala Pro Ala Thr Gly Ser
 210 215 220
 Ile Val Ala Ser Ser Glu Tyr Gln Trp Gln Asp Ser Glu Trp Leu Arg
 225 230 235 240
 Glu Arg Ser Gln Thr Asp Leu Ala Ser Lys Pro Met Ser Val Tyr Glu
 245 250 255
 Val His Leu Gly Ser Trp Arg Trp Gly Lys Asn Tyr Glu Asp Leu Ala
 260 265 270
 Thr Glu Leu Val Asp Tyr Val Ala Asp Leu Gly Tyr Thr His Val Glu
 275 280 285
 Phe Leu Pro Val Ala Glu His Pro Phe Gly Gly Ser Trp Gly Tyr Gln
 290 295 300
 Val Thr Gly Tyr Tyr Ala Pro Thr Ser Arg Trp Gly Thr Pro Asp Gln
 305 310 315 320
 Phe Arg Ala Leu Val Asp Ala Phe His Ala Arg Gly Ile Gly Val Ile
 325 330 335
 Met Asp Trp Val Pro Ala His Phe Pro Lys Asp Asp Trp Ala Leu Ala
 340 345 350
 Arg Phe Asp Gly Glu Ala Leu Tyr Glu His Pro Asp Trp Arg Arg Gly
 355 360 365
 Glu Gln Lys Asp Trp Gly Thr Leu Val Phe Asp Phe Gly Arg Asn Glu
 370 375 380
 Val Arg Asn Phe Leu Val Ala Asn Ala Leu Tyr Trp Ile Glu Glu Phe
 385 390 395 400
 His Ile Asp Gly Leu Arg Val Asp Ala Val Ala Ser Met Leu Tyr Leu
 405 410 415
 Asp Tyr Ser Arg Glu His Gly Glu Trp Glu Pro Asn Ile Tyr Gly Gly

420										425					430				
Arg	Glu	Asn	Leu	Glu	Ala	Val	Gln	Phe	Leu	Gln	Glu	Met	Asn	Ala	Thr				
		435					440					445							
Val	Leu	Arg	Leu	His	Pro	Gly	Ala	Leu	Thr	Ile	Ala	Glu	Glu	Ser	Thr				
		450				455					460								
Ser	Trp	Pro	Gly	Val	Thr	Ala	Pro	Thr	Trp	Asp	Gly	Gly	Leu	Gly	Phe				
465					470					475					480				
Ser	Leu	Lys	Trp	Asn	Met	Gly	Trp	Met	His	Asp	Thr	Leu	Glu	Tyr	Phe				
				485					490					495					
Ser	Lys	Asn	Pro	Val	His	Arg	Ala	Phe	His	His	Ser	Glu	Leu	Thr	Phe				
			500					505					510						
Ser	Leu	Val	Tyr	Ala	Phe	Ser	Glu	Arg	Phe	Val	Leu	Pro	Ile	Ser	His				
		515					520				525								
Asp	Glu	Val	Val	His	Gly	Lys	Gly	Ser	Leu	Trp	Asp	Arg	Met	Pro	Gly				
	530					535				540									
Asp	Thr	Trp	Asn	Lys	Ala	Ala	Gly	Leu	Arg	Thr	Phe	Leu	Ala	Tyr	Met				
545					550					555					560				
Trp	Ser	His	Pro	Gly	Lys	Lys	Leu	Leu	Phe	Met	Gly	Gln	Glu	Phe	Gly				
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Gln	Arg	Glu	Glu	Trp	Ala	Glu	Gly	Gln	Gly	Leu	Pro	Trp	Asp	Ile	Val				
			580					585					590						
Asp	Gly	Trp	Gln	Gly	Glu	Tyr	His	Glu	Ala	Ile	Arg	Thr	Leu	Thr	Arg				
		595					600					605							
Ser	Leu	Asn	Gly	Val	Tyr	Ser	Asp	Ser	Pro	Ala	Leu	His	Thr	Gln	Asp				
		610				615					620								
Phe	Thr	Gly	Glu	Gly	Phe	Thr	Trp	Asn	Lys	Gly	Asp	Asp	Ala	Thr	Asn				
625					630					635					640				
Asn	Ile	Leu	Ala	Phe	Thr	Arg	Phe	Gly	Ser	Asp	Gly	Ser	Gln	Met	Leu				
				645					650					655					
Cys	Val	Phe	Asn	Leu	Ser	Gly	Thr	Ser	Gln	Pro	Glu	Tyr	Gln	Leu	Gly				
			660					665					670						
Val	Ala	Ala	Gly	Gly	Glu	Trp	Lys	Leu	Val	Leu	Asn	Thr	Asp	Asp	Ala				
		675					680					685							
Glu	Phe	Leu	Gly	Ala	Glu	Asn	Asp	Ile	Ala	Thr	Ser	Val	Gln	Ala	Ala				
		690				695					700								
Ala	Thr	Pro	Arg	Asp	Asn	Phe	Ala	Tyr	Ser	Leu	Ser	Leu	His	Val	Pro				
705					710					715					720				
Ala	Met	Ser	Ala	Gln	Phe	Tyr	Ser	Leu	Gln	Lys									
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<211> 1913
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (1)..(1890)
 <223> RXN01884

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 cgt ctc cgc gac cta gga atg cgc aac tac tgg ggc tac aac tct ttc 96
 Arg Leu Arg Asp Leu Gly Met Arg Asn Tyr Trp Gly Tyr Asn Ser Phe
 20 25 30
 ggc ttc ttt gcg ccc tac aac gat tac gct gcc aac aag aac ccc ggt 144
 Gly Phe Phe Ala Pro Tyr Asn Asp Tyr Ala Ala Asn Lys Asn Pro Gly
 35 40 45
 ggc gcc gtg gcc gag ttc aaa ggc ttg gtg cgc agc tac cac gaa gcg 192
 Gly Ala Val Ala Glu Phe Lys Gly Leu Val Arg Ser Tyr His Glu Ala
 50 55 60
 ggc ctc gaa gta att ttg gat gtg gtc tac aac cac acc gcc gag ggc 240
 Gly Leu Glu Val Ile Leu Asp Val Val Tyr Asn His Thr Ala Glu Gly
 65 70 75 80
 aac cac atg ggc ccc acc atc gcg ttc cga ggc att gac aac gag gcg 288
 Asn His Met Gly Pro Thr Ile Ala Phe Arg Gly Ile Asp Asn Glu Ala
 85 90 95
 tac tac cga ctg gtt gag ggc gat cgc cgt cat tac atg gac tac acc 336
 Tyr Tyr Arg Leu Val Glu Gly Asp Arg Arg His Tyr Met Asp Tyr Thr
 100 105 110
 ggt act ggt aac tcc ctc aat gtc cgc gac ccg cac tca ctg cag ctg 384
 Gly Thr Gly Asn Ser Leu Asn Val Arg Asp Pro His Ser Leu Gln Leu
 115 120 125
 att atg gat tcg ctg cgc tac tgg gtc acc gag atg cat gtc gac ggc 432
 Ile Met Asp Ser Leu Arg Tyr Trp Val Thr Glu Met His Val Asp Gly
 130 135 140
 ttc cgc ttc gac ctt gcc tct acc ctt gct cgt gaa ttt gat gat gtt 480
 Phe Arg Phe Asp Leu Ala Ser Thr Leu Ala Arg Glu Phe Asp Asp Val
 145 150 155 160
 gac cgc ctg gca acc ttc ttc gac ctg gtc caa caa gac ccg gtg gtc 528
 Asp Arg Leu Ala Thr Phe Phe Asp Leu Val Gln Gln Asp Pro Val Val
 165 170 175
 tcc cag gtc aag ctc att gct gag ccg tgg gat gtt ggc gaa ggc gga 576
 Ser Gln Val Lys Leu Ile Ala Glu Pro Trp Asp Val Gly Glu Gly Gly
 180 185 190
 tac caa gtg ggt aac ttc cca cca ctg tgg act gag tgg aac ggt aaa 624
 Tyr Gln Val Gly Asn Phe Pro Pro Leu Trp Thr Glu Trp Asn Gly Lys
 195 200 205

tac cgc gac act gtc cgt gat ttc tgg cgt ggt gag cca gca acc ttg	672
Tyr Arg Asp Thr Val Arg Asp Phe Trp Arg Gly Glu Pro Ala Thr Leu	
210 215 220	
ggt gaa ttc gct tcc cga cta act ggt tcc tct gat ttg tat gca aac	720
Gly Glu Phe Ala Ser Arg Leu Thr Gly Ser Ser Asp Leu Tyr Ala Asn	
225 230 235 240	
aac ggc cgt cgc ccc act gca tcg atc aac ttt gtg act gct cac gac	768
Asn Gly Arg Arg Pro Thr Ala Ser Ile Asn Phe Val Thr Ala His Asp	
245 250 255	
ggc ttc acc ctc aat gac ttg gtc agt tac aac gag aag cac aac atg	816
Gly Phe Thr Leu Asn Asp Leu Val Ser Tyr Asn Glu Lys His Asn Met	
260 265 270	
gcc aac ggt gaa gac ggt cgg gac ggt gaa tca cac aac cgt tcc tgg	864
Ala Asn Gly Glu Asp Gly Arg Asp Gly Glu Ser His Asn Arg Ser Trp	
275 280 285	
aac tgt ggc gtc gaa gga cca act gac gat cct gag att atg cag ctg	912
Asn Cys Gly Val Glu Gly Pro Thr Asp Asp Pro Glu Ile Met Gln Leu	
290 295 300	
cgt gct cag caa cga cgc aac ttc ctc acc acc ttg ttg ctg tcc cag	960
Arg Ala Gln Gln Arg Arg Asn Phe Leu Thr Thr Leu Leu Leu Ser Gln	
305 310 315 320	
ggc acc cct atg ttg tcc cac ggt gat gaa atg gcc cgt acc caa aac	1008
Gly Thr Pro Met Leu Ser His Gly Asp Glu Met Ala Arg Thr Gln Asn	
325 330 335	
ggc aac aac aac gtc tac tgc caa gac aat gaa ctg gcg tgg gtg aat	1056
Gly Asn Asn Asn Val Tyr Cys Gln Asp Asn Glu Leu Ala Trp Val Asn	
340 345 350	
tgg gat cag gct gaa gaa aac gct gac ttg gtg agc ttc acc agg cgt	1104
Trp Asp Gln Ala Glu Glu Asn Ala Asp Leu Val Ser Phe Thr Arg Arg	
355 360 365	
ttg ctg cgt atc cga gca aac cac cca gta ttt agg cgc agg cag ttc	1152
Leu Leu Arg Ile Arg Ala Asn His Pro Val Phe Arg Arg Arg Gln Phe	
370 375 380	
ctt gcc ggt ggc cct ttg ggc gcc gat gtt cgt gac cgc gat atc gca	1200
Leu Ala Gly Gly Pro Leu Gly Ala Asp Val Arg Asp Arg Asp Ile Ala	
385 390 395 400	
tgg ctg gta cca aat gga acc ttg atg act caa gat gac tgg gac ttc	1248
Trp Leu Val Pro Asn Gly Thr Leu Met Thr Gln Asp Asp Trp Asp Phe	
405 410 415	
gct ttc ggt aaa tca ctg cag gtg ttc ttc aac ggc gat gcc atc gaa	1296
Ala Phe Gly Lys Ser Leu Gln Val Phe Phe Asn Gly Asp Ala Ile Glu	
420 425 430	
gag cct gat tat cga gga cag aaa atc cac gat gac tcc ttc atc ttg	1344
Glu Pro Asp Tyr Arg Gly Gln Lys Ile His Asp Asp Ser Phe Ile Leu	
435 440 445	

atg ttc aac gct cac ttc gaa cct atc gat ttc aat ctc cct cct gag 1392
 Met Phe Asn Ala His Phe Glu Pro Ile Asp Phe Asn Leu Pro Pro Glu
 450 455 460

cat ttc ggt atg aag tgg aag ctt ttg gtc gat acc acc gaa gcg gtg 1440
 His Phe Gly Met Lys Trp Lys Leu Leu Val Asp Thr Thr Glu Ala Val
 465 470 475 480

ggc cac ccg ctg gag gat ctc acc atc gaa gct ggc gga acc atc act 1488
 Gly His Pro Leu Glu Asp Leu Thr Ile Glu Ala Gly Gly Thr Ile Thr
 485 490 495

gtt cct gcc cgt tcc acg atg ctg ctg cgc cag gtg gag gct ccg gac 1536
 Val Pro Ala Arg Ser Thr Met Leu Leu Arg Gln Val Glu Ala Pro Asp
 500 505 510

tac acc aag ctt gag gaa aag atc gct gct gaa aag cgt gag caa gaa 1584
 Tyr Thr Lys Leu Glu Glu Lys Ile Ala Ala Glu Lys Arg Glu Gln Glu
 515 520 525

ctt gcg gca gag aag gaa gct gct gag aag cgc gaa ttg gaa ctg gcg 1632
 Leu Ala Ala Glu Lys Glu Ala Ala Glu Lys Arg Glu Leu Glu Leu Ala
 530 535 540

gca gca aag gaa gct gaa gat gct gct gag gct ctc cac ctt gcg gca 1680
 Ala Ala Lys Glu Ala Glu Asp Ala Ala Glu Ala Leu His Leu Ala Ala
 545 550 555 560

gaa cgt gct tcg act cag gaa gct gaa ttg gcc cat caa cac ggt gct 1728
 Glu Arg Ala Ser Thr Gln Glu Ala Glu Leu Ala His Gln His Gly Ala
 565 570 575

gat gcg att gcc gat gag gta gcg gaa gaa cca caa gag ctg cca caa 1776
 Asp Ala Ile Ala Asp Glu Val Ala Glu Glu Pro Gln Glu Leu Pro Gln
 580 585 590

gat gaa gta gcg gca gag gtc gag act gag ccc gac acc gag cct gac 1824
 Asp Glu Val Ala Ala Glu Val Glu Thr Glu Pro Asp Thr Glu Pro Asp
 595 600 605

act gaa tct gac tcc gag cag gct gag gta gct tca gag gag cct gaa 1872
 Thr Glu Ser Asp Ser Glu Gln Ala Glu Val Ala Ser Glu Glu Pro Glu
 610 615 620

gcg gac gaa gaa gag aag tagtacaccg aaagtggcgt cgc 1913
 Ala Asp Glu Glu Glu Lys
 625 630

<210> 364

<211> 630

<212> PRT

<213> Corynebacterium glutamicum

<400> 364

Val Thr Ala Ile Glu Leu Met Pro Val His Gln Phe Leu Gln Asp Asp
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Arg Leu Arg Asp Leu Gly Met Arg Asn Tyr Trp Gly Tyr Asn Ser Phe
 20 25 30

517

355	360	365
Leu Leu Arg Ile Arg Ala Asn His Pro Val Phe Arg Arg Arg Gln Phe		
370	375	380
Leu Ala Gly Gly Pro Leu Gly Ala Asp Val Arg Asp Arg Asp Ile Ala		
385	390	395
Trp Leu Val Pro Asn Gly Thr Leu Met Thr Gln Asp Asp Trp Asp Phe		
	405	410
Ala Phe Gly Lys Ser Leu Gln Val Phe Phe Asn Gly Asp Ala Ile Glu		
	420	425
Glu Pro Asp Tyr Arg Gly Gln Lys Ile His Asp Asp Ser Phe Ile Leu		
	435	440
Met Phe Asn Ala His Phe Glu Pro Ile Asp Phe Asn Leu Pro Pro Glu		
	450	455
His Phe Gly Met Lys Trp Lys Leu Leu Val Asp Thr Thr Glu Ala Val		
	465	470
Gly His Pro Leu Glu Asp Leu Thr Ile Glu Ala Gly Gly Thr Ile Thr		
	485	490
Val Pro Ala Arg Ser Thr Met Leu Leu Arg Gln Val Glu Ala Pro Asp		
	500	505
Tyr Thr Lys Leu Glu Glu Lys Ile Ala Ala Glu Lys Arg Glu Gln Glu		
	515	520
Leu Ala Ala Glu Lys Glu Ala Ala Glu Lys Arg Glu Leu Glu Leu Ala		
	530	535
Ala Ala Lys Glu Ala Glu Asp Ala Ala Glu Ala Leu His Leu Ala Ala		
	545	550
Glu Arg Ala Ser Thr Gln Glu Ala Glu Leu Ala His Gln His Gly Ala		
	565	570
Asp Ala Ile Ala Asp Glu Val Ala Glu Glu Pro Gln Glu Leu Pro Gln		
	580	585
Asp Glu Val Ala Ala Glu Val Glu Thr Glu Pro Asp Thr Glu Pro Asp		
	595	600
Thr Glu Ser Asp Ser Glu Gln Ala Glu Val Ala Ser Glu Glu Pro Glu		
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Ala Asp Glu Glu Glu Lys		
625	630	

<210> 365

<211> 1496

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (1)..(1473)

<223> FRXA01884

<400> 365

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Met His Val Asp Gly Phe Arg Phe Asp Leu Ala Ser Thr Leu Ala Arg	
1 5 10 15	
gaa ttt gat gat gtt gac cgc ctg gca acc ttc ttc gac ctg gtc caa	96
Glu Phe Asp Asp Val Asp Arg Leu Ala Thr Phe Phe Asp Leu Val Gln	
20 25 30	
caa gac ccg gtg gtc tcc cag gtc aag ctc att gct gag ccg tgg gat	144
Gln Asp Pro Val Val Ser Gln Val Lys Leu Ile Ala Glu Pro Trp Asp	
35 40 45	
gtt ggc gaa ggc gga tac caa gtg ggt aac ttc cca cca ctg tgg act	192
Val Gly Glu Gly Gly Tyr Gln Val Gly Asn Phe Pro Pro Leu Trp Thr	
50 55 60	
gag tgg aac ggt aaa tac cgc gac act gtc cgt gat ttc tgg cgt ggt	240
Glu Trp Asn Gly Lys Tyr Arg Asp Thr Val Arg Asp Phe Trp Arg Gly	
65 70 75 80	
gag cca gca acc ttg ggt gaa ttc gct tcc cga cta act ggt tcc tct	288
Glu Pro Ala Thr Leu Gly Glu Phe Ala Ser Arg Leu Thr Gly Ser Ser	
85 90 95	
gat ttg tat gca aac aac ggc cgt cgc ccc act gca tcg atc aac ttt	336
Asp Leu Tyr Ala Asn Asn Gly Arg Arg Pro Thr Ala Ser Ile Asn Phe	
100 105 110	
gtg act gct cac gac ggc ttc acc ctc aat gac ttg gtc agt tac aac	384
Val Thr Ala His Asp Gly Phe Thr Leu Asn Asp Leu Val Ser Tyr Asn	
115 120 125	
gag aag cac aac atg gcc aac ggt gaa gac ggt cgg gac ggt gaa tca	432
Glu Lys His Asn Met Ala Asn Gly Glu Asp Gly Arg Asp Gly Glu Ser	
130 135 140	
cac aac cgt tcc tgg aac tgt ggc gtc gaa gga cca act gac gat cct	480
His Asn Arg Ser Trp Asn Cys Gly Val Glu Gly Pro Thr Asp Asp Pro	
145 150 155 160	
gag att atg cag ctg cgt gct cag caa cga cgc aac ttc ctc acc acc	528
Glu Ile Met Gln Leu Arg Ala Gln Gln Arg Arg Asn Phe Leu Thr Thr	
165 170 175	
ttg ttg ctg tcc cag ggc acc cct atg ttg tcc cac ggt gat gaa atg	576
Leu Leu Leu Ser Gln Gly Thr Pro Met Leu Ser His Gly Asp Glu Met	
180 185 190	
gcc cgt acc caa aac ggc aac aac aac gtc tac tgc caa gac aat gaa	624
Ala Arg Thr Gln Asn Gly Asn Asn Asn Val Tyr Cys Gln Asp Asn Glu	
195 200 205	
ctg gcg tgg gtg aat tgg gat cag gct gaa gaa aac gct gac ttg gtg	672
Leu Ala Trp Val Asn Trp Asp Gln Ala Glu Glu Asn Ala Asp Leu Val	
210 215 220	
agc ttc acc agg cgt ttg ctg cgt atc cga gca aac cac cca gta ttt	720

Ser Phe Thr Arg Arg Leu Leu Arg Ile Arg Ala Asn His Pro Val Phe	
225 230 235 240	
agg cgc agg cag ttc ctt gcc ggt ggc cct ttg ggc gcc gat gtt cgt	768
Arg Arg Arg Gln Phe Leu Ala Gly Gly Pro Leu Gly Ala Asp Val Arg	
245 250 255	
gac cgc gat atc gca tgg ctg gta cca aat gga acc ttg atg act caa	816
Asp Arg Asp Ile Ala Trp Leu Val Pro Asn Gly Thr Leu Met Thr Gln	
260 265 270	
gat gac tgg gac ttc gct ttc ggt aaa tca ctg cag gtg ttc ttc aac	864
Asp Asp Trp Asp Phe Ala Phe Gly Lys Ser Leu Gln Val Phe Phe Asn	
275 280 285	
ggc gat gcc atc gaa gag cct gat tat cga gga cag aaa atc cac gat	912
Gly Asp Ala Ile Glu Glu Pro Asp Tyr Arg Gly Gln Lys Ile His Asp	
290 295 300	
gac tcc ttc atc ttg atg ttc aac gct cac ttc gaa cct atc gat ttc	960
Asp Ser Phe Ile Leu Met Phe Asn Ala His Phe Glu Pro Ile Asp Phe	
305 310 315 320	
aat ctc cct cct gag cat ttc ggt atg aag tgg aag ctt ttg gtc gat	1008
Asn Leu Pro Pro Glu His Phe Gly Met Lys Trp Lys Leu Leu Val Asp	
325 330 335	
acc acc gaa gcg gtg ggc cac ccg ctg gag gat ctc acc atc gaa gct	1056
Thr Thr Glu Ala Val Gly His Pro Leu Glu Asp Leu Thr Ile Glu Ala	
340 345 350	
ggc gga acc atc act gtt cct gcc cgt tcc acg atg ctg ctg cgc cag	1104
Gly Gly Thr Ile Thr Val Pro Ala Arg Ser Thr Met Leu Leu Arg Gln	
355 360 365	
gtg gag gct ccg gac tac acc aag ctt gag gaa aag atc gct gct gaa	1152
Val Glu Ala Pro Asp Tyr Thr Lys Leu Glu Glu Lys Ile Ala Ala Glu	
370 375 380	
aag cgt gag caa gaa ctt gcg gca gag aag gaa gct gct gag aag cgc	1200
Lys Arg Glu Gln Glu Leu Ala Ala Glu Lys Glu Ala Ala Glu Lys Arg	
385 390 395 400	
gaa ttg gaa ctg gcg gca gca aag gaa gct gaa gat gct gct gag gct	1248
Glu Leu Glu Leu Ala Ala Ala Lys Glu Ala Glu Asp Ala Ala Glu Ala	
405 410 415	
ctc cac ctt gcg gca gaa cgt gct tcg act cag gaa gct gaa ttg gcc	1296
Leu His Leu Ala Ala Glu Arg Ala Ser Thr Gln Glu Ala Glu Leu Ala	
420 425 430	
cat caa cac ggt gct gat gcg att gcc gat gag gta gcg gaa gaa cca	1344
His Gln His Gly Ala Asp Ala Ile Ala Asp Glu Val Ala Glu Glu Pro	
435 440 445	
caa gag ctg cca caa gat gaa gta gcg gca gag gtc gag act gag ccc	1392
Gln Glu Leu Pro Gln Asp Glu Val Ala Ala Glu Val Glu Thr Glu Pro	
450 455 460	
gac acc gag cct gac act gaa tct gac tcc gag cag gct gag gta gct	1440
Asp Thr Glu Pro Asp Thr Glu Ser Asp Ser Glu Gln Ala Glu Val Ala	

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465              470              475              480
tca gag gag cct gaa gcg gac gaa gaa gag aag tagtacaccg aaagtggcgt 1493
Ser Glu Glu Pro Glu Ala Asp Glu Glu Lys
              485              490

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cqc	1496
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<210> 366
<211> 491
<212> PRT
<213> Corynebacterium glutamicum
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<400> 366
Met His Val Asp Gly Phe Arg Phe Asp Leu Ala Ser Thr Leu Ala Arg
1 5 10 15

Glu Phe Asp Asp Val Asp Arg Leu Ala Thr Phe Phe Asp Leu Val Gln
20 25 30

Gln Asp Pro Val Val Ser Gln Val Lys Leu Ile Ala Glu Pro Trp Asp
35 40 45

Val Gly Glu Gly Gly Tyr Gln Val Gly Asn Phe Pro Pro Leu Trp Thr
50 55 60

Glu Trp Asn Gly Lys Tyr Arg Asp Thr Val Arg Asp Phe Trp Arg Gly
65 70 75 80

Glu Pro Ala Thr Leu Gly Glu Phe Ala Ser Arg Leu Thr Gly Ser Ser
85 90 95

Asp Leu Tyr Ala Asn Asn Gly Arg Arg Pro Thr Ala Ser Ile Asn Phe
100 105 110

Val Thr Ala His Asp Gly Phe Thr Leu Asn Asp Leu Val Ser Tyr Asn
115 120 125

Glu Lys His Asn Met Ala Asn Gly Glu Asp Gly Arg Asp Gly Glu Ser
130 135 140

His Asn Arg Ser Trp Asn Cys Gly Val Glu Gly Pro Thr Asp Asp Pro
145 150 155 160

Glu Ile Met Gln Leu Arg Ala Gln Gln Arg Arg Asn Phe Leu Thr Thr
165 170 175

Leu Leu Leu Ser Gln Gly Thr Pro Met Leu Ser His Gly Asp Glu Met
180 185 190

Ala Arg Thr Gln Asn Gly Asn Asn Val Tyr Cys Gln Asp Asn Glu
195 200 205

Leu Ala Trp Val Asn Trp Asp Gln Ala Glu Glu Asn Ala Asp Leu Val
210 215 220

Ser Phe Thr Arg Arg Leu Leu Arg Ile Arg Ala Asn His Pro Val Phe
225 230 235 240

Arg Arg Arg Gln Phe Leu Ala Gly Gly Pro Leu Gly Ala Asp Val Arg

<400> 367
agaaaaccct gccgatgcaa actttgagga gagattcaat caaggaatag aaatcattct 60

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gggtgggtcta gacgcgcttg ggcatataag atgacgttcc atg aca tca acg att 115
                                   Met Thr Ser Thr Ile
                                   1 5

gag cac tcg tac caa gtt tgg cct gga cat gct tat cct ctg ggt tca 163
Glu His Ser Tyr Gln Val Trp Pro Gly His Ala Tyr Pro Leu Gly Ser
          10          15          20

acc tat gac ggt gct gga acg aac ttc gca ctc ttc tcc gac gtt gca 211
Thr Tyr Asp Gly Ala Gly Thr Asn Phe Ala Leu Phe Ser Asp Val Ala
          25          30          35

gag cgt gtt gag ctg tgt cta tta gat gca gat aac aac gag act cga 259
Glu Arg Val Glu Leu Cys Leu Leu Asp Ala Asp Asn Asn Glu Thr Arg
          40          45          50

att cca ctc gaa gag cgc gat gcc cac att tgg cat tgc tac ctt cct 307
Ile Pro Leu Glu Glu Arg Asp Ala His Ile Trp His Cys Tyr Leu Pro
          55          60          65

ggc gtt caa cct gga cag cgc tac gga ttc cga gtt cat ggc ccg tgg 355
Gly Val Gln Pro Gly Gln Arg Tyr Gly Phe Arg Val His Gly Pro Trp
          70          75          80          85

aac cca gat gag ggt aag cgg tgc gac gcg aac aaa ctt cta gtt gat 403
Asn Pro Asp Glu Gly Lys Arg Cys Asp Ala Asn Lys Leu Leu Val Asp
          90          95          100

ccc tat gct cgt gct ttc gat gga gat ttt gat gga cat ccg tca cta 451
Pro Tyr Ala Arg Ala Phe Asp Gly Asp Phe Asp Gly His Pro Ser Leu
          105          110          115

ttt tct tac gac atc acc aat cca aat gac ccc aac ggt cgc aat acc 499
Phe Ser Tyr Asp Ile Thr Asn Pro Asn Asp Pro Asn Gly Arg Asn Thr
          120          125          130

gaa gac agc att gat cac aca atg aag tct gtc gtg gtg aac cca ttc 547
Glu Asp Ser Ile Asp His Thr Met Lys Ser Val Val Val Asn Pro Phe
          135          140          145

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<210> 368

<211> 149

<212> PRT

<213> Corynebacterium glutamicum

<400> 368

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Met Thr Ser Thr Ile Glu His Ser Tyr Gln Val Trp Pro Gly His Ala
 1          5          10          15

Tyr Pro Leu Gly Ser Thr Tyr Asp Gly Ala Gly Thr Asn Phe Ala Leu
 20          25          30

Phe Ser Asp Val Ala Glu Arg Val Glu Leu Cys Leu Leu Asp Ala Asp
 35          40          45

Asn Asn Glu Thr Arg Ile Pro Leu Glu Glu Arg Asp Ala His Ile Trp
 50          55          60

His Cys Tyr Leu Pro Gly Val Gln Pro Gly Gln Arg Tyr Gly Phe Arg
 65          70          75          80

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[illegible]

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<210> 369
<211> 1635
<212> DNA
<213> Corynebacterium glutamicum
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<220>
<221> CDS
<222> (101)..(1612)
<223> RXN01550
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Ala Ala Leu His Thr Glu Ile Ile Lys Ala Glu Thr Leu Ala Asp Trp	
120 125 130	
tac gca ctg tgg cca gag aag ttc aac aac aag act aac ggt gtt acc	547
Tyr Ala Leu Trp Pro Glu Lys Phe Asn Asn Lys Thr Asn Gly Val Thr	
135 140 145	
cca cgc cgt tgg ctg cgc atg atc aac cca ggt ctg tct gac ctg ctc	595
Pro Arg Arg Trp Leu Arg Met Ile Asn Pro Gly Leu Ser Asp Leu Leu	
150 155 160 165	
act cga ctt tcc ggt tcc gat gat tgg gta acc gat ctg gat gag ctg	643
Thr Arg Leu Ser Gly Ser Asp Asp Trp Val Thr Asp Leu Asp Glu Leu	
170 175 180	
aag aag ctg cgc tcc tat gcc gac gat aag tcc gtg ctt gaa gaa ctc	691
Lys Lys Leu Arg Ser Tyr Ala Asp Asp Lys Ser Val Leu Glu Glu Leu	
185 190 195	
cgc gct atc aag gct gct aat aag caa gac ttc gcc gag tgg atc ctc	739
Arg Ala Ile Lys Ala Ala Asn Lys Gln Asp Phe Ala Glu Trp Ile Leu	
200 205 210	
gag cgc cag ggc att gag att gat cca gaa tcc atc ttt gac gtg cag	787
Glu Arg Gln Gly Ile Glu Ile Asp Pro Glu Ser Ile Phe Asp Val Gln	
215 220 225	
att aag cgc ctc cac gag tac aag cgc cag ctc atg aac gcg ctc tac	835
Ile Lys Arg Leu His Glu Tyr Lys Arg Gln Leu Met Asn Ala Leu Tyr	
230 235 240 245	
gta cta gac ctt tac ttc cgt att aag gaa gat ggc ctc acc gac atc	883
Val Leu Asp Leu Tyr Phe Arg Ile Lys Glu Asp Gly Leu Thr Asp Ile	
250 255 260	
cca gca cgc act gtc atc ttt ggc gcc aag gcc gcg ccg ggt tat gtc	931
Pro Ala Arg Thr Val Ile Phe Gly Ala Lys Ala Ala Pro Gly Tyr Val	
265 270 275	
cgc gcc aag gcg att atc aag ctc atc aac tct att gct gac ttg gta	979
Arg Ala Lys Ala Ile Ile Lys Leu Ile Asn Ser Ile Ala Asp Leu Val	
280 285 290	
aac aac gat cct gag gtc tcc ccg ctg ctc aag gtg gtc ttt gta gag	1027
Asn Asn Asp Pro Glu Val Ser Pro Leu Leu Lys Val Val Phe Val Glu	
295 300 305	
aac tac aac gtc tcc cct gct gag cac atc ttg cct gcg tct gat gtc	1075
Asn Tyr Asn Val Ser Pro Ala Glu His Ile Leu Pro Ala Ser Asp Val	
310 315 320 325	
tcc gaa cag att tcc acc gcc ggc aag gaa gcc agc ggt acc tcc aac	1123
Ser Glu Gln Ile Ser Thr Ala Gly Lys Glu Ala Ser Gly Thr Ser Asn	
330 335 340	
atg aag ttc atg atg aac ggc gcc ctc acc ctg ggc acc atg gac ggc	1171
Met Lys Phe Met Met Asn Gly Ala Leu Thr Leu Gly Thr Met Asp Gly	
345 350 355	

gcc aac gta gag atc gtg gat tct gtg ggc gag gaa aac gcc tat atc 1219
 Ala Asn Val Glu Ile Val Asp Ser Val Gly Glu Glu Asn Ala Tyr Ile
 360 365 370

ttc ggt gct cgc gtg gaa gaa ttg cca gcc ctg cgc gaa agc tac gag 1267
 Phe Gly Ala Arg Val Glu Glu Leu Pro Ala Leu Arg Glu Ser Tyr Glu
 375 380 385

cca tat gag ctc tat gag acc gtc cct ggc ctc aag cgc gca ttg gac 1315
 Pro Tyr Glu Leu Tyr Glu Thr Val Pro Gly Leu Lys Arg Ala Leu Asp
 390 395 400 405

gcc ctg gat aac ggc acc ctc aac gac aac aac agt ggt ttg ttc tac 1363
 Ala Leu Asp Asn Gly Thr Leu Asn Asp Asn Asn Ser Gly Leu Phe Tyr
 410 415 420

gac ctc aag cat tcc ttg atc cac ggt tat gga aaa gac gcc agc gac 1411
 Asp Leu Lys His Ser Leu Ile His Gly Tyr Gly Lys Asp Ala Ser Asp
 425 430 435

acc tac tac gtg ctt ggc gat ttc gca gat tac cgc gag acc cgc gac 1459
 Thr Tyr Tyr Val Leu Gly Asp Phe Ala Asp Tyr Arg Glu Thr Arg Asp
 440 445 450

cgt atg gcc gcc gac tac gcc tcc gat ccc ctg ggt tgg gca cgc atg 1507
 Arg Met Ala Ala Asp Tyr Ala Ser Asp Pro Leu Gly Trp Ala Arg Met
 455 460 465

gcc tgg atc aac att tgc gag tcc ggc cgt ttc tcc tcc gac cgc acc 1555
 Ala Trp Ile Asn Ile Cys Glu Ser Gly Arg Phe Ser Ser Asp Arg Thr
 470 475 480 485

atc cgc gat tat gcc acc gag atc tgg aag ctc gag cca act cct gct 1603
 Ile Arg Asp Tyr Ala Thr Glu Ile Trp Lys Leu Glu Pro Thr Pro Ala
 490 495 500

gtt aag aag taggttttaa cctccgcttc taa 1635
 Val Lys Lys

<210> 370

<211> 504

<212> PRT

<213> Corynebacterium glutamicum

<400> 370

Val Gln Leu Asn Asp Thr His Pro Val Leu Ala Ile Pro Glu Leu Met
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Arg Leu Leu Met Asp Glu His Asp Met Gly Trp Glu Glu Ser Trp Ala
 20 25 30

Ile Val Phe Lys Thr Phe Ala Tyr Thr Asn His Thr Val Leu Thr Glu
 35 40 45

Ala Leu Glu Gln Trp Asp Gln Gln Ile Phe Gln Gln Leu Phe Trp Arg
 50 55 60

Val Trp Glu Ile Ile Thr Glu Ile Asp Arg Arg Phe Arg Leu Glu Arg
 65 70 75 80

Ala Ala Asp Gly Leu Asp Glu Glu Thr Ile Asp Arg Met Ala Pro Ile
 85 90 95
 Gln His Gly Thr Val His Met Ala Trp Ile Ala Cys Tyr Ala Ala Tyr
 100 105 110
 Ser Ile Asn Gly Val Ala Ala Leu His Thr Glu Ile Ile Lys Ala Glu
 115 120 125
 Thr Leu Ala Asp Trp Tyr Ala Leu Trp Pro Glu Lys Phe Asn Asn Lys
 130 135 140
 Thr Asn Gly Val Thr Pro Arg Arg Trp Leu Arg Met Ile Asn Pro Gly
 145 150 155 160
 Leu Ser Asp Leu Leu Thr Arg Leu Ser Gly Ser Asp Asp Trp Val Thr
 165 170 175
 Asp Leu Asp Glu Leu Lys Lys Leu Arg Ser Tyr Ala Asp Asp Lys Ser
 180 185 190
 Val Leu Glu Glu Leu Arg Ala Ile Lys Ala Ala Asn Lys Gln Asp Phe
 195 200 205
 Ala Glu Trp Ile Leu Glu Arg Gln Gly Ile Glu Ile Asp Pro Glu Ser
 210 215 220
 Ile Phe Asp Val Gln Ile Lys Arg Leu His Glu Tyr Lys Arg Gln Leu
 225 230 235 240
 Met Asn Ala Leu Tyr Val Leu Asp Leu Tyr Phe Arg Ile Lys Glu Asp
 245 250 255
 Gly Leu Thr Asp Ile Pro Ala Arg Thr Val Ile Phe Gly Ala Lys Ala
 260 265 270
 Ala Pro Gly Tyr Val Arg Ala Lys Ala Ile Ile Lys Leu Ile Asn Ser
 275 280 285
 Ile Ala Asp Leu Val Asn Asn Asp Pro Glu Val Ser Pro Leu Leu Lys
 290 295 300
 Val Val Phe Val Glu Asn Tyr Asn Val Ser Pro Ala Glu His Ile Leu
 305 310 315 320
 Pro Ala Ser Asp Val Ser Glu Gln Ile Ser Thr Ala Gly Lys Glu Ala
 325 330 335
 Ser Gly Thr Ser Asn Met Lys Phe Met Met Asn Gly Ala Leu Thr Leu
 340 345 350
 Gly Thr Met Asp Gly Ala Asn Val Glu Ile Val Asp Ser Val Gly Glu
 355 360 365
 Glu Asn Ala Tyr Ile Phe Gly Ala Arg Val Glu Glu Leu Pro Ala Leu
 370 375 380
 Arg Glu Ser Tyr Glu Pro Tyr Glu Leu Tyr Glu Thr Val Pro Gly Leu
 385 390 395 400

<400> 371																	
atc	ttc	caa	cag	ctg	ttc	tgg	cgc	gtg	tgg	gaa	atc	atc	aca	gag	atc	48	
Ile	Phe	Gln	Gln	Leu	Phe	Trp	Arg	Val	Trp	Glu	Ile	Ile	Thr	Glu	Ile		
1				5				10						15			
gat cgc cgc ttc cgt ttg gag cgc gca gcc gat gga ctg gat gaa gag																	96
Asp	Arg	Arg	Phe	Arg	Leu	Glu	Arg	Ala	Ala	Asp	Gly	Leu	Asp	Glu	Glu		
		20						25				30					
acc atc gac cgc atg gct cca atc cag cgc ggc act gtt cat atg gca																	144
Thr	Ile	Asp	Arg	Met	Ala	Pro	Ile	Gln	Arg	Gly	Thr	Val	His	Met	Ala		
		35				40						45					
tgg att gcc tgt tac gcg gca tat tcc atc aat ggc gtg gca gcg ctg																	192
Trp	Ile	Ala	Cys	Tyr	Ala	Ala	Tyr	Ser	Ile	Asn	Gly	Val	Ala	Ala	Leu		
50						55				60							
cac acc gag atc atc aag gcc gag acc ttg gct gac tgg tac gca ctg																	240
His	Thr	Glu	Ile	Ile	Lys	Ala	Glu	Thr	Leu	Ala	Asp	Trp	Tyr	Ala	Leu		
65				70						75				80			
tgg cca gag aag ttc aac aac aag act aac ggt gtt acc cca cgc cgt																	288
Trp	Pro	Glu	Lys	Phe	Asn	Asn	Lys	Thr	Asn	Gly	Val	Thr	Pro	Arg	Arg		
				85				90						95			
tgg ctg cgc atg atc aac cca ggt ctg tct gac ctg ctc act cga ctt																	336
Trp	Leu	Arg	Met	Ile	Asn	Pro	Gly	Leu	Ser	Asp	Leu	Leu	Thr	Arg	Leu		
		100						105				110					

tcc ggt tcc gat gat tgg gta acc gat ctg gat gag ctg aag aag ctg	384
Ser Gly Ser Asp Asp Trp Val Thr Asp Leu Asp Glu Leu Lys Lys Leu	
115 120 125	
cgc tcc tat gcc gac gat aag tcc gtg ctt gaa gaa ctc cgc gct atc	432
Arg Ser Tyr Ala Asp Asp Lys Ser Val Leu Glu Glu Leu Arg Ala Ile	
130 135 140	
aag gct gct aat aag caa gac ttc gcc gag tgg atc ctc gag cgc cag	480
Lys Ala Ala Asn Lys Gln Asp Phe Ala Glu Trp Ile Leu Glu Arg Gln	
145 150 155 160	
ggc att gag att gat cca gaa tcc atc ttt gac gtg cag att aag cgc	528
Gly Ile Glu Ile Asp Pro Glu Ser Ile Phe Asp Val Gln Ile Lys Arg	
165 170 175	
ctc cac gag tac aag cgc cag ctc atg aac gcg ctc tac gta cta gac	576
Leu His Glu Tyr Lys Arg Gln Leu Met Asn Ala Leu Tyr Val Leu Asp	
180 185 190	
ctt tac ttc cgt att aag gaa gat ggc ctc acc gac atc cca gca cgc	624
Leu Tyr Phe Arg Ile Lys Glu Asp Gly Leu Thr Asp Ile Pro Ala Arg	
195 200 205	
act gtc atc ttt ggc gcc aag gcc gcg ccg ggt tat gtc cgc gcc aag	672
Thr Val Ile Phe Gly Ala Lys Ala Ala Pro Gly Tyr Val Arg Ala Lys	
210 215 220	
gcg att atc aag ctc atc aac tct att gct gac ttg gta aac aac gat	720
Ala Ile Ile Lys Leu Ile Asn Ser Ile Ala Asp Leu Val Asn Asn Asp	
225 230 235 240	
cct gag gtc tcc ccg ctg ctc aag gtg gtc ttt gta gag aac tac aac	768
Pro Glu Val Ser Pro Leu Leu Lys Val Val Phe Val Glu Asn Tyr Asn	
245 250 255	
gtc tcc cct gct gag cac atc ttg cct gcg tct gat gtc tcc gaa cag	816
Val Ser Pro Ala Glu His Ile Leu Pro Ala Ser Asp Val Ser Glu Gln	
260 265 270	
att tcc acc gcc ggc aag gaa gcc agc ggt acc tcc aac atg aag ttc	864
Ile Ser Thr Ala Gly Lys Glu Ala Ser Gly Thr Ser Asn Met Lys Phe	
275 280 285	
atg atg aac ggc gcc ctc acc ctg ggc acc atg gac ggc gcc aac gta	912
Met Met Asn Gly Ala Leu Thr Leu Gly Thr Met Asp Gly Ala Asn Val	
290 295 300	
gag atc gtg gat tct gtg ggc gag gaa aac gcc tat atc ttc ggt gct	960
Glu Ile Val Asp Ser Val Gly Glu Glu Asn Ala Tyr Ile Phe Gly Ala	
305 310 315 320	
cgc gtg gaa gaa ttg cca gcc ctg cgc gaa agc tac gag cca tat gag	1008
Arg Val Glu Glu Leu Pro Ala Leu Arg Glu Ser Tyr Glu Pro Tyr Glu	
325 330 335	
ctc tat gag acc gtc cct ggc ctc aag cgc gca ttg gac gcc ctg gat	1056
Leu Tyr Glu Thr Val Pro Gly Leu Lys Arg Ala Leu Asp Ala Leu Asp	
340 345 350	
aac ggc acc ctc aac gac aac aac agt ggt ttg ttc tac gac ctc aag	1104

Asn Gly Thr Leu Asn Asp Asn Asn Ser Gly Leu Phe Tyr Asp Leu Lys
 355 360 365
 cat tcc ttg atc cac ggt tat gga aaa gac gcc agc gac acc tac tac 1152
 His Ser Leu Ile His Gly Tyr Gly Lys Asp Ala Ser Asp Thr Tyr Tyr
 370 375 380
 gtg ctt ggc gat ttc gca gat tac cgc gag acc cgc gac cgt atg gcc 1200
 Val Leu Gly Asp Phe Ala Asp Tyr Arg Glu Thr Arg Asp Arg Met Ala
 385 390 395 400
 gcc gac tac gcc tcc gat ccc ctg ggt tgg gca cgc atg gcc tgg atc 1248
 Ala Asp Tyr Ala Ser Asp Pro Leu Gly Trp Ala Arg Met Ala Trp Ile
 405 410 415
 aac att tgc gag tcc ggc cgt ttc tcc tcc gac cgc acc atc cgc gat 1296
 Asn Ile Cys Glu Ser Gly Arg Phe Ser Ser Asp Arg Thr Ile Arg Asp
 420 425 430
 tat gcc acc gag atc tgg aag ctg gag cca act cct gct gtt aag aag 1344
 Tyr Ala Thr Glu Ile Trp Lys Leu Glu Pro Thr Pro Ala Val Lys Lys
 435 440 445
 taggttttaa cctccgcttc taa 1367

<210> 372

<211> 448

<212> PRT

<213> Corynebacterium glutamicum

<400> 372

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 Asp Arg Arg Phe Arg Leu Glu Arg Ala Ala Asp Gly Leu Asp Glu Glu
 20 25 30
 Thr Ile Asp Arg Met Ala Pro Ile Gln Arg Gly Thr Val His Met Ala
 35 40 45
 Trp Ile Ala Cys Tyr Ala Ala Tyr Ser Ile Asn Gly Val Ala Ala Leu
 50 55 60
 His Thr Glu Ile Ile Lys Ala Glu Thr Leu Ala Asp Trp Tyr Ala Leu
 65 70 75 80
 Trp Pro Glu Lys Phe Asn Asn Lys Thr Asn Gly Val Thr Pro Arg Arg
 85 90 95
 Trp Leu Arg Met Ile Asn Pro Gly Leu Ser Asp Leu Leu Thr Arg Leu
 100 105 110
 Ser Gly Ser Asp Asp Trp Val Thr Asp Leu Asp Glu Leu Lys Lys Leu
 115 120 125
 Arg Ser Tyr Ala Asp Asp Lys Ser Val Leu Glu Glu Leu Arg Ala Ile
 130 135 140
 Lys Ala Ala Asn Lys Gln Asp Phe Ala Glu Trp Ile Leu Glu Arg Gln
 145 150 155 160

Gly Ile Glu Ile Asp Pro Glu Ser Ile Phe Asp Val Gln Ile Lys Arg
 165 170 175
 Leu His Glu Tyr Lys Arg Gln Leu Met Asn Ala Leu Tyr Val Leu Asp
 180 185 190
 Leu Tyr Phe Arg Ile Lys Glu Asp Gly Leu Thr Asp Ile Pro Ala Arg
 195 200 205
 Thr Val Ile Phe Gly Ala Lys Ala Ala Pro Gly Tyr Val Arg Ala Lys
 210 215 220
 Ala Ile Ile Lys Leu Ile Asn Ser Ile Ala Asp Leu Val Asn Asn Asp
 225 230 235 240
 Pro Glu Val Ser Pro Leu Leu Lys Val Val Phe Val Glu Asn Tyr Asn
 245 250 255
 Val Ser Pro Ala Glu His Ile Leu Pro Ala Ser Asp Val Ser Glu Gln
 260 265 270
 Ile Ser Thr Ala Gly Lys Glu Ala Ser Gly Thr Ser Asn Met Lys Phe
 275 280 285
 Met Met Asn Gly Ala Leu Thr Leu Gly Thr Met Asp Gly Ala Asn Val
 290 295 300
 Glu Ile Val Asp Ser Val Gly Glu Glu Asn Ala Tyr Ile Phe Gly Ala
 305 310 315 320
 Arg Val Glu Glu Leu Pro Ala Leu Arg Glu Ser Tyr Glu Pro Tyr Glu
 325 330 335
 Leu Tyr Glu Thr Val Pro Gly Leu Lys Arg Ala Leu Asp Ala Leu Asp
 340 345 350
 Asn Gly Thr Leu Asn Asp Asn Asn Ser Gly Leu Phe Tyr Asp Leu Lys
 355 360 365
 His Ser Leu Ile His Gly Tyr Gly Lys Asp Ala Ser Asp Thr Tyr Tyr
 370 375 380
 Val Leu Gly Asp Phe Ala Asp Tyr Arg Glu Thr Arg Asp Arg Met Ala
 385 390 395 400
 Ala Asp Tyr Ala Ser Asp Pro Leu Gly Trp Ala Arg Met Ala Trp Ile
 405 410 415
 Asn Ile Cys Glu Ser Gly Arg Phe Ser Ser Asp Arg Thr Ile Arg Asp
 420 425 430
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<210> 373

<211> 2348

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (1)..(2325)

<223> RXN02100

<400> 373

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gac aag ctg tgg tac cag gac acc gca gat gca acc gat gct gtc gga	96
Asp Lys Leu Trp Tyr Gln Asp Thr Ala Asp Ala Thr Asp Ala Val Gly	
20 25 30	
gat cca ctc gtt gcg tac ttc tcc atg gag ttt ggc att cac cca agc	144
Asp Pro Leu Val Ala Tyr Phe Ser Met Glu Phe Gly Ile His Pro Ser	
35 40 45	
ctg cca atc tac tct ggc gga ctt ggt gtg ctt gcg ggc gag aac atg	192
Leu Pro Ile Tyr Ser Gly Gly Leu Gly Val Leu Ala Gly Glu Asn Met	
50 55 60	
aag tct gca tct gac ttg ggt gtg cca ctg atc ggt gtt ggt ttg ctc	240
Lys Ser Ala Ser Asp Leu Gly Val Pro Leu Ile Gly Val Gly Leu Leu	
65 70 75 80	
tac acc cac ggc tac ttc acc cag tca ctg tcc ggt gac ggt tgg cag	288
Tyr Thr His Gly Tyr Phe Thr Gln Ser Leu Ser Gly Asp Gly Trp Gln	
85 90 95	
cag gaa gag tac aag tac cac gat cca gca gaa ctg ccg att gag gca	336
Gln Glu Glu Tyr Lys Tyr His Asp Pro Ala Glu Leu Pro Ile Glu Ala	
100 105 110	
gtt aaa gat aag aac ggc gag cag gtc act gtt tct gtc acc tac cca	384
Val Lys Asp Lys Asn Gly Glu Gln Val Thr Val Ser Val Thr Tyr Pro	
115 120 125	
ggt gcg cag gaa gta aag att gca ctg tgg gta gca aac gtt ggc cgc	432
Gly Ala Gln Glu Val Lys Ile Ala Leu Trp Val Ala Asn Val Gly Arg	
130 135 140	
atc cca ttg ctg ctg ctt gat acc aac atc gag gca aac cca gaa gag	480
Ile Pro Leu Leu Leu Leu Asp Thr Asn Ile Glu Ala Asn Pro Glu Glu	
145 150 155 160	
ctc cgc aac gtt act gac cgc ctg tac ggt ggc gac aat gag cac cgc	528
Leu Arg Asn Val Thr Asp Arg Leu Tyr Gly Gly Asp Asn Glu His Arg	
165 170 175	
atc aag cag gaa ctc gtt ctc ggt gtt ggt ggc gtc cgc gct gtc aac	576
Ile Lys Gln Glu Leu Val Leu Gly Val Gly Gly Val Arg Ala Val Asn	
180 185 190	
gca ttc tgc gaa gct cgt ggt ctg aag cgc tca tct gtt gca cac ctc	624
Ala Phe Cys Glu Ala Arg Gly Leu Lys Arg Ser Ser Val Ala His Leu	
195 200 205	

aac gaa ggc cac gca ggt ttc ctg acc ctg gag cgt atc cgc gag cgc	672
Asn Glu Gly His Ala Gly Phe Leu Thr Leu Glu Arg Ile Arg Glu Arg	
210 215 220	
atc gca gag ggc atg gag tac cca gca gca ttc gag cag gtt cgt gcg	720
Ile Ala Glu Gly Met Glu Tyr Pro Ala Ala Phe Glu Gln Val Arg Ala	
225 230 235 240	
tcc aac atc ttc acc acc cac acc cca gtc cca gca ggc atc gac cgc	768
Ser Asn Ile Phe Thr Thr His Thr Pro Val Pro Ala Gly Ile Asp Arg	
245 250 255	
ttc gac atg gag atg gtg cgt cgt tat ctc ggt ggc ggt cag cca gaa	816
Phe Asp Met Glu Met Val Arg Arg Tyr Leu Gly Gly Gly Gln Pro Glu	
260 265 270	
gat cag cag ctg tgc gtt ggt gtt cca att gag aag gca ctt gag ctt	864
Asp Gln Gln Leu Cys Val Gly Val Pro Ile Glu Lys Ala Leu Glu Leu	
275 280 285	
ggt caa gag tcc gat cca cac cgc ttc aac atg gct cat atg ggc ctt	912
Gly Gln Glu Ser Asp Pro His Arg Phe Asn Met Ala His Met Gly Leu	
290 295 300	
cgc gcg agc caa cat gct aat ggc gtc gca aag ctt cat ggt gaa gta	960
Arg Ala Ser Gln His Ala Asn Gly Val Ala Lys Leu His Gly Glu Val	
305 310 315 320	
agc cgt gac atg ttc gcc ggc ctg tac ccc gga tat gag cct cgt gaa	1008
Ser Arg Asp Met Phe Ala Gly Leu Tyr Pro Gly Tyr Glu Pro Arg Glu	
325 330 335	
gtg ccc atc ggg cac gtc acc aac ggt gtt cac ctg ccg acg tgg gtc	1056
Val Pro Ile Gly His Val Thr Asn Gly Val His Leu Pro Thr Trp Val	
340 345 350	
aag cca gag atg aag gaa ctc atc gat cgc gtc act ggc ggc gct gat	1104
Lys Pro Glu Met Lys Glu Leu Ile Asp Arg Val Thr Gly Gly Ala Asp	
355 360 365	
ctt gcg gtt gct gat tct tgg tca aac cca cag gct gtc gag tct gag	1152
Leu Ala Val Ala Asp Ser Trp Ser Asn Pro Gln Ala Val Glu Ser Glu	
370 375 380	
aag atc tgg aag gtg cgc aac aag ttc cgt gct gac cta gtg gag gtt	1200
Lys Ile Trp Lys Val Arg Asn Lys Phe Arg Ala Asp Leu Val Glu Val	
385 390 395 400	
gct cgc gct gca act gca aag tcc tgg tct cac cgt gga cac acc gaa	1248
Ala Arg Ala Ala Thr Ala Lys Ser Trp Ser His Arg Gly His Thr Glu	
405 410 415	
gca gaa ctt gcg tgg acc tcc cgc gtt ctg gat cca aac gtg ctg acc	1296
Ala Glu Leu Ala Trp Thr Ser Arg Val Leu Asp Pro Asn Val Leu Thr	
420 425 430	
att ggt ttc gca cgt cgc gta tcc acc tac aag cgc ttg acc ttg atg	1344
Ile Gly Phe Ala Arg Arg Val Ser Thr Tyr Lys Arg Leu Thr Leu Met	
435 440 445	
ctg cgc aac cct gaa cgc ctg cgt tcc atc ttg ctt aat gag gaa cgc	1392

Leu Arg Asn Pro Glu Arg Leu Arg Ser Ile Leu Leu Asn Glu Glu Arg	
450 455 460	
cca gtt cag ttc gtt att gct ggt aag gca cac cca cat gac atg ggt	1440
Pro Val Gln Phe Val Ile Ala Gly Lys Ala His Pro His Asp Met Gly	
465 470 475 480	
ggc aag aag ctc atg cag gaa atc gtc cac ttc gct gat caa gct ggt	1488
Gly Lys Lys Leu Met Gln Glu Ile Val His Phe Ala Asp Gln Ala Gly	
485 490 495	
gtc cgt gac cgt ttc ctc ttc ctg cct gat tac gac atc aac ctg gcc	1536
Val Arg Asp Arg Phe Leu Phe Leu Pro Asp Tyr Asp Ile Asn Leu Ala	
500 505 510	
agc tac ctg atc tct ggt gct gac gtg tgg ctg aac aac cca gtg cgc	1584
Ser Tyr Leu Ile Ser Gly Ala Asp Val Trp Leu Asn Asn Pro Val Arg	
515 520 525	
cct cag gaa gca tcg gga acc tcc ggt atg aag gcc gtc atg aat ggt	1632
Pro Gln Glu Ala Ser Gly Thr Ser Gly Met Lys Ala Val Met Asn Gly	
530 535 540	
ggc ctg acc ctg tcc atc tct gat ggt tgg tgg gat gaa atg cct aag	1680
Gly Leu Thr Leu Ser Ile Ser Asp Gly Trp Trp Asp Glu Met Pro Lys	
545 550 555 560	
gag acc acc ggc tgg acc atc cca acc gtt gag tcc cag gac ttg gaa	1728
Glu Thr Thr Gly Trp Thr Ile Pro Thr Val Glu Ser Gln Asp Leu Glu	
565 570 575	
tgc cgc gac cac ctg gaa tcc cag gcg ctg tac gac ctg ctg gaa aac	1776
Cys Arg Asp His Leu Glu Ser Gln Ala Leu Tyr Asp Leu Leu Glu Asn	
580 585 590	
gaa gtt gca ccg ctg ttt tac aag cgc gac aag aac ggc atc cca cag	1824
Glu Val Ala Pro Leu Phe Tyr Lys Arg Asp Lys Asn Gly Ile Pro Gln	
595 600 605	
gac tgg ctg gac ctg gtt cgc gaa tcc tgg acc acc ctg tca cca atg	1872
Asp Trp Leu Asp Leu Val Arg Glu Ser Trp Thr Thr Leu Ser Pro Met	
610 615 620	
gtc acc tcc acc cgc atg gtg cgc gac tac acc acc cag tac tac cgc	1920
Val Thr Ser Thr Arg Met Val Arg Asp Tyr Thr Thr Gln Tyr Tyr Arg	
625 630 635 640	
cca acc aaa cac cag gca gag ctc att gcg cag cct gca gaa gca gcg	1968
Pro Thr Lys His Gln Ala Glu Leu Ile Ala Gln Pro Ala Glu Ala Ala	
645 650 655	
gat tac gcg gca tgg ctt gag cac atc aaa gca gag tgg gct ggc gtc	2016
Asp Tyr Ala Ala Trp Leu Glu His Ile Lys Ala Glu Trp Ala Gly Val	
660 665 670	
aag gtc tca gac ctg aag atc agc gag agc gcc atc acg gcg cag gag	2064
Lys Val Ser Asp Leu Lys Ile Ser Glu Ser Ala Ile Thr Ala Gln Glu	
675 680 685	
ctt gaa gtc agc gtt cgc gtt gat tcc ggt tcg ctt aac gac gac gag	2112
Leu Glu Val Ser Val Arg Val Asp Ser Gly Ser Leu Asn Asp Asp Glu	

690	695	700	
ttc caa gct cag gca ctc ttt ggt gcg ctc gga cac aac ggt gac atc			2160
Phe Gln Ala Gln Ala Leu Phe Gly Ala Leu Gly His Asn Gly Asp Ile			
705	710	715	720
gaa gat cca gaa atc acc gtt ttg acc cca cgc ggc gat ggc gcc tac			2208
Glu Asp Pro Glu Ile Thr Val Leu Thr Pro Arg Gly Asp Gly Ala Tyr			
725	730		735
gcg gca aag gtc agc act gac ctg cca ggc aac tac ggc atc act gcc			2256
Ala Ala Lys Val Ser Thr Asp Leu Pro Gly Asn Tyr Gly Ile Thr Ala			
740	745		750
cgc gtt gtt cca aac aac agg atg ctg gtc agc cca gcg gaa acc cgc			2304
Arg Val Val Pro Asn Asn Arg Met Leu Val Ser Pro Ala Glu Thr Arg			
755	760		765
ctg atc acc tac ttg gag aac tagggcgaaa ctagctttac caa			2348
Leu Ile Thr Tyr Leu Glu Asn			
770	775		
<210> 374			
<211> 775			
<212> PRT			
<213> Corynebacterium glutamicum			
<400> 374			
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Asp Lys Leu Trp Tyr Gln Asp Thr Ala Asp Ala Thr Asp Ala Val Gly			
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Asp Pro Leu Val Ala Tyr Phe Ser Met Glu Phe Gly Ile His Pro Ser			
35	40		45
Leu Pro Ile Tyr Ser Gly Gly Leu Gly Val Leu Ala Gly Glu Asn Met			
50	55		60
Lys Ser Ala Ser Asp Leu Gly Val Pro Leu Ile Gly Val Gly Leu Leu			
65	70	75	80
Tyr Thr His Gly Tyr Phe Thr Gln Ser Leu Ser Gly Asp Gly Trp Gln			
85	90		95
Gln Glu Glu Tyr Lys Tyr His Asp Pro Ala Glu Leu Pro Ile Glu Ala			
100	105		110
Val Lys Asp Lys Asn Gly Glu Gln Val Thr Val Ser Val Thr Tyr Pro			
115	120		125
Gly Ala Gln Glu Val Lys Ile Ala Leu Trp Val Ala Asn Val Gly Arg			
130	135		140
Ile Pro Leu Leu Leu Leu Asp Thr Asn Ile Glu Ala Asn Pro Glu Glu			
145	150	155	160
Leu Arg Asn Val Thr Asp Arg Leu Tyr Gly Gly Asp Asn Glu His Arg			
165	170		175

Ile Lys Gln Glu Leu Val Leu Gly Val Gly Gly Val Arg Ala Val Asn
 180 185 190
 Ala Phe Cys Glu Ala Arg Gly Leu Lys Arg Ser Ser Val Ala His Leu
 195 200 205
 Asn Glu Gly His Ala Gly Phe Leu Thr Leu Glu Arg Ile Arg Glu Arg
 210 215 220
 Ile Ala Glu Gly Met Glu Tyr Pro Ala Ala Phe Glu Gln Val Arg Ala
 225 230 235 240
 Ser Asn Ile Phe Thr Thr His Thr Pro Val Pro Ala Gly Ile Asp Arg
 245 250 255
 Phe Asp Met Glu Met Val Arg Arg Tyr Leu Gly Gly Gly Gln Pro Glu
 260 265 270
 Asp Gln Gln Leu Cys Val Gly Val Pro Ile Glu Lys Ala Leu Glu Leu
 275 280 285
 Gly Gln Glu Ser Asp Pro His Arg Phe Asn Met Ala His Met Gly Leu
 290 295 300
 Arg Ala Ser Gln His Ala Asn Gly Val Ala Lys Leu His Gly Glu Val
 305 310 315 320
 Ser Arg Asp Met Phe Ala Gly Leu Tyr Pro Gly Tyr Glu Pro Arg Glu
 325 330 335
 Val Pro Ile Gly His Val Thr Asn Gly Val His Leu Pro Thr Trp Val
 340 345 350
 Lys Pro Glu Met Lys Glu Leu Ile Asp Arg Val Thr Gly Gly Ala Asp
 355 360 365
 Leu Ala Val Ala Asp Ser Trp Ser Asn Pro Gln Ala Val Glu Ser Glu
 370 375 380
 Lys Ile Trp Lys Val Arg Asn Lys Phe Arg Ala Asp Leu Val Glu Val
 385 390 395 400
 Ala Arg Ala Ala Thr Ala Lys Ser Trp Ser His Arg Gly His Thr Glu
 405 410 415
 Ala Glu Leu Ala Trp Thr Ser Arg Val Leu Asp Pro Asn Val Leu Thr
 420 425 430
 Ile Gly Phe Ala Arg Arg Val Ser Thr Tyr Lys Arg Leu Thr Leu Met
 435 440 445
 Leu Arg Asn Pro Glu Arg Leu Arg Ser Ile Leu Leu Asn Glu Glu Arg
 450 455 460
 Pro Val Gln Phe Val Ile Ala Gly Lys Ala His Pro His Asp Met Gly
 465 470 475 480
 Gly Lys Lys Leu Met Gln Glu Ile Val His Phe Ala Asp Gln Ala Gly
 485 490 495

Val Arg Asp Arg Phe Leu Phe Leu Pro Asp Tyr Asp Ile Asn Leu Ala
 500 505 510
 Ser Tyr Leu Ile Ser Gly Ala Asp Val Trp Leu Asn Asn Pro Val Arg
 515 520 525
 Pro Gln Glu Ala Ser Gly Thr Ser Gly Met Lys Ala Val Met Asn Gly
 530 535 540
 Gly Leu Thr Leu Ser Ile Ser Asp Gly Trp Trp Asp Glu Met Pro Lys
 545 550 555 560
 Glu Thr Thr Gly Trp Thr Ile Pro Thr Val Glu Ser Gln Asp Leu Glu
 565 570 575
 Cys Arg Asp His Leu Glu Ser Gln Ala Leu Tyr Asp Leu Leu Glu Asn
 580 585 590
 Glu Val Ala Pro Leu Phe Tyr Lys Arg Asp Lys Asn Gly Ile Pro Gln
 595 600 605
 Asp Trp Leu Asp Leu Val Arg Glu Ser Trp Thr Thr Leu Ser Pro Met
 610 615 620
 Val Thr Ser Thr Arg Met Val Arg Asp Tyr Thr Thr Gln Tyr Tyr Arg
 625 630 635 640
 Pro Thr Lys His Gln Ala Glu Leu Ile Ala Gln Pro Ala Glu Ala Ala
 645 650 655
 Asp Tyr Ala Ala Trp Leu Glu His Ile Lys Ala Glu Trp Ala Gly Val
 660 665 670
 Lys Val Ser Asp Leu Lys Ile Ser Glu Ser Ala Ile Thr Ala Gln Glu
 675 680 685
 Leu Glu Val Ser Val Arg Val Asp Ser Gly Ser Leu Asn Asp Asp Glu
 690 695 700
 Phe Gln Ala Gln Ala Leu Phe Gly Ala Leu Gly His Asn Gly Asp Ile
 705 710 715 720
 Glu Asp Pro Glu Ile Thr Val Leu Thr Pro Arg Gly Asp Gly Ala Tyr
 725 730 735
 Ala Ala Lys Val Ser Thr Asp Leu Pro Gly Asn Tyr Gly Ile Thr Ala
 740 745 750
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 755 760 765
 Leu Ile Thr Tyr Leu Glu Asn
 770 775

<210> 375

<211> 941

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (1)..(918)

<223> FRXA02100

<400> 375

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cag gaa atc gtc cac ttc gct gat caa gct ggt gtc cgt gac cgt ttc	96
Gln Glu Ile Val His Phe Ala Asp Gln Ala Gly Val Arg Asp Arg Phe	
20 25 30	
ctc ttc ctg cct gat tac gac atc aac ctg gcc agc tac ctg atc tct	144
Leu Phe Leu Pro Asp Tyr Asp Ile Asn Leu Ala Ser Tyr Leu Ile Ser	
35 40 45	
ggt gct gac gtg tgg ctg aac aac cca gtg cgc cct cag gaa gca tcg	192
Gly Ala Asp Val Trp Leu Asn Asn Pro Val Arg Pro Gln Glu Ala Ser	
50 55 60	
gga acc tcc ggt atg aag gcc gtc atg aat ggt ggc ctg acc ctg tcc	240
Gly Thr Ser Gly Met Lys Ala Val Met Asn Gly Gly Leu Thr Leu Ser	
65 70 75 80	
atc tct gat ggt tgg tgg gat gaa atg cct aag gag acc acc ggc tgg	288
Ile Ser Asp Gly Trp Trp Asp Glu Met Pro Lys Glu Thr Thr Gly Trp	
85 90 95	
acc atc cca acc gtt gag tcc cag gac ttg gaa tgc cgc gac cac ctg	336
Thr Ile Pro Thr Val Glu Ser Gln Asp Leu Glu Cys Arg Asp His Leu	
100 105 110	
gaa tcc cag gcg ctg tac gac ctg ctg gaa aac gaa gtt gca ccg ctg	384
Glu Ser Gln Ala Leu Tyr Asp Leu Leu Glu Asn Glu Val Ala Pro Leu	
115 120 125	
ttt tac aag cgc gac aag aac ggc atc cca cag gac tgg ctg gac ctg	432
Phe Tyr Lys Arg Asp Lys Asn Gly Ile Pro Gln Asp Trp Leu Asp Leu	
130 135 140	
gtt cgc gaa tcc tgg acc acc ctg tca cca atg gtc acc tcc acc cgc	480
Val Arg Glu Ser Trp Thr Thr Leu Ser Pro Met Val Thr Ser Thr Arg	
145 150 155 160	
atg gtg cgc gac tac acc acc cag tac tac cgc cca acc aaa cac cag	528
Met Val Arg Asp Tyr Thr Thr Gln Tyr Tyr Arg Pro Thr Lys His Gln	
165 170 175	
gca gag ctc att gcg cag cct gca gaa gca gcg gat tac gcg gca tgg	576
Ala Glu Leu Ile Ala Gln Pro Ala Glu Ala Ala Asp Tyr Ala Ala Trp	
180 185 190	
ctt gag cac atc aaa gca gag tgg gct ggc gtc aag gtc tca gac ctg	624
Leu Glu His Ile Lys Ala Glu Trp Ala Gly Val Lys Val Ser Asp Leu	
195 200 205	
aag atc agc gag agc gcc atc acg gcg cag gag ctt gaa gtc agc gtt	672
Lys Ile Ser Glu Ser Ala Ile Thr Ala Gln Glu Leu Glu Val Ser Val	
210 215 220	

cgc gtt gat tcc ggt tcg ctt aac gac gac gag ttc caa gct cag gca 720
 Arg Val Asp Ser Gly Ser Leu Asn Asp Asp Glu Phe Gln Ala Gln Ala
 225 230 235 240

ctc ttt ggt gcg ctc gga cac aac ggt gac atc gaa gat cca gaa atc 768
 Leu Phe Gly Ala Leu Gly His Asn Gly Asp Ile Glu Asp Pro Glu Ile
 245 250 255

acc gtt ttg acc cca cgc ggc gat ggc gcc tac gcg gca aag gtc agc 816
 Thr Val Leu Thr Pro Arg Gly Asp Gly Ala Tyr Ala Ala Lys Val Ser
 260 265 270

act gac ctg cca ggc aac tac ggc atc act gcc cgc gtt gtt cca aac 864
 Thr Asp Leu Pro Gly Asn Tyr Gly Ile Thr Ala Arg Val Val Pro Asn
 275 280 285

aac agg atg ctg gtc agc cca gcg gaa acc cgc ctg atc acc tac ttg 912
 Asn Arg Met Leu Val Ser Pro Ala Glu Thr Arg Leu Ile Thr Tyr Leu
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 Glu Asn
 305

<210> 376
 <211> 306
 <212> PRT
 <213> Corynebacterium glutamicum

<400> 376
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Leu Phe Leu Pro Asp Tyr Asp Ile Asn Leu Ala Ser Tyr Leu Ile Ser
 35 40 45

Gly Ala Asp Val Trp Leu Asn Asn Pro Val Arg Pro Gln Glu Ala Ser
 50 55 60

Gly Thr Ser Gly Met Lys Ala Val Met Asn Gly Gly Leu Thr Leu Ser
 65 70 75 80

Ile Ser Asp Gly Trp Trp Asp Glu Met Pro Lys Glu Thr Thr Gly Trp
 85 90 95

Thr Ile Pro Thr Val Glu Ser Gln Asp Leu Glu Cys Arg Asp His Leu
 100 105 110

Glu Ser Gln Ala Leu Tyr Asp Leu Leu Glu Asn Glu Val Ala Pro Leu
 115 120 125

Phe Tyr Lys Arg Asp Lys Asn Gly Ile Pro Gln Asp Trp Leu Asp Leu
 130 135 140

Val Arg Glu Ser Trp Thr Thr Leu Ser Pro Met Val Thr Ser Thr Arg
 145 150 155 160

Met Val Arg Asp Tyr Thr Thr Gln Tyr Tyr Arg Pro Thr Lys His Gln
 165 170 175

Ala Glu Leu Ile Ala Gln Pro Ala Glu Ala Ala Asp Tyr Ala Ala Trp
 180 185 190

Leu Glu His Ile Lys Ala Glu Trp Ala Gly Val Lys Val Ser Asp Leu
 195 200 205

Lys Ile Ser Glu Ser Ala Ile Thr Ala Gln Glu Leu Glu Val Ser Val
 210 215 220

Arg Val Asp Ser Gly Ser Leu Asn Asp Asp Glu Phe Gln Ala Gln Ala
 225 230 235 240

Leu Phe Gly Ala Leu Gly His Asn Gly Asp Ile Glu Asp Pro Glu Ile
 245 250 255

Thr Val Leu Thr Pro Arg Gly Asp Gly Ala Tyr Ala Ala Lys Val Ser
 260 265 270

Thr Asp Leu Pro Gly Asn Tyr Gly Ile Thr Ala Arg Val Val Pro Asn
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Glu Asn
 305

<210> 377
 <211> 1206
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
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 <222> (1)..(1206)
 <223> FRXA02113

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gac aag ctg tgg tac cag gac acc gca gat gca acc gat gct gtc gga 96
 Asp Lys Leu Trp Tyr Gln Asp Thr Ala Asp Ala Thr Asp Ala Val Gly
 20 25 30

gat cca ctc gtt gcg tac ttc tcc atg gag ttt ggc att cac cca agc 144
 Asp Pro Leu Val Ala Tyr Phe Ser Met Glu Phe Gly Ile His Pro Ser
 35 40 45

ctg cca atc tac tct ggc gga ctt ggt gtg ctt gcg ggc gag aac atg 192
 Leu Pro Ile Tyr Ser Gly Gly Leu Gly Val Leu Ala Gly Glu Asn Met
 50 55 60

aag tct gca tct gac ttg ggt gtg cca ctg atc ggt gtt ggt ttg ctc 240
 Lys Ser Ala Ser Asp Leu Gly Val Pro Leu Ile Gly Val Gly Leu Leu
 65 70 75 80

tac acc cac ggc tac ttc acc cag tca ctg tcc ggt gac ggt tgg cag	288
Tyr Thr His Gly Tyr Phe Thr Gln Ser Leu Ser Gly Asp Gly Trp Gln	
85 90 95	
cag gaa gag tac aag tac cac gat cca gca gaa ctg ccg att gag gca	336
Gln Glu Glu Tyr Lys Tyr His Asp Pro Ala Glu Leu Pro Ile Glu Ala	
100 105 110	
gtt aaa gat aag aac ggc gag cag gtc act gtt tct gtc acc tac cca	384
Val Lys Asp Lys Asn Gly Glu Gln Val Thr Val Ser Val Thr Tyr Pro	
115 120 125	
ggt gcg cag gaa gta aag att gca ctg tgg gta gca aac gtt ggc cgc	432
Gly Ala Gln Glu Val Lys Ile Ala Leu Trp Val Ala Asn Val Gly Arg	
130 135 140	
atc cca ttg ctg ctg ctt gat acc aac atc gag gca aac cca gaa gag	480
Ile Pro Leu Leu Leu Asp Thr Asn Ile Glu Ala Asn Pro Glu Glu	
145 150 155 160	
ctc cgc aac gtt act gac cgc ctg tac ggt ggc gac aat gag cac cgc	528
Leu Arg Asn Val Thr Asp Arg Leu Tyr Gly Gly Asp Asn Glu His Arg	
165 170 175	
atc aag cag gaa ctc gtt ctc ggt gtt ggt ggc gtc cgc gct gtc aac	576
Ile Lys Gln Glu Leu Val Leu Gly Val Gly Gly Val Arg Ala Val Asn	
180 185 190	
gca ttc tgc gaa gct cgt ggt ctg aag cgc tca tct gtt gca cac ctc	624
Ala Phe Cys Glu Ala Arg Gly Leu Lys Arg Ser Ser Val Ala His Leu	
195 200 205	
aac gaa ggc cac gca ggt ttc ctg acc ctg gag cgt atc cgc gag cgc	672
Asn Glu Gly His Ala Gly Phe Leu Thr Leu Glu Arg Ile Arg Glu Arg	
210 215 220	
atc gca gag ggc atg gag tac cca gca gca ttc gag cag gtt cgt gcg	720
Ile Ala Glu Gly Met Glu Tyr Pro Ala Ala Phe Glu Gln Val Arg Ala	
225 230 235 240	
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Ser Asn Ile Phe Thr Thr His Thr Pro Val Pro Ala Gly Ile Asp Arg	
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Phe Asp Met Glu Met Val Arg Arg Tyr Leu Gly Gly Gly Gln Pro Glu	
260 265 270	
gat cag cag ctg tgc gtt ggt gtt cca att gag aag gca ctt gag ctt	864
Asp Gln Gln Leu Cys Val Gly Val Pro Ile Glu Lys Ala Leu Glu Leu	
275 280 285	
ggt caa gag tcc gat cca cac cgc ttc aac atg gct cat atg ggc ctt	912
Gly Gln Glu Ser Asp Pro His Arg Phe Asn Met Ala His Met Gly Leu	
290 295 300	
cgc gcg agc caa cat gct aat ggc gtc gca aag ctt cat ggt gaa gta	960
Arg Ala Ser Gln His Ala Asn Gly Val Ala Lys Leu His Gly Glu Val	
305 310 315 320	

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agc cgt gac atg ttc gcc ggc ctg tac ccc gga tat gag cct cgt gaa 1008
Ser Arg Asp Met Phe Ala Gly Leu Tyr Pro Gly Tyr Glu Pro Arg Glu
                325                      330                      335

gtg ccc atc ggg cac gtc acc aac ggt gtt cac ctg ccg acg tgg gtc 1056
Val Pro Ile Gly His Val Thr Asn Gly Val His Leu Pro Thr Trp Val
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aag cca gag atg aag gaa ctc atc gat cgc gtc act ggc ggc gct gat 1104
Lys Pro Glu Met Lys Glu Leu Ile Asp Arg Val Thr Gly Gly Ala Asp
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ctt gcg gtt gct gat tct tgg tca aac cca cag gct gtc gag tct gag 1152
Leu Ala Val Ala Asp Ser Trp Ser Asn Pro Gln Ala Val Glu Ser Glu
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aag atc tgg aag gtg cgc aac aag ttc cgt gct gac cta gtg gag gtt 1200
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gct cgc
Ala Arg
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<212> PRT

<213> Corynebacterium glutamicum

<400> 378

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Asp Pro Leu Val Ala Tyr Phe Ser Met Glu Phe Gly Ile His Pro Ser
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Leu Pro Ile Tyr Ser Gly Gly Leu Gly Val Leu Ala Gly Glu Asn Met
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Lys Ser Ala Ser Asp Leu Gly Val Pro Leu Ile Gly Val Gly Leu Leu
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Tyr Thr His Gly Tyr Phe Thr Gln Ser Leu Ser Gly Asp Gly Trp Gln
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Gln Glu Glu Tyr Lys Tyr His Asp Pro Ala Glu Leu Pro Ile Glu Ala
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Val Lys Asp Lys Asn Gly Glu Gln Val Thr Val Ser Val Thr Tyr Pro
115                      120                      125

Gly Ala Gln Glu Val Lys Ile Ala Leu Trp Val Ala Asn Val Gly Arg
130                      135                      140

Ile Pro Leu Leu Leu Leu Asp Thr Asn Ile Glu Ala Asn Pro Glu Glu
145                      150                      155                      160

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Leu Arg Asn Val Thr Asp Arg Leu Tyr Gly Gly Asp Asn Glu His Arg
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 Ile Lys Gln Glu Leu Val Leu Gly Val Gly Gly Val Arg Ala Val Asn
 180 185 190
 Ala Phe Cys Glu Ala Arg Gly Leu Lys Arg Ser Ser Val Ala His Leu
 195 200 205
 Asn Glu Gly His Ala Gly Phe Leu Thr Leu Glu Arg Ile Arg Glu Arg
 210 215 220
 Ile Ala Glu Gly Met Glu Tyr Pro Ala Ala Phe Glu Gln Val Arg Ala
 225 230 235 240
 Ser Asn Ile Phe Thr Thr His Thr Pro Val Pro Ala Gly Ile Asp Arg
 245 250 255
 Phe Asp Met Glu Met Val Arg Arg Tyr Leu Gly Gly Gly Gln Pro Glu
 260 265 270
 Asp Gln Gln Leu Cys Val Gly Val Pro Ile Glu Lys Ala Leu Glu Leu
 275 280 285
 Gly Gln Glu Ser Asp Pro His Arg Phe Asn Met Ala His Met Gly Leu
 290 295 300
 Arg Ala Ser Gln His Ala Asn Gly Val Ala Lys Leu His Gly Glu Val
 305 310 315 320
 Ser Arg Asp Met Phe Ala Gly Leu Tyr Pro Gly Tyr Glu Pro Arg Glu
 325 330 335
 Val Pro Ile Gly His Val Thr Asn Gly Val His Leu Pro Thr Trp Val
 340 345 350
 Lys Pro Glu Met Lys Glu Leu Ile Asp Arg Val Thr Gly Gly Ala Asp
 355 360 365
 Leu Ala Val Ala Asp Ser Trp Ser Asn Pro Gln Ala Val Glu Ser Glu
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 Lys Ile Trp Lys Val Arg Asn Lys Phe Arg Ala Asp Leu Val Glu Val
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Ala Arg

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 <223> RXA02147

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Met Phe Gly Arg Arg	
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tgg gtg agc gtt gtg gcg tca tgt gtt atc gca agc acg ctg att ctg	163
Trp Val Ser Val Val Ala Ser Cys Val Ile Ala Ser Thr Leu Ile Leu	
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Val Pro Ser His Ser Gly Ala Glu Glu Val Asp Gln Leu Ile Ala Asp	
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atc gag cat gtc tct cag gaa acg tct gcc cag aat gag gaa gtc aaa	259
Ile Glu His Val Ser Gln Glu Thr Ser Ala Gln Asn Glu Glu Val Lys	
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Gln Leu Glu Ile Asp Ile Glu Ala Arg Glu Val Thr Ile Lys Glu Val	
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cag gag cag tcg gta agc tac cgt gag gcg gct gat caa gca tcg gag	355
Gln Glu Gln Ser Val Ser Tyr Arg Glu Ala Ala Asp Gln Ala Ser Glu	
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aat gtc gaa gct tat cgt tcg gag atc aat cgg atc gct cag gcg aag	403
Asn Val Glu Ala Tyr Arg Ser Glu Ile Asn Arg Ile Ala Gln Ala Lys	
90 95 100	
tat cgt ggc aca gtc acg gat cct ttg agc att gcg gtg tct gca gaa	451
Tyr Arg Gly Thr Val Thr Asp Pro Leu Ser Ile Ala Val Ser Ala Glu	
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Asp Pro Gln Asn Val Ile Asp Arg Met Ser Tyr Leu Ser Thr Leu Thr	
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aag tcc act agt gat gtg gtt gaa tcc ctc aac gcg gag act gag aag	547
Lys Ser Thr Ser Asp Val Val Glu Ser Leu Asn Ala Glu Thr Glu Lys	
135 140 145	
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Ser Ala Glu Ala Val Tyr Gln Ala Asn Arg Thr Lys Ala Glu Ala Glu	
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Phe Gln Leu Gly Gln Leu Lys Val Arg Gln Ala Glu Leu Glu Ser Glu	
170 175 180	
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Lys Glu Ala Leu Asp Gly Arg Lys Ser Glu Ile Arg Asp Arg Val Asp	
185 190 195	
gcc ctg acg cca cag gag cgg gaa atg tgg gtt gct aag aat ggt cca	739
Ala Leu Thr Pro Gln Glu Arg Glu Met Trp Val Ala Lys Asn Gly Pro	
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ttg gac att gat ctg act gat ttg ctt ggt ctt tcc gct gcg act tcg	787
Leu Asp Ile Asp Leu Thr Asp Leu Leu Gly Leu Ser Ala Ala Thr Ser	
215 220 225	

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 Gly Ala Val Asp Ala Ala Leu Ser Lys Leu Gly Ser Pro Tyr Gly Trp
 230 235 240 245
 ggt ggc att ggc cca aat gag ttt gat tgc tca ggt ttg atc tat tgg 883
 Gly Gly Ile Gly Pro Asn Glu Phe Asp Cys Ser Gly Leu Ile Tyr Trp
 250 255 260
 gcg tat cag cag atg ggt aag act ttg cca cgt acg tct caa gct cag 931
 Ala Tyr Gln Gln Met Gly Lys Thr Leu Pro Arg Thr Ser Gln Ala Gln
 265 270 275
 atg gct ggc gga acg ccg gtg agc aga gat gag ctg cag cct ggc gat 979
 Met Ala Gly Gly Thr Pro Val Ser Arg Asp Glu Leu Gln Pro Gly Asp
 280 285 290
 gtc att gga tat tac cca ggt gct act cac gtg gga ctg tat att ggg 1027
 Val Ile Gly Tyr Tyr Pro Gly Ala Thr His Val Gly Leu Tyr Ile Gly
 295 300 305
 gac gga aag att gtg cac gcc tca gac tac gga atc cct gtg cag gtg 1075
 Asp Gly Lys Ile Val His Ala Ser Asp Tyr Gly Ile Pro Val Gln Val
 310 315 320 325
 gta tct gtt gat tca gca ccg ttt tat ggt gcg cgt cgc tac 1117
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 <213> Corynebacterium glutamicum

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 Asn Glu Glu Val Lys Gln Leu Glu Ile Asp Ile Glu Ala Arg Glu Val
 50 55 60
 Thr Ile Lys Glu Val Gln Glu Gln Ser Val Ser Tyr Arg Glu Ala Ala
 65 70 75 80
 Asp Gln Ala Ser Glu Asn Val Glu Ala Tyr Arg Ser Glu Ile Asn Arg
 85 90 95
 Ile Ala Gln Ala Lys Tyr Arg Gly Thr Val Thr Asp Pro Leu Ser Ile
 100 105 110
 Ala Val Ser Ala Glu Asp Pro Gln Asn Val Ile Asp Arg Met Ser Tyr
 115 120 125

Leu Ser Thr Leu Thr Lys Ser Thr Ser Asp Val Val Glu Ser Leu Asn
 130 135 140
 Ala Glu Thr Glu Lys Ser Ala Glu Ala Val Tyr Gln Ala Asn Arg Thr
 145 150 155 160
 Lys Ala Glu Ala Glu Phe Gln Leu Gly Gln Leu Lys Val Arg Gln Ala
 165 170 175
 Glu Leu Glu Ser Glu Lys Glu Ala Leu Asp Gly Arg Lys Ser Glu Ile
 180 185 190
 Arg Asp Arg Val Asp Ala Leu Thr Pro Gln Glu Arg Glu Met Trp Val
 195 200 205
 Ala Lys Asn Gly Pro Leu Asp Ile Asp Leu Thr Asp Leu Leu Gly Leu
 210 215 220
 Ser Ala Ala Thr Ser Gly Ala Val Asp Ala Ala Leu Ser Lys Leu Gly
 225 230 235 240
 Ser Pro Tyr Gly Trp Gly Gly Ile Gly Pro Asn Glu Phe Asp Cys Ser
 245 250 255
 Gly Leu Ile Tyr Trp Ala Tyr Gln Gln Met Gly Lys Thr Leu Pro Arg
 260 265 270
 Thr Ser Gln Ala Gln Met Ala Gly Gly Thr Pro Val Ser Arg Asp Glu
 275 280 285
 Leu Gln Pro Gly Asp Val Ile Gly Tyr Tyr Pro Gly Ala Thr His Val
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 Met Thr Ile Pro Gly
 1 5
 gct tcc aca cag act gat atc cct ctg gac aca ctt ctt gag gat tac 163

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Ser	Leu	Asp	Trp	Leu	Cys	Leu	Pro	Arg	Phe	Asp	Ser	Gln	Ala	Met	Phe	
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Thr	Arg	Leu	Leu	Gly	Asp	Arg	Glu	His	Gly	His	Trp	Ser	Leu	Arg	Val	
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Pro	Gly	Gly	Glu	Val	Ile	Ser	Gln	Asn	Tyr	Leu	Gly	Asp	Ser	Phe	Val	
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gtg	cag	acc	gtg	tgg	cgt	tca	gag	acc	ggg	act	gcc	cgg	gtt	gtt	gat	403
Val	Gln	Thr	Val	Trp	Arg	Ser	Glu	Thr	Gly	Thr	Ala	Arg	Val	Val	Asp	
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Phe	Met	Pro	Ile	His	Gly	Gln	Glu	Gln	Pro	Asp	Ile	Thr	Asp	Leu	Val	
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Arg	Ser	Val	His	Cys	Val	Glu	Gly	Glu	Val	Asp	Val	Glu	Ser	Ile	Leu	
		120					125					130				
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Arg	Leu	Arg	Phe	Asp	Tyr	Gly	Glu	Ser	Thr	Pro	Tyr	Phe	Arg	Thr	Ser	
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act	gtc	gac	ggc	atc	agc	atc	gtg	cag	gct	gtc	gcc	ggc	ccc	aat	gcg	595
Thr	Val	Asp	Gly	Ile	Ser	Ile	Val	Gln	Ala	Val	Ala	Gly	Pro	Asn	Ala	
	150				155					160					165	
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Val	Tyr	Val	Arg	Gly	Pro	Glu	Met	Pro	His	Arg	Pro	Ala	Lys	Asp	Cys	
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cac	agt	ggc	acc	ttc	cac	ctg	acg	gcc	ggc	gaa	tcc	gtg	gaa	tgg	gtt	691
His	Ser	Gly	Thr	Phe	His	Leu	Thr	Ala	Gly	Glu	Ser	Val	Glu	Trp	Val	
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ctc	acc	tgg	gca	cgg	tcg	ttc	gaa	cgg	cat	ccc	ccc	atg	cgg	gat	tac	739
Leu	Thr	Trp	Ala	Pro	Ser	Phe	Glu	Pro	His	Pro	Pro	Met	Pro	Asp	Tyr	
		200					205					210				
acc	cgc	tct	ttg	gag	agc	acc	ttg	agc	ttc	tgg	gca	tca	tgg	gtt	gaa	787
Thr	Arg	Ser	Leu	Glu	Ser	Thr	Leu	Ser	Phe	Trp	Ala	Ser	Trp	Val	Glu	
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Glu	Leu	Pro	His	Gln	Arg	Leu	Tyr	Asp	Ala	Glu	Val	Arg	Arg	Ser	Met	
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Leu	Val	Leu	Arg	Ala	Leu	Thr	Asp	Leu	Gln	Thr	Gly	Gly	Ile	Val	Ala	

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Ala	Pro	Thr	Thr	Ser	Leu	Pro	Glu	Asp	Phe	Gly	Gly	Ile	Arg	Asn	Trp					
265					270					275										
gac	tac	cgc	tac	gtg	tgg	ctg	cgc	gac	tcc	gca	ctc	acc	att	gaa	gcc	979				
Asp	Tyr	Arg	Tyr	Val	Trp	Leu	Arg	Asp	Ser	Ala	Leu	Thr	Ile	Glu	Ala					
280					285					290										
ctc	gtg	gaa	tac	gga	ttc	tcc	caa	gca	gcc	ctc	caa	tgg	cgc	acc	tgg	1027				
Leu	Val	Glu	Tyr	Gly	Phe	Ser	Gln	Ala	Ala	Leu	Gln	Trp	Arg	Thr	Trp					
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Gly	Leu	Gly	Gly	Glu	Arg	His	Leu	Pro	Glu	Arg	Glu	Leu	Gln	His	Leu					
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Thr	Ile	Arg	Arg	Ala	Gly	Cys	Leu	Glu	Asp	Glu	Phe	Ser	Trp	Gly	Met					
375	380					385														
caa	aaa	gcc	atc	ctc	gat	ttc	caa	gaa	gcc	aac	ttc	gac	cgc	aag	gat	1315				
Gln	Lys	Ala	Ile	Leu	Asp	Phe	Gln	Glu	Ala	Asn	Phe	Asp	Arg	Lys	Asp					
390	395					400					405									
caa	ggc	atc	tgg	gaa	atg	cgc	tcc	gaa	ccg	caa	tat	ttc	acc	cac	ggc	1363				
Gln	Gly	Ile	Trp	Glu	Met	Arg	Ser	Glu	Pro	Gln	Tyr	Phe	Thr	His	Gly					
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cgc	gcc	atg	atg	tgg	gcc	ggc	ttc	gac	cgc	ggc	atc	aaa	gcc	atc	gaa	1411				
Arg	Ala	Met	Met	Trp	Ala	Gly	Phe	Asp	Arg	Gly	Ile	Lys	Ala	Ile	Glu					
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gaa	ttc	aac	ctc	gac	ggc	ccc	atc	gag	cgc	tgg	cgt	gaa	ctc	cgc	gcc	1459				
Glu	Phe	Asn	Leu	Asp	Gly	Pro	Ile	Glu	Arg	Trp	Arg	Glu	Leu	Arg	Ala					
440					445					450										
aaa	ctc	cgc	gaa	gaa	atc	atg	acc	aac	ggc	ttc	aac	gaa	gag	atc	caa	1507				
Lys	Leu	Arg	Glu	Glu	Ile	Met	Thr	Asn	Gly	Phe	Asn	Glu	Glu	Ile	Gln					
455					460					465										
tcc	ttc	acc	cag	tgc	tac	gac	aac	acc	caa	gtc	gac	gcc	tcg	ctg	ctt	1555				
Ser	Phe	Thr	Gln	Cys	Tyr	Asp	Asn	Thr	Gln	Val	Asp	Ala	Ser	Leu	Leu					
470	475					480					485									
cag	ctc	gcc	caa	ata	ggc	ttc	atc	ggc	ttc	gac	gat	cca	aaa	atg	ctc	1603				
Gln	Leu	Ala	Gln	Ile	Gly	Phe	Ile	Gly	Phe	Asp	Asp	Pro	Lys	Met	Leu					
490					495					500										

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 Ser Thr Val Ala Arg Ile Glu Gln Glu Leu Leu Asp Ala His Gly Phe
 505 510 515

 ctt cac agg tac cac acc gac ggg tct gac ggc ctt gcc ggc gac gaa 1699
 Leu His Arg Tyr His Thr Asp Gly Ser Asp Gly Leu Ala Gly Asp Glu
 520 525 530

 tac ccc ttc ctc atc tgt tca ttc tgg ctg gta gaa caa tac gca agc 1747
 Tyr Pro Phe Leu Ile Cys Ser Phe Trp Leu Val Glu Gln Tyr Ala Ser
 535 540 545

 tcc aac cgc ctc gac gag gcc aaa gaa aag atg aac cgc atc ctt gcc 1795
 Ser Asn Arg Leu Asp Glu Ala Lys Glu Lys Met Asn Arg Ile Leu Ala
 550 555 560 565

 gtc caa agc cca ctt ggc cta ctg gct gag gaa tac tcc acc cac cat 1843
 Val Gln Ser Pro Leu Gly Leu Leu Ala Glu Glu Tyr Ser Thr His His
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 ggc agg ctc gct gga aac tac cct cag gcc ttt tcc cac att ggt ctg 1891
 Gly Arg Leu Ala Gly Asn Tyr Pro Gln Ala Phe Ser His Ile Gly Leu
 585 590 595

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<211> 612

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 382

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 35 40 45

 Ser Gln Ala Met Phe Thr Arg Leu Leu Gly Asp Arg Glu His Gly His
 50 55 60

 Trp Ser Leu Arg Val Pro Gly Gly Glu Val Ile Ser Gln Asn Tyr Leu
 65 70 75 80

 Gly Asp Ser Phe Val Val Gln Thr Val Trp Arg Ser Glu Thr Gly Thr
 85 90 95

 Ala Arg Val Val Asp Phe Met Pro Ile His Gly Gln Glu Gln Pro Asp
 100 105 110

 Ile Thr Asp Leu Val Arg Ser Val His Cys Val Glu Gly Glu Val Asp
 115 120 125

Val Glu Ser Ile Leu Arg Leu Arg Phe Asp Tyr Gly Glu Ser Thr Pro
 130 135 140
 Tyr Phe Arg Thr Ser Thr Val Asp Gly Ile Ser Ile Val Gln Ala Val
 145 150 155 160
 Ala Gly Pro Asn Ala Val Tyr Val Arg Gly Pro Glu Met Pro His Arg
 165 170 175
 Pro Ala Lys Asp Cys His Ser Gly Thr Phe His Leu Thr Ala Gly Glu
 180 185 190
 Ser Val Glu Trp Val Leu Thr Trp Ala Pro Ser Phe Glu Pro His Pro
 195 200 205
 Pro Met Pro Asp Tyr Thr Arg Ser Leu Glu Ser Thr Leu Ser Phe Trp
 210 215 220
 Ala Ser Trp Val Glu Glu Leu Pro His Gln Arg Leu Tyr Asp Ala Glu
 225 230 235 240
 Val Arg Arg Ser Met Leu Val Leu Arg Ala Leu Thr Asp Leu Gln Thr
 245 250 255
 Gly Gly Ile Val Ala Ala Pro Thr Thr Ser Leu Pro Glu Asp Phe Gly
 260 265 270
 Gly Ile Arg Asn Trp Asp Tyr Arg Tyr Val Trp Leu Arg Asp Ser Ala
 275 280 285
 Leu Thr Ile Glu Ala Leu Val Glu Tyr Gly Phe Ser Gln Ala Ala Leu
 290 295 300
 Gln Trp Arg Thr Trp Leu Leu Arg Ala Ile Ala Gly Asp Pro Glu Asn
 305 310 315 320
 Leu Arg Ile Met Tyr Gly Leu Gly Gly Glu Arg His Leu Pro Glu Arg
 325 330 335
 Glu Leu Gln His Leu Arg Gly Tyr Glu Asn Ser Val Pro Val Arg Val
 340 345 350
 Gly Asn Gly Ala Ala Glu Gln Tyr Gln Ala Asp Val Val Gly Glu Val
 355 360 365
 Met Val Ala Leu Glu Thr Ile Arg Arg Ala Gly Cys Leu Glu Asp Glu
 370 375 380
 Phe Ser Trp Gly Met Gln Lys Ala Ile Leu Asp Phe Gln Glu Ala Asn
 385 390 395 400
 Phe Asp Arg Lys Asp Gln Gly Ile Trp Glu Met Arg Ser Glu Pro Gln
 405 410 415
 Tyr Phe Thr His Gly Arg Ala Met Met Trp Ala Gly Phe Asp Arg Gly
 420 425 430
 Ile Lys Ala Ile Glu Glu Phe Asn Leu Asp Gly Pro Ile Glu Arg Trp
 435 440 445

Arg Glu Leu Arg Ala Lys Leu Arg Glu Glu Ile Met Thr Asn Gly Phe
 450 455 460
 Asn Glu Glu Ile Gln Ser Phe Thr Gln Cys Tyr Asp Asn Thr Gln Val
 465 470 475 480
 Asp Ala Ser Leu Leu Gln Leu Ala Gln Ile Gly Phe Ile Gly Phe Asp
 485 490 495
 Asp Pro Lys Met Leu Ser Thr Val Ala Arg Ile Glu Gln Glu Leu Leu
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 Asp Ala His Gly Phe Leu His Arg Tyr His Thr Asp Gly Ser Asp Gly
 515 520 525
 Leu Ala Gly Asp Glu Tyr Pro Phe Leu Ile Cys Ser Phe Trp Leu Val
 530 535 540
 Glu Gln Tyr Ala Ser Ser Asn Arg Leu Asp Glu Ala Lys Glu Lys Met
 545 550 555 560
 Asn Arg Ile Leu Ala Val Gln Ser Pro Leu Gly Leu Leu Ala Glu Glu
 565 570 575
 Tyr Ser Thr His His Gly Arg Leu Ala Gly Asn Tyr Pro Gln Ala Phe
 580 585 590
 Ser His Ile Gly Leu Ile Ser Ala Ala Arg Ala Ile Asn Phe Glu Glu
 595 600 605
 Ala Arg Asn Arg
 610

<210> 383
 <211> 658
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(658)
 <223> RXA01888

<400> 383
 agtagatact agataccacc cattgatgcc gtcaaggggt ttcctgtaaa gatgtaagag 60
 attaagaaaa gaggtagata tggcgtcaaa gcgaccgaca atg gct gat gtg gca 115
 Met Ala Asp Val Ala
 1 5
 aaa gct gct gga gta tcc act gcg ctg gtc tcc atc gtg ttt cgc gat 163
 Lys Ala Ala Gly Val Ser Thr Ala Leu Val Ser Ile Val Phe Arg Asp
 10 15 20
 gcc ccc gga gca agt gaa tcc acc cgc aac cat gtg aaa gaa aaa gcc 211
 Ala Pro Gly Ala Ser Glu Ser Thr Arg Asn His Val Lys Glu Lys Ala
 25 30 35
 gcc gaa ctc gga tac att cct gat cga cga gcc caa aaa ctt cgc caa 259
 Ala Glu Leu Gly Tyr Ile Pro Asp Arg Arg Ala Gln Lys Leu Arg Gln

40	45	50	
aac cgc tcc gga ctc atc ggt gtg gca ttc gaa atg cac caa gca ttc			307
Asn Arg Ser Gly Leu Ile Gly Val Ala Phe Glu Met His Gln Ala Phe			
55	60	65	
cac ggc gat atc gtc gaa cac ctc tat ccc acc gcc cga aaa cat ggc			355
His Gly Asp Ile Val Glu His Leu Tyr Pro Thr Ala Arg Lys His Gly			
70	75	80	85
ttc gac ctg tac ctt agc gcg atc aca ccg act cgc act gaa aaa gat			403
Phe Asp Leu Tyr Leu Ser Ala Ile Thr Pro Thr Arg Thr Glu Lys Asp			
	90	95	100
gcc gtc aac gcc ctg atc agg gaa cga tgc gaa gca gta att ctt cta			451
Ala Val Asn Ala Leu Ile Arg Glu Arg Cys Glu Ala Val Ile Leu Leu			
	105	110	115
gga tct cgc atg tca cct agt gat ttg gaa aca atc gca cag caa ctt			499
Gly Ser Arg Met Ser Pro Ser Asp Leu Glu Thr Ile Ala Gln Gln Leu			
	120	125	130
ccc gtc caa gta att gcc cgc ggt tcc gga acc ccc aaa gtc agt tcc			547
Pro Val Gln Val Ile Ala Arg Gly Ser Gly Thr Pro Lys Val Ser Ser			
	135	140	145
gtc cat gtc gac gac gca gtt ggc gcc caa tta gcc ctc aac cac ctc			595
Val His Val Asp Asp Ala Val Gly Ala Gln Leu Ala Leu Asn His Leu			
150	155	160	165
atc gaa tta ggc cac gaa cac atc atc tac atc gat ggt ggc gac gcc			643
Ile Glu Leu Gly His Glu His Ile Ile Tyr Ile Asp Gly Gly Asp Ala			
	170	175	180
cct ggc acc cag gaa			658
Pro Gly Thr Gln Glu			
	185		

<210> 384

<211> 186

<212> PRT

<213> Corynebacterium glutamicum

<400> 384

Met Ala Asp Val Ala Lys Ala Ala Gly Val Ser Thr Ala Leu Val Ser
1 5 10 15

Ile Val Phe Arg Asp Ala Pro Gly Ala Ser Glu Ser Thr Arg Asn His
20 25 30

Val Lys Glu Lys Ala Ala Glu Leu Gly Tyr Ile Pro Asp Arg Arg Ala
35 40 45

Gln Lys Leu Arg Gln Asn Arg Ser Gly Leu Ile Gly Val Ala Phe Glu
50 55 60

Met His Gln Ala Phe His Gly Asp Ile Val Glu His Leu Tyr Pro Thr
65 70 75 80

Ala Arg Lys His Gly Phe Asp Leu Tyr Leu Ser Ala Ile Thr Pro Thr

85	90	95
Arg Thr Glu Lys Asp Ala Val Asn Ala Leu Ile Arg Glu Arg Cys Glu 100 105 110		
Ala Val Ile Leu Leu Gly Ser Arg Met Ser Pro Ser Asp Leu Glu Thr 115 120 125		
Ile Ala Gln Gln Leu Pro Val Gln Val Ile Ala Arg Gly Ser Gly Thr 130 135 140		
Pro Lys Val Ser Ser Val His Val Asp Asp Ala Val Gly Ala Gln Leu 145 150 155 160		
Ala Leu Asn His Leu Ile Glu Leu Gly His Glu His Ile Ile Tyr Ile 165 170 175		
Asp Gly Gly Asp Ala Pro Gly Thr Gln Glu 180 185		
 <210> 385 <211> 1503 <212> DNA <213> Corynebacterium glutamicum		
 <220> <221> CDS <222> (101)..(1480) <223> RXN01927		
 <400> 385 gagcagcggg atcttttgcg taattcgcgc gcgcagatcc atgtgattga ccacaatggg 60		
gatgaaattt tggatacccc aacggaagag gatttttaag atg gct ttg gtt ctt 115 Met Ala Leu Val Leu 1 5		
gga atc gat agt tcc acc caa tcc tgc aag gct ttg ctt gtc gac gcc 163 Gly Ile Asp Ser Ser Thr Gln Ser Cys Lys Ala Leu Leu Val Asp Ala 10 15 20		
gcc acc ggc cag gtt atc gac gaa ggc cgc gcg agt cac ccg agc ggg 211 Ala Thr Gly Gln Val Ile Asp Glu Gly Arg Ala Ser His Pro Ser Gly 25 30 35		
tcg gag gta gat cca cgt gcg tgg atc gct gcg ctg gat caa gct acc 259 Ser Glu Val Asp Pro Arg Ala Trp Ile Ala Ala Leu Asp Gln Ala Thr 40 45 50		
gag ggg ttg tta gaa cgc gcg gac gct gta tct att gca ggc cag cag 307 Glu Gly Leu Leu Glu Arg Ala Asp Ala Val Ser Ile Ala Gly Gln Gln 55 60 65		
cac ggc atg gtg gcg ttg gat gaa aac gat gaa atc gtt cgc ccg gcg 355 His Gly Met Val Ala Leu Asp Glu Asn Asp Glu Ile Val Arg Pro Ala 70 75 80 85		
ttg tta tgg aat gac act cgt tct gcc cag gct gcg ttg gat ctc aat 403 Leu Leu Trp Asn Asp Thr Arg Ser Ala Gln Ala Ala Leu Asp Leu Asn 90 95 100		

gag gag atc ggc ggc gat cag gct gcg gta gat gcc acg gga agt gtg	451
Glu Glu Ile Gly Gly Asp Gln Ala Ala Val Asp Ala Thr Gly Ser Val	
105 110 115	
tat gtt gct tct tta act gcc acc aaa atg cgg tgg atg cgt gat cat	499
Tyr Val Ala Ser Leu Thr Ala Thr Lys Met Arg Trp Met Arg Asp His	
120 125 130	
gaa cca gaa aat gca gcg cgc acg gcg tcg gtg atg ttg cct cat gat	547
Glu Pro Glu Asn Ala Ala Arg Thr Ala Ser Val Met Leu Pro His Asp	
135 140 145	
ttc ctc acc tgg cat ttg atg gga cgc gga cgc aaa gtc acc gac cat	595
Phe Leu Thr Trp His Leu Met Gly Arg Gly Arg Lys Val Thr Asp His	
150 155 160 165	
ggt gat gct tct gga acg ggc tac tac agc acg cgt gat cgt gcg tgg	643
Gly Asp Ala Ser Gly Thr Gly Tyr Tyr Ser Thr Arg Asp Arg Ala Trp	
170 175 180	
cgc acc gat cta gct gcc ttg gcg ctg ggc cat gag gtg gaa ctt cct	691
Arg Thr Asp Leu Ala Ala Leu Ala Leu Gly His Glu Val Glu Leu Pro	
185 190 195	
gaa ctc ctg gcc cca aat gcg att gcg gga aca act cca ggt gga gtg	739
Glu Leu Leu Ala Pro Asn Ala Ile Ala Gly Thr Thr Pro Gly Gly Val	
200 205 210	
aaa gtt gct gca ggc acg gga gat aat gct gcg gct gcg ctt ggc ctt	787
Lys Val Ala Ala Gly Thr Gly Asp Asn Ala Ala Ala Ala Leu Gly Leu	
215 220 225	
gat ttg cag cct ggt gat gtc agc gtg tcg atc gcc acc tct ggc gtt	835
Asp Leu Gln Pro Gly Asp Val Ser Val Ser Ile Gly Thr Ser Gly Val	
230 235 240 245	
gcc ggc atg acc gtt caa cat agc gtc cac gat cca tct ggt ttg gtc	883
Ala Gly Met Thr Val Gln His Ser Val His Asp Pro Ser Gly Leu Val	
250 255 260	
act ggt ttc gcc gat gcc acg ggt gcg tat ttc ccg ctg gcc tgc acg	931
Thr Gly Phe Ala Asp Ala Thr Gly Ala Tyr Phe Pro Leu Ala Cys Thr	
265 270 275	
ctt aat ggc gca ccg gtg ttg gaa ttc ggc cgc cgc att ctg ggc gtg	979
Leu Asn Gly Ala Pro Val Leu Glu Phe Gly Arg Arg Ile Leu Gly Val	
280 285 290	
gaa tgg gaa gag ttc gat gcg ctt gca ctg gct gct caa ccc ggt tca	1027
Glu Trp Glu Glu Phe Asp Ala Leu Ala Leu Ala Ala Gln Pro Gly Ser	
295 300 305	
ggt ggc gtg acg ctc cag cct tat ttg gag ggc gag cgt acg ccg aat	1075
Gly Gly Val Thr Leu Gln Pro Tyr Leu Glu Gly Glu Arg Thr Pro Asn	
310 315 320 325	
cgt ccc gca gca cgt ggc gtt ttg gct gga cta aac tgt gca acg acc	1123
Arg Pro Ala Ala Arg Gly Val Leu Ala Gly Leu Asn Cys Ala Thr Thr	
330 335 340	

cgc gag gac ttt gcc cga gca act gtt gaa ggc ttg ttg ttg gca ttg 1171
 Arg Glu Asp Phe Ala Arg Ala Thr Val Glu Gly Leu Leu Leu Ala Leu
 345 350 355
 gat gat gct gta acg gcg ctg gtt gag gcc acg gga gtg ccc gtt cag 1219
 Asp Asp Ala Val Thr Ala Leu Val Glu Ala Thr Gly Val Pro Val Gln
 360 365 370
 cgc atc cag ctc atc ggt ggc ggc gcg cgt tca cag gcg gtt cgt gag 1267
 Arg Ile Gln Leu Ile Gly Gly Gly Ala Arg Ser Gln Ala Val Arg Glu
 375 380 385
 att gcc cct gag att ttc ggc cat gag att gtg gtt cca gaa ccc gct 1315
 Ile Ala Pro Glu Ile Phe Gly His Glu Ile Val Val Pro Glu Pro Ala
 390 395 400 405
 gaa tat gtg gcg ttg ggt gca gct cgt cag gcg gca tgg gcg ctg tcg 1363
 Glu Tyr Val Ala Leu Gly Ala Ala Arg Gln Ala Ala Trp Ala Leu Ser
 410 415 420
 ggt gag gcc acg cca ccg cag tgg cca act ccc ggt tcc gat ccg cac 1411
 Gly Glu Ala Thr Pro Pro Gln Trp Pro Thr Pro Gly Ser Asp Pro His
 425 430 435
 cgc gca cct aaa aac act gag ctg agc acg cgt tat gcg aag ctg cgt 1459
 Arg Ala Pro Lys Asn Thr Glu Leu Ser Thr Arg Tyr Ala Lys Leu Arg
 440 445 450
 gct gca acg cag ggt tgg tac tagagctcga tattgtcgat caa 1503
 Ala Ala Thr Gln Gly Trp Tyr
 455 460

<210> 386

<211> 460

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 386

Met Ala Leu Val Leu Gly Ile Asp Ser Ser Thr Gln Ser Cys Lys Ala
 1 5 10 15
 Leu Leu Val Asp Ala Ala Thr Gly Gln Val Ile Asp Glu Gly Arg Ala
 20 25 30
 Ser His Pro Ser Gly Ser Glu Val Asp Pro Arg Ala Trp Ile Ala Ala
 35 40 45
 Leu Asp Gln Ala Thr Glu Gly Leu Leu Glu Arg Ala Asp Ala Val Ser
 50 55 60
 Ile Ala Gly Gln Gln His Gly Met Val Ala Leu Asp Glu Asn Asp Glu
 65 70 75 80
 Ile Val Arg Pro Ala Leu Leu Trp Asn Asp Thr Arg Ser Ala Gln Ala
 85 90 95
 Ala Leu Asp Leu Asn Glu Glu Ile Gly Gly Asp Gln Ala Ala Val Asp
 100 105 110
 Ala Thr Gly Ser Val Tyr Val Ala Ser Leu Thr Ala Thr Lys Met Arg

115	120	125
Trp Met Arg Asp His Glu Pro Glu Asn Ala Ala Arg Thr Ala Ser Val		
130	135	140
Met Leu Pro His Asp Phe Leu Thr Trp His Leu Met Gly Arg Gly Arg		
145	150	155
Lys Val Thr Asp His Gly Asp Ala Ser Gly Thr Gly Tyr Tyr Ser Thr		
	165	170
Arg Asp Arg Ala Trp Arg Thr Asp Leu Ala Ala Leu Ala Leu Gly His		
	180	185
Glu Val Glu Leu Pro Glu Leu Leu Ala Pro Asn Ala Ile Ala Gly Thr		
	195	200
Thr Pro Gly Gly Val Lys Val Ala Ala Gly Thr Gly Asp Asn Ala Ala		
	210	215
Ala Ala Leu Gly Leu Asp Leu Gln Pro Gly Asp Val Ser Val Ser Ile		
225	230	235
Gly Thr Ser Gly Val Ala Gly Met Thr Val Gln His Ser Val His Asp		
	245	250
Pro Ser Gly Leu Val Thr Gly Phe Ala Asp Ala Thr Gly Ala Tyr Phe		
	260	265
Pro Leu Ala Cys Thr Leu Asn Gly Ala Pro Val Leu Glu Phe Gly Arg		
	275	280
Arg Ile Leu Gly Val Glu Trp Glu Glu Phe Asp Ala Leu Ala Leu Ala		
	290	295
Ala Gln Pro Gly Ser Gly Gly Val Thr Leu Gln Pro Tyr Leu Glu Gly		
305	310	315
Glu Arg Thr Pro Asn Arg Pro Ala Ala Arg Gly Val Leu Ala Gly Leu		
	325	330
Asn Cys Ala Thr Thr Arg Glu Asp Phe Ala Arg Ala Thr Val Glu Gly		
	340	345
Leu Leu Leu Ala Leu Asp Asp Ala Val Thr Ala Leu Val Glu Ala Thr		
	355	360
Gly Val Pro Val Gln Arg Ile Gln Leu Ile Gly Gly Gly Ala Arg Ser		
	370	375
Gln Ala Val Arg Glu Ile Ala Pro Glu Ile Phe Gly His Glu Ile Val		
385	390	395
Val Pro Glu Pro Ala Glu Tyr Val Ala Leu Gly Ala Ala Arg Gln Ala		
	405	410
Ala Trp Ala Leu Ser Gly Glu Ala Thr Pro Pro Gln Trp Pro Thr Pro		
	420	425
Gly Ser Asp Pro His Arg Ala Pro Lys Asn Thr Glu Leu Ser Thr Arg		
	435	440
		445

Tyr Ala Lys Leu Arg Ala Ala Thr Gln Gly Trp Tyr
 450 455 460

<210> 387
 <211> 1139
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (1)..(1116)
 <223> FRXA01927

<400> 387
 aat gac act cgt tct gcc cag gct gcg ttg gat ctc aat gag gag atc 48
 Asn Asp Thr Arg Ser Ala Gln Ala Ala Leu Asp Leu Asn Glu Glu Ile
 1 5 10 15
 ggc ggc gat cag gct gcg gta gat gcc acg gga agt gtg tat gtt gct 96
 Gly Gly Asp Gln Ala Ala Val Asp Ala Thr Gly Ser Val Tyr Val Ala
 20 25 30
 tct tta act gcc acc aaa atg cgg tgg atg cgt gat cat gaa cca gaa 144
 Ser Leu Thr Ala Thr Lys Met Arg Trp Met Arg Asp His Glu Pro Glu
 35 40 45
 aat gca gcg cgc acg gcg tcg gtg atg ttg cct cat gat ttc ctc acc 192
 Asn Ala Ala Arg Thr Ala Ser Val Met Leu Pro His Asp Phe Leu Thr
 50 55 60
 tgg cat ttg atg gga cgc gga cgc aaa gtc acc gac cat ggt gat gct 240
 Trp His Leu Met Gly Arg Gly Arg Lys Val Thr Asp His Gly Asp Ala
 65 70 75 80
 tct gga acg ggc tac tac agc acg cgt gat cgt gcg tgg cgc acc gat 288
 Ser Gly Thr Gly Tyr Tyr Ser Thr Arg Asp Arg Ala Trp Arg Thr Asp
 85 90 95
 cta gct gcc ttg gcg ctg ggc cat gag gtg gaa ctt cct gaa ctc ctg 336
 Leu Ala Ala Leu Ala Leu Gly His Glu Val Glu Leu Pro Glu Leu Leu
 100 105 110
 gcc cca aat gcg att gcg gga aca act cca ggt gga gtg aaa gtt gct 384
 Ala Pro Asn Ala Ile Ala Gly Thr Thr Pro Gly Gly Val Lys Val Ala
 115 120 125
 gca ggc acg gga gat aat gct gcg gct gcg ctt ggc ctt gat ttg cag 432
 Ala Gly Thr Gly Asp Asn Ala Ala Ala Leu Gly Leu Asp Leu Gln
 130 135 140
 cct ggt gat gtc agc gtg tcg atc ggc acc tct ggc gtt gcc ggc atg 480
 Pro Gly Asp Val Ser Val Ser Ile Gly Thr Ser Gly Val Ala Gly Met
 145 150 155 160
 acc gtt caa cat agc gtc cac gat cca tct ggt ttg gtc act ggt ttc 528
 Thr Val Gln His Ser Val His Asp Pro Ser Gly Leu Val Thr Gly Phe
 165 170 175
 gcc gat gcc acg ggt gcg tat ttc ccg ctg gcc tgc acg ctt aat ggc 576

Ala Asp Ala Thr Gly Ala Tyr Phe Pro Leu Ala Cys Thr Leu Asn Gly
180 185 190

gca ccg gtg ttg gaa ttc ggc cgc cgc att ctg ggc gtg gaa tgg gaa 624
Ala Pro Val Leu Glu Phe Gly Arg Arg Ile Leu Gly Val Glu Trp Glu
195 200 205

gag ttc gat gcg ctt gca ctg gct gct caa ccc ggt tca ggt ggc gtg 672
Glu Phe Asp Ala Leu Ala Leu Ala Ala Gln Pro Gly Ser Gly Gly Val
210 215 220

acg ctc cag cct tat ttg gag ggc gag cgt acg ccg aat cgt ccc gca 720
Thr Leu Gln Pro Tyr Leu Glu Gly Glu Arg Thr Pro Asn Arg Pro Ala
225 230 235 240

gca cgt ggc gtt ttg gct gga cta aac tgt gca acg acc cgc gag gac 768
Ala Arg Gly Val Leu Ala Gly Leu Asn Cys Ala Thr Thr Arg Glu Asp
245 250 255

ttt gcc cga gca act gtt gaa ggc ttg ttg ttg gca ttg gat gat gct 816
Phe Ala Arg Ala Thr Val Glu Gly Leu Leu Leu Ala Leu Asp Asp Ala
260 265 270

gta acg gcg ctg gtt gag gcc acg gga gtg ccc gtt cag cgc atc cag 864
Val Thr Ala Leu Val Glu Ala Thr Gly Val Pro Val Gln Arg Ile Gln
275 280 285

ctc atc ggt ggc ggc gcg cgt tca cag gcg gtt cgt gag att gcc cct 912
Leu Ile Gly Gly Gly Ala Arg Ser Gln Ala Val Arg Glu Ile Ala Pro
290 295 300

gag att ttc ggc cat gag att gtg gtt cca gaa ccc gct gaa tat gtg 960
Glu Ile Phe Gly His Glu Ile Val Val Pro Glu Pro Ala Glu Tyr Val
305 310 315 320

gcg ttg ggt gca gct cgt cag gcg gca tgg gcg ctg tcg ggt gag gcc 1008
Ala Leu Gly Ala Ala Arg Gln Ala Ala Trp Ala Leu Ser Gly Glu Ala
325 330 335

acg cca ccg cag tgg cca act ccc ggt tcc gat ccg cac cgc gca cct 1056
Thr Pro Pro Gln Trp Pro Thr Pro Gly Ser Asp Pro His Arg Ala Pro
340 345 350

aaa aac act gag ctg agc acg cgt tat gcg aag ctg cgt gct gca acg 1104
Lys Asn Thr Glu Leu Ser Thr Arg Tyr Ala Lys Leu Arg Ala Ala Thr
355 360 365

cag ggt tgg tac tagagctcga tattgtcgat caa 1139
Gln Gly Trp Tyr
370

<210> 388

<211> 372

<212> PRT

<213> Corynebacterium glutamicum

<400> 388

Asn Asp Thr Arg Ser Ala Gln Ala Ala Leu Asp Leu Asn Glu Glu Ile
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Gly Gly Asp Gln Ala Ala Val Asp Ala Thr Gly Ser Val Tyr Val Ala
 20 25 30
 Ser Leu Thr Ala Thr Lys Met Arg Trp Met Arg Asp His Glu Pro Glu
 35 40 45
 Asn Ala Ala Arg Thr Ala Ser Val Met Leu Pro His Asp Phe Leu Thr
 50 55 60
 Trp His Leu Met Gly Arg Gly Arg Lys Val Thr Asp His Gly Asp Ala
 65 70 75 80
 Ser Gly Thr Gly Tyr Tyr Ser Thr Arg Asp Arg Ala Trp Arg Thr Asp
 85 90 95
 Leu Ala Ala Leu Ala Leu Gly His Glu Val Glu Leu Pro Glu Leu Leu
 100 105 110
 Ala Pro Asn Ala Ile Ala Gly Thr Thr Pro Gly Gly Val Lys Val Ala
 115 120 125
 Ala Gly Thr Gly Asp Asn Ala Ala Ala Ala Leu Gly Leu Asp Leu Gln
 130 135 140
 Pro Gly Asp Val Ser Val Ser Ile Gly Thr Ser Gly Val Ala Gly Met
 145 150 155 160
 Thr Val Gln His Ser Val His Asp Pro Ser Gly Leu Val Thr Gly Phe
 165 170 175
 Ala Asp Ala Thr Gly Ala Tyr Phe Pro Leu Ala Cys Thr Leu Asn Gly
 180 185 190
 Ala Pro Val Leu Glu Phe Gly Arg Arg Ile Leu Gly Val Glu Trp Glu
 195 200 205
 Glu Phe Asp Ala Leu Ala Leu Ala Ala Gln Pro Gly Ser Gly Gly Val
 210 215 220
 Thr Leu Gln Pro Tyr Leu Glu Gly Glu Arg Thr Pro Asn Arg Pro Ala
 225 230 235 240
 Ala Arg Gly Val Leu Ala Gly Leu Asn Cys Ala Thr Thr Arg Glu Asp
 245 250 255
 Phe Ala Arg Ala Thr Val Glu Gly Leu Leu Leu Ala Leu Asp Asp Ala
 260 265 270
 Val Thr Ala Leu Val Glu Ala Thr Gly Val Pro Val Gln Arg Ile Gln
 275 280 285
 Leu Ile Gly Gly Gly Ala Arg Ser Gln Ala Val Arg Glu Ile Ala Pro
 290 295 300
 Glu Ile Phe Gly His Glu Ile Val Val Pro Glu Pro Ala Glu Tyr Val
 305 310 315 320
 Ala Leu Gly Ala Ala Arg Gln Ala Ala Trp Ala Leu Ser Gly Glu Ala
 325 330 335
 Thr Pro Pro Gln Trp Pro Thr Pro Gly Ser Asp Pro His Arg Ala Pro

340 345 350
 Lys Asn Thr Glu Leu Ser Thr Arg Tyr Ala Lys Leu Arg Ala Ala Thr
 355 360 365
 Gln Gly Trp Tyr
 370

 <210> 389
 <211> 844
 <212> DNA
 <213> Corynebacterium glutamicum

 <220>
 <221> CDS
 <222> (101)..(844)
 <223> RXA02729

 <400> 389
 gaattaattg caggcacggt acctagcgtg acgaaaacta cgatccccac tgcccttatt 60

 catcgtgaat caatcatcaa ctccacttta aggaagaagg atg gac tcc cca atg 115
 Met Asp Ser Pro Met 5
 1

 agt aac tca acc ggt acc gac att gtc gtt gtc gga tcc atc aat gcc 163
 Ser Asn Ser Thr Gly Thr Asp Ile Val Val Val Gly Ser Ile Asn Ala 20
 10 15

 gat ctc acc gca aaa gtt caa cgc cac cct gaa cct gga gaa acc ctc 211
 Asp Leu Thr Ala Lys Val Gln Arg His Pro Glu Pro Gly Glu Thr Leu 35
 25 30

 ctg ggt agc ggc ggc aca gtg agt gct ggt ggc aaa ggc gcc aac caa 259
 Leu Gly Ser Gly Gly Thr Val Ser Ala Gly Gly Lys Gly Ala Asn Gln 50
 40 45

 gct gtg gcg gca gcg caa tta ggt gcc aaa gtc acc atg atc ggt gcg 307
 Ala Val Ala Ala Ala Gln Leu Gly Ala Lys Val Thr Met Ile Gly Ala 65
 55 60

 gtc gga acc gat caa atg gct ggc gag gcg ctg aca cat ttg cgt caa 355
 Val Gly Thr Asp Gln Met Ala Gly Glu Ala Leu Thr His Leu Arg Gln 85
 70 75 80

 tca gga gca gat atg tcc gcg att gcc act gtg gac ggt ccc act ggt 403
 Ser Gly Ala Asp Met Ser Ala Ile Ala Thr Val Asp Gly Pro Thr Gly 100
 90 95

 ctt gcc atc atc act gtg tct gac gat ggg gaa aac acc atc atc gtt 451
 Leu Ala Ile Ile Thr Val Ser Asp Asp Gly Glu Asn Thr Ile Ile Val 115
 105 110

 atc cct ggc gct aac gct tct gtc acc gcg gaa ttt gtt gat aaa cac 499
 Ile Pro Gly Ala Asn Ala Ser Val Thr Ala Glu Phe Val Asp Lys His 130
 120 125

 tcc caa ctc att gag aac gcc ggc att gtg ttg ctt cag ggt gag atc 547
 Ser Gln Leu Ile Glu Asn Ala Gly Ile Val Leu Leu Gln Gly Glu Ile 145
 135 140

cct gcc gat ggt ttc gag cgt gcc gtt gat ctt tca caa gga cgt gtg 595
 Pro Ala Asp Gly Phe Glu Arg Ala Val Asp Leu Ser Gln Gly Arg Val
 150 155 160 165
 gtg atc aat ctg gct cca gtt gtg ccc gtg gga cat gat cag ctg cgt 643
 Val Ile Asn Leu Ala Pro Val Val Pro Val Gly His Asp Gln Leu Arg
 170 175 180
 cgt gcc gat cca ttg ctg gtc aac gaa cac gaa ggc gct ctg gtg ctg 691
 Arg Ala Asp Pro Leu Leu Val Asn Glu His Glu Gly Ala Leu Val Leu
 185 190 195
 gac atg ctt gga act cca gcg acc acg tct gat ccc caa agt ttg gtc 739
 Asp Met Leu Gly Thr Pro Ala Thr Thr Ser Asp Pro Gln Ser Leu Val
 200 205 210
 act gaa ttg ctg gag cag ggt ttt act tcc gtg gtg atg aca ctt ggt 787
 Thr Glu Leu Leu Glu Gln Gly Phe Thr Ser Val Val Met Thr Leu Gly
 215 220 225
 gcc gaa ggt gct ctg gtt ggc acg ccg ggc caa ctc acg gca att cct 835
 Ala Glu Gly Ala Leu Val Gly Thr Pro Gly Gln Leu Thr Ala Ile Pro
 230 235 240 245
 acc cca aag 844
 Thr Pro Lys

<210> 390
 <211> 248
 <212> PRT
 <213> Corynebacterium glutamicum

<400> 390
 Met Asp Ser Pro Met Ser Asn Ser Thr Gly Thr Asp Ile Val Val Val
 1 5 10 15
 Gly Ser Ile Asn Ala Asp Leu Thr Ala Lys Val Gln Arg His Pro Glu
 20 25 30
 Pro Gly Glu Thr Leu Leu Gly Ser Gly Gly Thr Val Ser Ala Gly Gly
 35 40 45
 Lys Gly Ala Asn Gln Ala Val Ala Ala Ala Gln Leu Gly Ala Lys Val
 50 55 60
 Thr Met Ile Gly Ala Val Gly Thr Asp Gln Met Ala Gly Glu Ala Leu
 65 70 75 80
 Thr His Leu Arg Gln Ser Gly Ala Asp Met Ser Ala Ile Ala Thr Val
 85 90 95
 Asp Gly Pro Thr Gly Leu Ala Ile Ile Thr Val Ser Asp Asp Gly Glu
 100 105 110
 Asn Thr Ile Ile Val Ile Pro Gly Ala Asn Ala Ser Val Thr Ala Glu
 115 120 125
 Phe Val Asp Lys His Ser Gln Leu Ile Glu Asn Ala Gly Ile Val Leu

130	135	140	
Leu Gln Gly Glu Ile Pro Ala Asp Gly Phe Glu Arg Ala Val Asp Leu 145 150 155 160			
Ser Gln Gly Arg Val Val Ile Asn Leu Ala Pro Val Val Pro Val Gly 165 170 175			
His Asp Gln Leu Arg Arg Ala Asp Pro Leu Leu Val Asn Glu His Glu 180 185 190			
Gly Ala Leu Val Leu Asp Met Leu Gly Thr Pro Ala Thr Thr Ser Asp 195 200 205			
Pro Gln Ser Leu Val Thr Glu Leu Leu Glu Gln Gly Phe Thr Ser Val 210 215 220			
Val Met Thr Leu Gly Ala Glu Gly Ala Leu Val Gly Thr Pro Gly Gln 225 230 235 240			
Leu Thr Ala Ile Pro Thr Pro Lys 245			
<210> 391			
<211> 1026			
<212> DNA			
<213> Corynebacterium glutamicum			
<220>			
<221> CDS			
<222> (101)..(1003)			
<223> RXA02797			
<400> 391			
acagtctcat gaagccataa taaccacctt ctacaaagat cgacgtagaa tggaataacc 60			
ccttatgaaa acgtttgcat aactccgcta aggatgttcc atg aat aat cga att 115			
Met Asn Asn Arg Ile 5			
1			
gtc gta gtc ggc tcc atc aac gct gat ctt aat gtt ctc gtt gac cgc 163			
Val Val Val Gly Ser Ile Asn Ala Asp Leu Asn Val Leu Val Asp Arg 20			
10 15			
cac cca gca cct ggc gaa aca ctg ttg ggc agt ggt gga cac atc act 211			
His Pro Ala Pro Gly Glu Thr Leu Leu Gly Ser Gly Gly His Ile Thr 35			
25 30			
gca gga ggc aaa ggc gcc aac cag gca gta gct gcc gct ctt caa ggt 259			
Ala Gly Gly Lys Gly Ala Asn Gln Ala Val Ala Ala Ala Leu Gln Gly 50			
40 45 50			
gca gac gtc gcc ttt gtc ggc gct gtg ggc aag gat cct tac gct gcc 307			
Ala Asp Val Ala Phe Val Gly Ala Val Gly Lys Asp Pro Tyr Ala Ala 65			
55 60 65			
cca gcc tta gaa ttc ctt cgt tct tca ggc gtc gac ctt acg gca gta 355			
Pro Ala Leu Glu Phe Leu Arg Ser Ser Gly Val Asp Leu Thr Ala Val 85			
70 75 80 85			

tcc gaa gta gat gac acc acc ggg ctt gca gtt atc acc gtt gcc aaa 403
 Ser Glu Val Asp Asp Thr Thr Gly Leu Ala Val Ile Thr Val Ala Lys
 90 95 100
 gac ggc gag aac aat atc gtt gtc atc ccc ggc gcg aat tcc ctg gtc 451
 Asp Gly Glu Asn Asn Ile Val Val Ile Pro Gly Ala Asn Ser Leu Val
 105 110 115
 aat tgt gat tat gta agc agc caa tcc gct ctt tta gct gaa gct gga 499
 Asn Cys Asp Tyr Val Ser Ser Gln Ser Ala Leu Leu Ala Glu Ala Gly
 120 125 130
 atc ctg ttg ctg caa ggt gag atc cct gcg gat ggc ttc aaa gag gcc 547
 Ile Leu Leu Leu Gln Gly Glu Ile Pro Ala Asp Gly Phe Lys Glu Ala
 135 140 145
 att cac cac acc atg ggt cgc gtc gtg gtg aat cta gcg ccc gtc atc 595
 Ile His His Thr Met Gly Arg Val Val Val Asn Leu Ala Pro Val Ile
 150 155 160 165
 gag gta gag aag tcc gcg tta ctt gag gct gat ccg atc atc gcc aat 643
 Glu Val Glu Lys Ser Ala Leu Leu Glu Ala Asp Pro Ile Ile Ala Asn
 170 175 180
 gag cac gag gcc ggc ctg att ctg gat caa ttc ggg gca ggc atc gat 691
 Glu His Glu Ala Gly Leu Ile Leu Asp Gln Phe Gly Ala Gly Ile Asp
 185 190 195
 tcc atg gat ccc cac gag ctc gcg caa gct ctc ctc gac gcc ggt ttc 739
 Ser Met Asp Pro His Glu Leu Ala Gln Ala Leu Leu Asp Ala Gly Phe
 200 205 210
 gcc tct gtt gtt tta acg ctt gga tcc gca ggc gcg ttg gtc gcc gat 787
 Ala Ser Val Val Leu Thr Leu Gly Ser Ala Gly Ala Leu Val Ala Asp
 215 220 225
 gcc acc ggt atc acg gac atc gcc aca cca acg gtg cag gca gtt gac 835
 Ala Thr Gly Ile Thr Asp Ile Ala Thr Pro Thr Val Gln Ala Val Asp
 230 235 240 245
 acc acg gga gcc ggt gac gct ttt gcc gga gcc ttc tgc gca cga cta 883
 Thr Thr Gly Ala Gly Asp Ala Phe Ala Gly Ala Phe Cys Ala Arg Leu
 250 255 260
 att aaa ggc gat tcg ctt atc gac gcc gcc acc cac gca gca cgc gtc 931
 Ile Lys Gly Asp Ser Leu Ile Asp Ala Ala Thr His Ala Ala Arg Val
 265 270 275
 ggc gct tac tcg gtg caa acc gcc gga gcg caa gcg tcc tat ccg gac 979
 Gly Ala Tyr Ser Val Gln Thr Ala Gly Ala Gln Ala Ser Tyr Pro Asp
 280 285 290
 gcg agc gtt tca ctt ccc tct gtt taaaaaaaaact atttaagaag agg 1026
 Ala Ser Val Ser Leu Pro Ser Val
 295 300

<210> 392

<211> 301

<212> PRT

<213> Corynebacterium glutamicum

<400> 392

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Met Asn Asn Arg Ile Val Val Val Gly Ser Ile Asn Ala Asp Leu Asn
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Gly Gly His Ile Thr Ala Gly Gly Lys Gly Ala Asn Gln Ala Val Ala
          35           40           45

Ala Ala Leu Gln Gly Ala Asp Val Ala Phe Val Gly Ala Val Gly Lys
          50           55           60

Asp Pro Tyr Ala Ala Pro Ala Leu Glu Phe Leu Arg Ser Ser Gly Val
          65           70           75           80

Asp Leu Thr Ala Val Ser Glu Val Asp Asp Thr Thr Gly Leu Ala Val
          85           90           95

Ile Thr Val Ala Lys Asp Gly Glu Asn Asn Ile Val Val Ile Pro Gly
          100          105          110

Ala Asn Ser Leu Val Asn Cys Asp Tyr Val Ser Ser Gln Ser Ala Leu
          115          120          125

Leu Ala Glu Ala Gly Ile Leu Leu Leu Gln Gly Glu Ile Pro Ala Asp
          130          135          140

Gly Phe Lys Glu Ala Ile His His Thr Met Gly Arg Val Val Val Asn
          145          150          155          160

Leu Ala Pro Val Ile Glu Val Glu Lys Ser Ala Leu Leu Glu Ala Asp
          165          170          175

Pro Ile Ile Ala Asn Glu His Glu Ala Gly Leu Ile Leu Asp Gln Phe
          180          185          190

Gly Ala Gly Ile Asp Ser Met Asp Pro His Glu Leu Ala Gln Ala Leu
          195          200          205

Leu Asp Ala Gly Phe Ala Ser Val Val Leu Thr Leu Gly Ser Ala Gly
          210          215          220

Ala Leu Val Ala Asp Ala Thr Gly Ile Thr Asp Ile Ala Thr Pro Thr
          225          230          235          240

Val Gln Ala Val Asp Thr Thr Gly Ala Gly Asp Ala Phe Ala Gly Ala
          245          250          255

Phe Cys Ala Arg Leu Ile Lys Gly Asp Ser Leu Ile Asp Ala Ala Thr
          260          265          270

His Ala Ala Arg Val Gly Ala Tyr Ser Val Gln Thr Ala Gly Ala Gln
          275          280          285

Ala Ser Tyr Pro Asp Ala Ser Val Ser Leu Pro Ser Val
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<211> 1161
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<220>
 <221> CDS
 <222> (101)..(1138)
 <223> RXA02730

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 cgattacata aaggtagata atgagataaa gcgaggcgct atg gcg acg gaa aaa 115
 Met Ala Thr Glu Lys
 1 5
 ttc cga ccg act ctt aaa gat gtc gct cgt caa gca ggt gtc tcc atc 163
 Phe Arg Pro Thr Leu Lys Asp Val Ala Arg Gln Ala Gly Val Ser Ile
 10 15 20
 gcc aca gca tca cga gca cta gcg gat aat ccg gcg gtt gct gca tcg 211
 Ala Thr Ala Ser Arg Ala Leu Ala Asp Asn Pro Ala Val Ala Ala Ser
 25 30 35
 act cgt gaa aga atc caa caa tta gcc tct gat ctg ggt tac cgg gcc 259
 Thr Arg Glu Arg Ile Gln Gln Leu Ala Ser Asp Leu Gly Tyr Arg Ala
 40 45 50
 aat gct caa gct cgt gcg ctt cgc agt tct cgc agc aac acc att ggt 307
 Asn Ala Gln Ala Arg Ala Leu Arg Ser Ser Arg Ser Asn Thr Ile Gly
 55 60 65
 gtg att gtt ccc agt ttg att aac cat tac ttc gcc gca atg gtt act 355
 Val Ile Val Pro Ser Leu Ile Asn His Tyr Phe Ala Ala Met Val Thr
 70 75 80 85
 gaa att caa agc acc gcc agc aaa gct gga ctt gcc acg att atc acc 403
 Glu Ile Gln Ser Thr Ala Ser Lys Ala Gly Leu Ala Thr Ile Ile Thr
 90 95 100
 aac agc aat gaa gat gcg acc act atg tct ggg tct ttg gag ttt ctc 451
 Asn Ser Asn Glu Asp Ala Thr Thr Met Ser Gly Ser Leu Glu Phe Leu
 105 110 115
 acc tcg cat ggt gtc gat gga atc atc tgc gta cct aat gag gaa tgc 499
 Thr Ser His Gly Val Asp Gly Ile Ile Cys Val Pro Asn Glu Glu Cys
 120 125 130
 gcg aat caa cta gag gac ttg cag aag caa gga atg cca gtg gtg ttg 547
 Ala Asn Gln Leu Glu Asp Leu Gln Lys Gln Gly Met Pro Val Val Leu
 135 140 145
 gtt gac cga gag ctt cca gga gac tcc acc atc cca acg gcg acc tct 595
 Val Asp Arg Glu Leu Pro Gly Asp Ser Thr Ile Pro Thr Ala Thr Ser
 150 155 160 165
 aac ccc caa cca gga atc gcc gca gca gta gaa ctc ctg gct cac aac 643
 Asn Pro Gln Pro Gly Ile Ala Ala Ala Val Glu Leu Leu Ala His Asn
 170 175 180
 aac gcg ttg ccg att ggt tac ctc tca ggt ccc atg gac acc tca aca 691

Asn Ala Leu Pro Ile Gly Tyr Leu Ser Gly Pro Met Asp Thr Ser Thr
 185 190 195
 ggt aga gag cga tta gag gat ttc aaa gca gcc tgc gcc aac tcc aaa 739
 Gly Arg Glu Arg Leu Glu Asp Phe Lys Ala Ala Cys Ala Asn Ser Lys
 200 205 210
 att ggc gaa cag ctc gtt ttt ctg ggt ggg tac gaa caa agc gtt gga 787
 Ile Gly Glu Gln Leu Val Phe Leu Gly Gly Tyr Glu Gln Ser Val Gly
 215 220 225
 ttt gaa ggc gct acg aaa ttg ctc gat caa gga gct aaa act ctt ttt 835
 Phe Glu Gly Ala Thr Lys Leu Leu Asp Gln Gly Ala Lys Thr Leu Phe
 230 235 240 245
 gcc ggc gat tct atg atg acg atc ggt gtc att gaa gcc tgc cat aag 883
 Ala Gly Asp Ser Met Met Thr Ile Gly Val Ile Glu Ala Cys His Lys
 250 255 260
 gct ggt ttg gtt atc ggc aag gat gtc agc gtg att ggt ttt gat aca 931
 Ala Gly Leu Val Ile Gly Lys Asp Val Ser Val Ile Gly Phe Asp Thr
 265 270 275
 cat ccg ctt ttt gcc ctg caa cct cat ccg ttg aca gtg att gat caa 979
 His Pro Leu Phe Ala Leu Gln Pro His Pro Leu Thr Val Ile Asp Gln
 280 285 290
 aat gta gaa caa cta gcc caa cga gca gtg tct atc ctc acc gaa tta 1027
 Asn Val Glu Gln Leu Ala Gln Arg Ala Val Ser Ile Leu Thr Glu Leu
 295 300 305
 att gca ggc acg gta cct agc gtg acg aaa act acg atc ccc act gcc 1075
 Ile Ala Gly Thr Val Pro Ser Val Thr Lys Thr Thr Ile Pro Thr Ala
 310 315 320 325
 ctt att cat cgt gaa tca atc atc aac tcc act tta agg aag aag gat 1123
 Leu Ile His Arg Glu Ser Ile Ile Asn Ser Thr Leu Arg Lys Lys Asp
 330 335 340
 gga ctc ccc aat gag taactcaacc ggtaccgaca ttg 1161
 Gly Leu Pro Asn Glu
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<210> 394

<211> 346

<212> PRT

<213> Corynebacterium glutamicum

<400> 394

Met Ala Thr Glu Lys Phe Arg Pro Thr Leu Lys Asp Val Ala Arg Gln
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 Ala Gly Val Ser Ile Ala Thr Ala Ser Arg Ala Leu Ala Asp Asn Pro
 20 25 30
 Ala Val Ala Ala Ser Thr Arg Glu Arg Ile Gln Gln Leu Ala Ser Asp
 35 40 45
 Leu Gly Tyr Arg Ala Asn Ala Gln Ala Arg Ala Leu Arg Ser Ser Arg
 50 55 60

Ser Asn Thr Ile Gly Val Ile Val Pro Ser Leu Ile Asn His Tyr Phe
 65 70 75 80
 Ala Ala Met Val Thr Glu Ile Gln Ser Thr Ala Ser Lys Ala Gly Leu
 85 90 95
 Ala Thr Ile Ile Thr Asn Ser Asn Glu Asp Ala Thr Thr Met Ser Gly
 100 105 110
 Ser Leu Glu Phe Leu Thr Ser His Gly Val Asp Gly Ile Ile Cys Val
 115 120 125
 Pro Asn Glu Glu Cys Ala Asn Gln Leu Glu Asp Leu Gln Lys Gln Gly
 130 135 140
 Met Pro Val Val Leu Val Asp Arg Glu Leu Pro Gly Asp Ser Thr Ile
 145 150 155 160
 Pro Thr Ala Thr Ser Asn Pro Gln Pro Gly Ile Ala Ala Ala Val Glu
 165 170 175
 Leu Leu Ala His Asn Asn Ala Leu Pro Ile Gly Tyr Leu Ser Gly Pro
 180 185 190
 Met Asp Thr Ser Thr Gly Arg Glu Arg Leu Glu Asp Phe Lys Ala Ala
 195 200 205
 Cys Ala Asn Ser Lys Ile Gly Glu Gln Leu Val Phe Leu Gly Gly Tyr
 210 215 220
 Glu Gln Ser Val Gly Phe Glu Gly Ala Thr Lys Leu Leu Asp Gln Gly
 225 230 235 240
 Ala Lys Thr Leu Phe Ala Gly Asp Ser Met Met Thr Ile Gly Val Ile
 245 250 255
 Glu Ala Cys His Lys Ala Gly Leu Val Ile Gly Lys Asp Val Ser Val
 260 265 270
 Ile Gly Phe Asp Thr His Pro Leu Phe Ala Leu Gln Pro His Pro Leu
 275 280 285
 Thr Val Ile Asp Gln Asn Val Glu Gln Leu Ala Gln Arg Ala Val Ser
 290 295 300
 Ile Leu Thr Glu Leu Ile Ala Gly Thr Val Pro Ser Val Thr Lys Thr
 305 310 315 320
 Thr Ile Pro Thr Ala Leu Ile His Arg Glu Ser Ile Ile Asn Ser Thr
 325 330 335
 Leu Arg Lys Lys Asp Gly Leu Pro Asn Glu
 340 345

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<211> 483

<212> DNA

<213> Corynebacterium glutamicum

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<221> CDS

<222> (101)..(460)

<223> RXA02551

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ttaaaaaac accgtcgatt tcatttcctt ctctatttac	atg tcc gta tgt gaa	115
	Met Ser Val Cys Glu	
	1 5	

gcc cac aac ccc gaa aac tac tca acc ggt ggc ggt aac atc atc ggc	163
Ala His Asn Pro Glu Asn Tyr Ser Thr Gly Gly Gly Asn Ile Ile Gly	
10 15 20	

gga gtg gtc agc ccc act ctc gcg gct tcc gaa tgg ggt tgg caa gtt	211
Gly Val Val Ser Pro Thr Leu Ala Ala Ser Glu Trp Gly Trp Gln Val	
25 30 35	

gat ccc ctc ggt ttg cgc atc gtc ctg aac aac tac tgg gag cgc tgg	259
Asp Pro Leu Gly Leu Arg Ile Val Leu Asn Asn Tyr Trp Glu Arg Trp	
40 45 50	

cag aag cca ctg ttc atc gtc gaa aac gga cta gga gca aag gac gtg	307
Gln Lys Pro Leu Phe Ile Val Glu Asn Gly Leu Gly Ala Lys Asp Val	
55 60 65	

ctt atc gac gga ccc tcc ggc cca aca gta aac gat gac tac cgc atc	355
Leu Ile Asp Gly Pro Ser Gly Pro Thr Val Asn Asp Asp Tyr Arg Ile	
70 75 80 85	

aaa tac ctc gac gac ggc ggc tca gga atc ttg aag cgc tac aag aag	403
Lys Tyr Leu Asp Asp Gly Gly Ser Gly Ile Leu Lys Arg Tyr Lys Lys	
90 95 100	

aag tcc ttt gat tgg tgc cgc gac atc atc gcc acc aat ggc gaa agc	451
Lys Ser Phe Asp Trp Cys Arg Asp Ile Ile Ala Thr Asn Gly Glu Ser	
105 110 115	

ctg gaa tcc taagaaataa aggtaggtgt cac	483
Leu Glu Ser	
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<210> 396

<211> 120

<212> PRT

<213> Corynebacterium glutamicum

<400> 396

Met Ser Val Cys Glu Ala His Asn Pro Glu Asn Tyr Ser Thr Gly Gly	
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Gly Asn Ile Ile Gly Gly Val Val Ser Pro Thr Leu Ala Ala Ser Glu	
20 25 30	

Trp Gly Trp Gln Val Asp Pro Leu Gly Leu Arg Ile Val Leu Asn Asn	
35 40 45	

Tyr Trp Glu Arg Trp Gln Lys Pro Leu Phe Ile Val Glu Asn Gly Leu	
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50 55 60

Gly Ala Lys Asp Val Leu Ile Asp Gly Pro Ser Gly Pro Thr Val Asn
65 70 75 80

Asp Asp Tyr Arg Ile Lys Tyr Leu Asp Asp Gly Gly Ser Gly Ile Leu
85 90 95

Lys Arg Tyr Lys Lys Lys Ser Phe Asp Trp Cys Arg Asp Ile Ile Ala
100 105 110

Thr Asn Gly Glu Ser Leu Glu Ser
115 120

<210> 397
<211> 795
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(772)
<223> RXA01325

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gcgcagcgct cggacgatta cgaacttcag gagaactcgg ggtcattcgt tgcattctac 60

cctggaaatt ttccacact aagtcagggtc taagtagggt atg gat atg acg att 115
Met Asp Met Thr Ile
1 5

tcc cgc tcc acc atg gcc caa atc ctt gac tac acc ctc ctc gga cca 163
Ser Arg Ser Thr Met Ala Gln Ile Leu Asp Tyr Thr Leu Leu Gly Pro
10 15 20

gaa gta acc aac tcc gaa ctg gcc gca ttt ata gat tcc gca att gag 211
Glu Val Thr Asn Ser Glu Leu Ala Ala Phe Ile Asp Ser Ala Ile Glu
25 30 35

ctg gga gtc ggc acg atc tgt gtc ccc aac agc atg gtc aac cta act 259
Leu Gly Val Gly Thr Ile Cys Val Pro Asn Ser Met Val Asn Leu Thr
40 45 50

gca aaa gcc caa gaa gct gga att cga gtg gcc acc gtc gca gga ttc 307
Ala Lys Ala Gln Glu Ala Gly Ile Arg Val Ala Thr Val Ala Gly Phe
55 60 65

ccg cac ggc aaa acc ccc gcg ttg gtg aaa gcc gcc gaa gcg cgc ctt 355
Pro His Gly Lys Thr Pro Ala Leu Val Lys Ala Ala Glu Ala Arg Leu
70 75 80 85

gcc gta cag tcc gga gct tcc gaa gta gat gtt gtt ttg gat att gcg 403
Ala Val Gln Ser Gly Ala Ser Glu Val Asp Val Val Leu Asp Ile Ala
90 95 100

gta gtg aaa gag gga gat gcc aat agg ttg ctg cag gaa att gtg gca 451
Val Val Lys Glu Gly Asp Ala Asn Arg Leu Leu Gln Glu Ile Val Ala
105 110 115

atc agg gag gct gtt cca tct cct gtg gtg ctg aaa ttc atc ctc gaa 499


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Ile Arg Glu Ala Val Pro Ser Pro Val Val Leu Lys Phe Ile Leu Glu
    120                      125                      130

aca gct gtt gtg agt gat gaa gca att gtg act gca gtg aat gcg ttg   547
Thr Ala Val Val Ser Asp Glu Ala Ile Val Thr Ala Val Asn Ala Leu
    135                      140                      145

att gct gct ggt gct gac ttc gct aaa act tcc acg gga ttc cac cca   595
Ile Ala Ala Gly Ala Asp Phe Ala Lys Thr Ser Thr Gly Phe His Pro
    150                      155                      160                      165

gcg gga ggg gca act gtt gag gct gtt cgg gtg atg gct tcg gct tct   643
Ala Gly Gly Ala Thr Val Glu Ala Val Arg Val Met Ala Ser Ala Ser
    170                      175                      180

cgg gga agg gtt gga att aag gct gcc ggt ggg gtg aaa act tgg gaa   691
Arg Gly Arg Val Gly Ile Lys Ala Ala Gly Gly Val Lys Thr Trp Glu
    185                      190                      195

gat gcg gtg gcg ttt gtt gaa gca ggg gct act cgc att gga act tct   739
Asp Ala Val Ala Phe Val Glu Ala Gly Ala Thr Arg Ile Gly Thr Ser
    200                      205                      210

aat gcg gga gcc att ttg gag ggt gcg ccg gag tagtttgccg ttctaatacgg 792
Asn Ala Gly Ala Ile Leu Glu Gly Ala Pro Glu
    215                      220

gac                                                                    795

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<210> 398

<211> 224

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 398

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Thr Leu Leu Gly Pro Glu Val Thr Asn Ser Glu Leu Ala Ala Phe Ile
    20                      25                      30

Asp Ser Ala Ile Glu Leu Gly Val Gly Thr Ile Cys Val Pro Asn Ser
    35                      40                      45

Met Val Asn Leu Thr Ala Lys Ala Gln Glu Ala Gly Ile Arg Val Ala
    50                      55                      60

Thr Val Ala Gly Phe Pro His Gly Lys Thr Pro Ala Leu Val Lys Ala
    65                      70                      75                      80

Ala Glu Ala Arg Leu Ala Val Gln Ser Gly Ala Ser Glu Val Asp Val
    85                      90                      95

Val Leu Asp Ile Ala Val Val Lys Glu Gly Asp Ala Asn Arg Leu Leu
    100                      105                      110

Gln Glu Ile Val Ala Ile Arg Glu Ala Val Pro Ser Pro Val Val Leu
    115                      120                      125

Lys Phe Ile Leu Glu Thr Ala Val Val Ser Asp Glu Ala Ile Val Thr

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571

ggt tct ttg ggg ctt gcg gca acg ctg gcc act ctg gaa tct ggt gcg 451
 Gly Ser Leu Gly Leu Ala Ala Thr Leu Ala Thr Leu Glu Ser Gly Ala
 105 110 115

 cat ctt gcc ttg gct aac aaa gaa tcg ctg gtt gcc ggt ggt gag ttt 499
 His Leu Ala Leu Ala Asn Lys Glu Ser Leu Val Ala Gly Gly Glu Phe
 120 125 130

 gtt acc tca aag gca aag ctg ggg cag atc att ccg gtc gat tcg gag 547
 Val Thr Ser Lys Ala Lys Leu Gly Gln Ile Ile Pro Val Asp Ser Glu
 135 140 145

 cac tct gcc atg gcg cag tgt ttg cgt tcg ggt act cgt gat gag gtt 595
 His Ser Ala Met Ala Gln Cys Leu Arg Ser Gly Thr Arg Asp Glu Val
 150 155 160 165

 gcg cgg att gtg ctg aca gct tcg ggc gga cct ttc agg gct gga cca 643
 Ala Arg Ile Val Leu Thr Ala Ser Gly Gly Pro Phe Arg Ala Gly Pro
 170 175 180

 ggg aga aga tgt ggg agg tgactcccgga gcaggcagca gcg 684
 Gly Arg Arg Cys Gly Arg
 185

<210> 400

<211> 187

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 400

Val Thr Lys Lys Ile Leu Ile Leu Gly Ser Thr Gly Ser Ile Gly Thr
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 Gln Ala Leu Asp Val Ile Ala Asp Asn Ser Asp Lys Phe Glu Val Val
 20 25 30

 Gly Ile Ala Ala Gly Gly Ser Gln Pro Asp Leu Val Ile Ser Gln Ala
 35 40 45

 Gln Gln Leu Gly Leu Ala Ala Asp Lys Val Ala Val Ala Asp Ala Gln
 50 55 60

 Ala Ala Ala Val Ile Ser Lys Ala Leu Gly Gly Glu Ile Ile Ser Gly
 65 70 75 80

 Thr Asp Ala Ala Lys Ile Leu Val Glu Thr Thr Lys Ala Asp Thr Val
 85 90 95

 Leu Asn Ala Leu Val Gly Ser Leu Gly Leu Ala Ala Thr Leu Ala Thr
 100 105 110

 Leu Glu Ser Gly Ala His Leu Ala Leu Ala Asn Lys Glu Ser Leu Val
 115 120 125

 Ala Gly Gly Glu Phe Val Thr Ser Lys Ala Lys Leu Gly Gln Ile Ile
 130 135 140

 Pro Val Asp Ser Glu His Ser Ala Met Ala Gln Cys Leu Arg Ser Gly
 145 150 155 160

<400> 401																
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cagcttcggg	cggacctttc	agggctggac	cagggagaag	atg	tgg	gag	gtg	act								115
				Met	Trp	Glu	Val	Thr								
				1				5								
ccc	gag	cag	gca	gca	gcg	cac	cca	acg	tgg	gcg	atg	ggg	cag	atg	aac	163
Pro	Glu	Gln	Ala	Ala	Ala	His	Pro	Thr	Trp	Ala	Met	Gly	Gln	Met	Asn	
				10					15					20		
acg	ttg	aac	tcc	gcc	acc	ctt	att	aat	aaa	ggc	ctc	gaa	ctc	atc	gag	211
Thr	Leu	Asn	Ser	Ala	Thr	Leu	Ile	Asn	Lys	Gly	Leu	Glu	Leu	Ile	Glu	
			25					30					35			
gcg	acc	ctg	ctg	ttt	gaa	acg	gat	gcg	gat	ctc	att	gat	gtg	acg	gtg	259
Ala	Thr	Leu	Leu	Phe	Glu	Thr	Asp	Ala	Asp	Leu	Ile	Asp	Val	Thr	Val	
		40					45					50				
cat	ccg	cag	tcg	atc	atc	cac	tcc	atg	atc	acg	ttt	acg	gat	ggg	gcg	307
His	Pro	Gln	Ser	Ile	Ile	His	Ser	Met	Ile	Thr	Phe	Thr	Asp	Gly	Ala	
		55				60					65					
acc	atc	gcg	cag	gcg	tcg	cca	cca	tcg	atg	aaa	ctg	ccg	atc	gcg	ttg	355
Thr	Ile	Ala	Gln	Ala	Ser	Pro	Pro	Ser	Met	Lys	Leu	Pro	Ile	Ala	Leu	
	70				75					80					85	
gcg	ctt	gat	tgg	cca	cat	cgg	gtg	ccg	aag	gct	cag	ccg	gcg	ctg	gat	403
Ala	Leu	Asp	Trp	Pro	His	Arg	Val	Pro	Lys	Ala	Gln	Pro	Ala	Leu	Asp	
				90					95					100		
ttc	acc	gct	gct	cat	acc	tgg	gct	ttt	gag	ccg	gtg	gat	gat	gcc	gca	451
Phe	Thr	Ala	Ala	His	Thr	Trp	Ala	Phe	Glu	Pro	Val	Asp	Asp	Ala	Ala	
			105					110					115			
ttc	cct	gcg	gtg	cag	ctg	gct	agg	cac	gtc	gca	aag	caa	aaa	ggc	acg	499
Phe	Pro	Ala	Val	Gln	Leu	Ala	Arg	His	Val	Ala	Lys	Gln	Lys	Gly	Thr	
		120					125					130				
tac	ccc	gcg	gtg	tat	aac	gcc	gcc	aac	gag	gag	gcg	gct	gag	gcg	ttt	547
Tyr	Pro	Ala	Val	Tyr	Asn	Ala	Ala	Asn	Glu	Glu	Ala	Ala	Glu	Ala	Phe	
	135					140					145					

ttg cgc ggg cga atc aag ttt ccg cag atc gtg gac gtg gtg gac gag 595
 Leu Arg Gly Arg Ile Lys Phe Pro Gln Ile Val Asp Val Val Asp Glu
 150 155 160 165

 gtc ctc caa gga gct tct cag ttt gct ggt gta gca tca cac gtc gat 643
 Val Leu Gln Gly Ala Ser Gln Phe Ala Gly Val Ala Ser His Val Asp
 170 175 180

 gat att ttg gca acc gaa tct gag gca cgc gcg cgt gcg aat gct ttg 691
 Asp Ile Leu Ala Thr Glu Ser Glu Ala Arg Ala Arg Ala Asn Ala Leu
 185 190 195

 atc aac cgg ttg gca acc aac ttg taagctaagg agcttccgcc tcg 738
 Ile Asn Arg Leu Ala Thr Asn Leu
 200 205

<210> 402

<211> 205

<212> PRT

<213> Corynebacterium glutamicum

<400> 402

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 1 5 10 15

 Met Gly Gln Met Asn Thr Leu Asn Ser Ala Thr Leu Ile Asn Lys Gly
 20 25 30

 Leu Glu Leu Ile Glu Ala Thr Leu Leu Phe Glu Thr Asp Ala Asp Leu
 35 40 45

 Ile Asp Val Thr Val His Pro Gln Ser Ile Ile His Ser Met Ile Thr
 50 55 60

 Phe Thr Asp Gly Ala Thr Ile Ala Gln Ala Ser Pro Pro Ser Met Lys
 65 70 75 80

 Leu Pro Ile Ala Leu Ala Leu Asp Trp Pro His Arg Val Pro Lys Ala
 85 90 95

 Gln Pro Ala Leu Asp Phe Thr Ala Ala His Thr Trp Ala Phe Glu Pro
 100 105 110

 Val Asp Asp Ala Ala Phe Pro Ala Val Gln Leu Ala Arg His Val Ala
 115 120 125

 Lys Gln Lys Gly Thr Tyr Pro Ala Val Tyr Asn Ala Ala Asn Glu Glu
 130 135 140

 Ala Ala Glu Ala Phe Leu Arg Gly Arg Ile Lys Phe Pro Gln Ile Val
 145 150 155 160

 Asp Val Val Asp Glu Val Leu Gln Gly Ala Ser Gln Phe Ala Gly Val
 165 170 175

 Ala Ser His Val Asp Asp Ile Leu Ala Thr Glu Ser Glu Ala Arg Ala
 180 185 190

 Arg Ala Asn Ala Leu Ile Asn Arg Leu Ala Thr Asn Leu
 195 200 205

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Glu	Leu	Val	Lys	Ile	Gly	Ala	Gln	Asn	Glu	Asn	Val	Val	Ala	Ile	Thr														
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gcc	gcg	atg	gca	ggc	cct	acc	ggc	ctg	tcc	aag	ttc	gaa	gcc	aat	ttc					1171									
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tct	gcc	gca	ggc	ctc	gca	ttg	ggc	gga	aaa	cac	cct	gtg	gtg	gct	att					1267									
Ser	Ala	Ala	Gly	Leu	Ala	Leu	Gly	Gly	Lys	His	Pro	Val	Val	Ala	Ile														
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Tyr	Ser	Thr	Phe	Leu	Asn	Arg	Ala	Phe	Asp	Gln	Leu	Leu	Met	Asp	Val														
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Gly	Met	Leu	Asn	Gln	Pro	Val	Thr	Leu	Val	Leu	Asp	Arg	Ser	Gly	Val														
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acg ggt tcg gat gga gcg agc cac aat ggc gtc tgg gat atg gcg ctg 1411
 Thr Gly Ser Asp Gly Ala Ser His Asn Gly Val Trp Asp Met Ala Leu
 425 430 435

acc tcg atc gtt cca ggc gtg cag gtg gcg gca cca cgt gat gag gat 1459
 Thr Ser Ile Val Pro Gly Val Gln Val Ala Ala Pro Arg Asp Glu Asp
 440 445 450

tcc ttg cgt gag ctg ctc aat gag gct att tcc atc gat gat ggc ccc 1507
 Ser Leu Arg Glu Leu Leu Asn Glu Ala Ile Ser Ile Asp Asp Gly Pro
 455 460 465

aca gtt gtg cgt ttc ccc aag ggc gac ttg cca act cca att gtt gct 1555
 Thr Val Val Arg Phe Pro Lys Gly Asp Leu Pro Thr Pro Ile Val Ala
 470 475 480 485

atc gac acc ttg gaa gac ggc gtg gat gtc ctc gca tat gaa gac gcc 1603
 Ile Asp Thr Leu Glu Asp Gly Val Asp Val Leu Ala Tyr Glu Asp Ala
 490 495 500

act gac gtt gaa tca acc gac gat gcg cca tca gtt ctc atc att gcg 1651
 Thr Asp Val Glu Ser Thr Asp Asp Ala Pro Ser Val Leu Ile Ile Ala
 505 510 515

gta ggc gag cgc gca act gtt gca ctt gac gtt gct tcc agg att aaa 1699
 Val Gly Glu Arg Ala Thr Val Ala Leu Asp Val Ala Ser Arg Ile Lys
 520 525 530

cag cac ggc gtg aac gtc acg gtt gtt gac ccc cgc tgg att gtc ccc 1747
 Gln His Gly Val Asn Val Thr Val Val Asp Pro Arg Trp Ile Val Pro
 535 540 545

atc ccg cag tcc ttg gtc gcg ctg tct gat gat cat gac ctc gtg atc 1795
 Ile Pro Gln Ser Leu Val Ala Leu Ser Asp Asp His Asp Leu Val Ile
 550 555 560 565

acc atc gaa gac ggc gtc atc cac ggc ggc gtg gga tcc ttg ctc tct 1843
 Thr Ile Glu Asp Gly Val Ile His Gly Gly Val Gly Ser Leu Leu Ser
 570 575 580

gat gcg ctt aac gcc tct gag gtg gat acc cct cgc cga caa atc gcc 1891
 Asp Ala Leu Asn Ala Ser Glu Val Asp Thr Pro Arg Arg Gln Ile Ala
 585 590 595

gtg ccc cag aag tac ctg gat cac gcg tcc cgc aat gaa gtg ctc gcc 1939
 Val Pro Gln Lys Tyr Leu Asp His Ala Ser Arg Asn Glu Val Leu Ala
 600 605 610

gat tat ggc ctc gac gcc gac ggc att gaa acc act gtt gtt gga tgg 1987
 Asp Tyr Gly Leu Asp Ala Asp Gly Ile Glu Thr Thr Val Val Gly Trp
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<210> 404

<211> 636

<212> PRT

<213> Corynebacterium glutamicum

<400> 404

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Val Asp Lys Val Ala Ala Thr Gly Gly His Leu Gly Pro Asn Leu Gly
      35           40           45

Val Val Glu Leu Thr Ile Gly Leu His Arg Val Phe Asp Ser Pro Gln
      50           55           60

Asp Pro Ile Ile Phe Asp Thr Ser His Gln Ser Tyr Val His Lys Ile
      65           70           75           80

Leu Thr Gly Arg Ala Lys Asp Phe Asp Ser Leu Arg Gln Lys Asp Gly
      85           90           95

Leu Ser Gly Tyr Thr Cys Arg Ala Glu Ser Glu His Asp Trp Thr Glu
      100          105          110

Ser Ser His Ala Ser Ala Ala Leu Ser Tyr Ala Asp Gly Leu Ser Lys
      115          120          125

Ala Lys Gln Leu Asp Gly Asp Thr Thr His Ser Val Val Ala Val Val
      130          135          140

Gly Asp Gly Ala Leu Thr Gly Gly Met Cys Trp Glu Ala Leu Asn Asn
      145          150          155          160

Ile Ala Ala Gly Lys Asp Arg Lys Val Val Val Val Asn Asp Asn
      165          170          175

Gly Arg Ser Tyr Ser Pro Thr Ile Gly Gly Phe Ala Glu Asn Leu Ala
      180          185          190

Gly Leu Arg Met Gln Pro Phe Tyr Asp Arg Phe Met Glu Lys Gly Lys
      195          200          205

Thr Ser Leu Lys Ser Met Gly Trp Val Gly Glu Arg Thr Phe Glu Ala
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Leu His Ala Phe Lys Glu Gly Val Lys Ser Thr Val Ile Pro Thr Glu
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Met Phe Pro Glu Leu Gly Met Lys Tyr Val Gly Pro Val Asp Gly His
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Asn Gln Lys Ala Val Asp Asn Ala Leu Lys Tyr Ala His Asp Tyr Asp
      260          265          270

Gly Pro Ile Ile Val His Met Val Thr Glu Lys Gly Arg Gly Tyr Ala
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Pro Ala Glu Gln Asp Leu Asp Glu Leu Met His Ser Thr Gly Val Ile
      290          295          300

Asp Pro Leu Thr Gly Ala Pro Lys Ser Ala Ser Lys Pro Gly Trp Thr

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305		310		315		320
Ser Val Phe Ser Asp Glu Leu Val Lys Ile Gly Ala Gln Asn Glu Asn						
		325		330		335
Val Val Ala Ile Thr Ala Ala Met Ala Gly Pro Thr Gly Leu Ser Lys						
		340		345		350
Phe Glu Ala Asn Phe Pro Asn Arg Phe Phe Asp Val Gly Ile Ala Glu						
		355		360		365
Gln His Ala Val Thr Ser Ala Ala Gly Leu Ala Leu Gly Gly Lys His						
		370		375		380
Pro Val Val Ala Ile Tyr Ser Thr Phe Leu Asn Arg Ala Phe Asp Gln						
		385		390		395
Leu Leu Met Asp Val Gly Met Leu Asn Gln Pro Val Thr Leu Val Leu						
		405		410		415
Asp Arg Ser Gly Val Thr Gly Ser Asp Gly Ala Ser His Asn Gly Val						
		420		425		430
Trp Asp Met Ala Leu Thr Ser Ile Val Pro Gly Val Gln Val Ala Ala						
		435		440		445
Pro Arg Asp Glu Asp Ser Leu Arg Glu Leu Leu Asn Glu Ala Ile Ser						
		450		455		460
Ile Asp Asp Gly Pro Thr Val Val Arg Phe Pro Lys Gly Asp Leu Pro						
		465		470		475
Thr Pro Ile Val Ala Ile Asp Thr Leu Glu Asp Gly Val Asp Val Leu						
		485		490		495
Ala Tyr Glu Asp Ala Thr Asp Val Glu Ser Thr Asp Asp Ala Pro Ser						
		500		505		510
Val Leu Ile Ile Ala Val Gly Glu Arg Ala Thr Val Ala Leu Asp Val						
		515		520		525
Ala Ser Arg Ile Lys Gln His Gly Val Asn Val Thr Val Val Asp Pro						
		530		535		540
Arg Trp Ile Val Pro Ile Pro Gln Ser Leu Val Ala Leu Ser Asp Asp						
		545		550		555
His Asp Leu Val Ile Thr Ile Glu Asp Gly Val Ile His Gly Gly Val						
		565		570		575
Gly Ser Leu Leu Ser Asp Ala Leu Asn Ala Ser Glu Val Asp Thr Pro						
		580		585		590
Arg Arg Gln Ile Ala Val Pro Gln Lys Tyr Leu Asp His Ala Ser Arg						
		595		600		605
Asn Glu Val Leu Ala Asp Tyr Gly Leu Asp Ala Asp Gly Ile Glu Thr						
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Thr Val Val Gly Trp Leu Asp Ser Leu Phe Gly Glu						
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<210> 405
 <211> 1061
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (1)..(1038)
 <223> FRXA01562

<400> 405
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 ctc aca gga gct cct aaa tct gca tca aag ccc ggt tgg acc tct gtg 96
 Leu Thr Gly Ala Pro Lys Ser Ala Ser Lys Pro Gly Trp Thr Ser Val
 20 25 30
 ttc agc gat gag ctg gtc aag att ggt gcg cag aat gaa aac gtt gtt 144
 Phe Ser Asp Glu Leu Val Lys Ile Gly Ala Gln Asn Glu Asn Val Val
 35 40 45
 gcc atc acc gcc gcg atg gca ggt cct acc ggt ctg tcc aag ttc gaa 192
 Ala Ile Thr Ala Ala Met Ala Gly Pro Thr Gly Leu Ser Lys Phe Glu
 50 55 60
 gcc aat ttc ccc aac cga ttc ttt gat gtc ggc att gct gag cag cac 240
 Ala Asn Phe Pro Asn Arg Phe Phe Asp Val Gly Ile Ala Glu Gln His
 65 70 75 80
 gcg gta act tct gcc gca ggc ctc gca ttg ggt gga aaa cac cct gtg 288
 Ala Val Thr Ser Ala Ala Gly Leu Ala Leu Gly Gly Lys His Pro Val
 85 90 95
 gtg gct att tac tcc acg ttc ttg aac cgc gct ttt gat cag ctg ctc 336
 Val Ala Ile Tyr Ser Thr Phe Leu Asn Arg Ala Phe Asp Gln Leu Leu
 100 105 110
 atg gat gtg ggc atg ctc aac cag cct gtt act ttg gtg ctt gat cgc 384
 Met Asp Val Gly Met Leu Asn Gln Pro Val Thr Leu Val Leu Asp Arg
 115 120 125
 tca ggt gtc acg ggt tcg gat gga gcg agc cac aat ggc gtc tgg gat 432
 Ser Gly Val Thr Gly Ser Asp Gly Ala Ser His Asn Gly Val Trp Asp
 130 135 140
 atg gcg ctg acc tcg atc gtt cca ggc gtg cag gtg gcg gca cca cgt 480
 Met Ala Leu Thr Ser Ile Val Pro Gly Val Gln Val Ala Ala Pro Arg
 145 150 155 160
 gat gag gat tcc ttg cgt gag ctg ctc aat gag gct att tcc atc gat 528
 Asp Glu Asp Ser Leu Arg Glu Leu Leu Asn Glu Ala Ile Ser Ile Asp
 165 170 175
 gat ggc ccc aca gtt gtg cgt ttc ccc aag ggc gac ttg cca act cca 576
 Asp Gly Pro Thr Val Val Arg Phe Pro Lys Gly Asp Leu Pro Thr Pro
 180 185 190

att gtt gct atc gac acc ttg gaa gac ggc gtg gat gtc ctc gca tat 624
 Ile Val Ala Ile Asp Thr Leu Glu Asp Gly Val Asp Val Leu Ala Tyr
 195 200 205
 gaa gac gcc act gac gtt gaa tca acc gac gat gcg cca tca gtt ctc 672
 Glu Asp Ala Thr Asp Val Glu Ser Thr Asp Asp Ala Pro Ser Val Leu
 210 215 220
 atc att gcg gta ggc gag cgc gca act gtt gca ctt gac gtt gct tcc 720
 Ile Ile Ala Val Gly Glu Arg Ala Thr Val Ala Leu Asp Val Ala Ser
 225 230 235 240
 agg att aaa cag cac ggc gtg aac gtc acg gtt gtt gac ccc cgc tgg 768
 Arg Ile Lys Gln His Gly Val Asn Val Thr Val Val Asp Pro Arg Trp
 245 250 255
 att gtc ccc atc ccg cag tcc ttg gtc gcg ctg tct gat gat cat gac 816
 Ile Val Pro Ile Pro Gln Ser Leu Val Ala Leu Ser Asp Asp His Asp
 260 265 270
 ctc gtg atc acc atc gaa gac ggc gtc atc cac ggc ggc gtg gga tcc 864
 Leu Val Ile Thr Ile Glu Asp Gly Val Ile His Gly Gly Val Gly Ser
 275 280 285
 ttg ctc tct gat gcg ctt aac gcc tct gag gtg gat acc cct cgc cga 912
 Leu Leu Ser Asp Ala Leu Asn Ala Ser Glu Val Asp Thr Pro Arg Arg
 290 295 300
 caa atc gcc gtg ccc cag aag tac ctg gat cac gcg tcc cgc aat gaa 960
 Gln Ile Ala Val Pro Gln Lys Tyr Leu Asp His Ala Ser Arg Asn Glu
 305 310 315 320
 gtg ctc gcc gat tat ggc ctc gac gcc gac ggc att gaa acc act gtt 1008
 Val Leu Ala Asp Tyr Gly Leu Asp Ala Asp Gly Ile Glu Thr Thr Val
 325 330 335
 gtt gga tgg ctg gat tcc ctg ttc ggg gaa taaaaccctg cttatcgacg 1058
 Val Gly Trp Leu Asp Ser Leu Phe Gly Glu
 340 345
 ccg 1061

<210> 406

<211> 346

<212> PRT

<213> Corynebacterium glutamicum

<400> 406

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 20 25 30

Phe Ser Asp Glu Leu Val Lys Ile Gly Ala Gln Asn Glu Asn Val Val
 35 40 45

Ala Ile Thr Ala Ala Met Ala Gly Pro Thr Gly Leu Ser Lys Phe Glu
 50 55 60

Ala Asn Phe Pro Asn Arg Phe Phe Asp Val Gly Ile Ala Glu Gln His
 65 70 75 80
 Ala Val Thr Ser Ala Ala Gly Leu Ala Leu Gly Gly Lys His Pro Val
 85 90 95
 Val Ala Ile Tyr Ser Thr Phe Leu Asn Arg Ala Phe Asp Gln Leu Leu
 100 105 110
 Met Asp Val Gly Met Leu Asn Gln Pro Val Thr Leu Val Leu Asp Arg
 115 120 125
 Ser Gly Val Thr Gly Ser Asp Gly Ala Ser His Asn Gly Val Trp Asp
 130 135 140
 Met Ala Leu Thr Ser Ile Val Pro Gly Val Gln Val Ala Ala Pro Arg
 145 150 155 160
 Asp Glu Asp Ser Leu Arg Glu Leu Leu Asn Glu Ala Ile Ser Ile Asp
 165 170 175
 Asp Gly Pro Thr Val Val Arg Phe Pro Lys Gly Asp Leu Pro Thr Pro
 180 185 190
 Ile Val Ala Ile Asp Thr Leu Glu Asp Gly Val Asp Val Leu Ala Tyr
 195 200 205
 Glu Asp Ala Thr Asp Val Glu Ser Thr Asp Asp Ala Pro Ser Val Leu
 210 215 220
 Ile Ile Ala Val Gly Glu Arg Ala Thr Val Ala Leu Asp Val Ala Ser
 225 230 235 240
 Arg Ile Lys Gln His Gly Val Asn Val Thr Val Val Asp Pro Arg Trp
 245 250 255
 Ile Val Pro Ile Pro Gln Ser Leu Val Ala Leu Ser Asp Asp His Asp
 260 265 270
 Leu Val Ile Thr Ile Glu Asp Gly Val Ile His Gly Gly Val Gly Ser
 275 280 285
 Leu Leu Ser Asp Ala Leu Asn Ala Ser Glu Val Asp Thr Pro Arg Arg
 290 295 300
 Gln Ile Ala Val Pro Gln Lys Tyr Leu Asp His Ala Ser Arg Asn Glu
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 Val Leu Ala Asp Tyr Gly Leu Asp Ala Asp Gly Ile Glu Thr Thr Val
 325 330 335
 Val Gly Trp Leu Asp Ser Leu Phe Gly Glu
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<210> 407

<211> 703

<212> DNA

<213> *Corynebacterium glutamicum*

<220>

<221> CDS

<222> (101)..(703)

<223> FRXA01705

<400> 407

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 Met Gly Ile Leu Asn
 1 5

agt att tca aca cct gct gac tta aag gcc ctt aat gat gag gat ttg 163
 Ser Ile Ser Thr Pro Ala Asp Leu Lys Ala Leu Asn Asp Glu Asp Leu
 10 15 20

gac gct ctt gcc aaa gaa atc cga act ttc ctg gtc gat aaa gtc gca 211
 Asp Ala Leu Ala Lys Glu Ile Arg Thr Phe Leu Val Asp Lys Val Ala
 25 30 35

gca act ggt ggc cac tta ggt cca aat ttg ggc gta gtg gaa tta acc 259
 Ala Thr Gly Gly His Leu Gly Pro Asn Leu Gly Val Val Glu Leu Thr
 40 45 50

atc ggt ctt cat cga gtt ttc gat tcg cct caa gac ccg atc atc ttt 307
 Ile Gly Leu His Arg Val Phe Asp Ser Pro Gln Asp Pro Ile Ile Phe
 55 60 65

gat act tct cac cag tcc tat gtg cat aag atc ctg acg ggt cgc gct 355
 Asp Thr Ser His Gln Ser Tyr Val His Lys Ile Leu Thr Gly Arg Ala
 70 75 80 85

aaa gat ttt gat tct ttg cgt caa aaa gat ggc ctt tct ggt tac acc 403
 Lys Asp Phe Asp Ser Leu Arg Gln Lys Asp Gly Leu Ser Gly Tyr Thr
 90 95 100

tgc cgt gct gaa agt gag cac gat tgg act gag tct tcg cat gct tcg 451
 Cys Arg Ala Glu Ser Glu His Asp Trp Thr Glu Ser Ser His Ala Ser
 105 110 115

gcg gcc ttg tct tat gcg gat ggt ttg tct aaa gcc aag cag ttg gat 499
 Ala Ala Leu Ser Tyr Ala Asp Gly Leu Ser Lys Ala Lys Gln Leu Asp
 120 125 130

ggc gat acc acg cat agt gtg gtt gct gtc gtt ggt gat ggc gct cta 547
 Gly Asp Thr Thr His Ser Val Val Ala Val Val Gly Asp Gly Ala Leu
 135 140 145

act ggc ggc atg tgt tgg gaa gca ctg aac aat att gct gct ggt aaa 595
 Thr Gly Gly Met Cys Trp Glu Ala Leu Asn Asn Ile Ala Ala Gly Lys
 150 155 160 165

gac cgc aaa gtt gtt gtc gta gtc aat gac aat ggc cgg agt tat tct 643
 Asp Arg Lys Val Val Val Val Val Asn Asp Asn Gly Arg Ser Tyr Ser
 170 175 180

cca acc att ggc gga ttt gcg gaa aac ctt gcg ggc ctt cgc atg cag 691
 Pro Thr Ile Gly Gly Phe Ala Glu Asn Leu Ala Gly Leu Arg Met Gln
 185 190 195

cct ttc tat gat 703
 Pro Phe Tyr Asp

200

<210> 408

<211> 201

<212> PRT

<213> Corynebacterium glutamicum

<400> 408

Met Gly Ile Leu Asn Ser Ile Ser Thr Pro Ala Asp Leu Lys Ala Leu
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Asn Asp Glu Asp Leu Asp Ala Leu Ala Lys Glu Ile Arg Thr Phe Leu
 20 25 30

Val Asp Lys Val Ala Ala Thr Gly Gly His Leu Gly Pro Asn Leu Gly
 35 40 45

Val Val Glu Leu Thr Ile Gly Leu His Arg Val Phe Asp Ser Pro Gln
 50 55 60

Asp Pro Ile Ile Phe Asp Thr Ser His Gln Ser Tyr Val His Lys Ile
 65 70 75 80

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Lys Ile Pro Gly Asp Leu Pro Leu Gly Trp His Lys Leu His Leu Lys
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Gln	Pro	Gly	Thr	Thr	Arg	Asp	Met	Tyr	Pro	Asn	Trp	Cys	Ile	Pro	Leu	
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Cys	Asp	Ser	Glu	Gly	Asn	Ser	Val	Leu	Ile	Glu	Ser	Leu	Arg	Glu	Asn	
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Lys Leu His Leu Lys Ser Asn Glu Arg Ser Ala Glu Cys Gly Leu Ile
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 Met Pro Arg Met Gln Ser Pro Ala Thr Gly Thr Tyr Ile Arg Phe Asp
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 His Asn Ala Leu Val Gly Ile Leu Ala Leu Glu Ala Glu Leu Ala Gly
 485 490 495
 Ala Val Val Ile Gly Glu Asp Leu Gly Thr Phe Glu Pro Trp Val Gln
 500 505 510
 Asp Ala Leu Ala Gln Arg Gly Ile Met Gly Thr Ser Ile Leu Trp Phe
 515 520 525
 Glu His Ser Pro Ser Gln Pro Gly Pro Arg Arg Gln Glu Glu Tyr Arg
 530 535 540
 Pro Leu Ala Leu Thr Thr Val Thr Thr His Asp Leu Pro Pro Thr Ala
 545 550 555 560
 Gly Tyr Leu Glu Gly Glu His Ile Ala Leu Arg Glu Arg Leu Gly Val
 565 570 575
 Leu Asn Thr Asp Pro Ala Ala Glu Leu Ala Glu Asp Leu Gln Trp Gln
 580 585 590
 Ala Glu Ile Leu Asp Val Ala Ala Ser Ala Asn Ala Leu Pro Ala Arg
 595 600 605
 Glu Tyr Val Gly Leu Glu Arg Asp Gln Arg Gly Glu Leu Ala Glu Leu
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 Leu Glu Gly Leu His Thr Phe Val Ala Lys Thr Pro Ser Ala Leu Thr
 625 630 635 640
 Cys Val Cys Leu Val Asp Met Val Gly Glu Lys Arg Ala Gln Asn Gln
 645 650 655
 Pro Gly Thr Thr Arg Asp Met Tyr Pro Asn Trp Cys Ile Pro Leu Cys
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<210> 413

<211> 1287

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(1264)

<223> RXN00043

<400> 413

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Met Ala Glu Val Val	
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cat tat caa gaa aat gca ggt caa gca gtt aaa aaa att gaa gga aga	163
His Tyr Gln Glu Asn Ala Gly Gln Ala Val Lys Lys Ile Glu Gly Arg	
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att gtt acc ccc cac ggg gtg att gat ggc ttt ctc caa ctc gaa aac	211
Ile Val Thr Pro His Gly Val Ile Asp Gly Phe Leu Gln Leu Glu Asn	
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ggc atc atc acg gaa ctc tct gga gaa cca gca cct aaa aac gca gga	259
Gly Ile Ile Thr Glu Leu Ser Gly Glu Pro Ala Pro Lys Asn Ala Gly	
40 45 50	
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Phe His Pro Glu Leu Pro Thr Ile Val Pro Ser Phe Ile Asp Leu His	
55 60 65	
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Asn His Gly Gly Asn Gly Gly Ala Phe Pro Thr Gly Thr Gln Asp Gln	
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gcg agg aat gcc gcg cag tat cac cgc gaa cat ggc acg acc gtg atg	403
Ala Arg Asn Ala Ala Gln Tyr His Arg Glu His Gly Thr Thr Val Met	
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Leu Ala Ser Met Val Ser Ala Pro Ala Asp Ala Leu Ala Ala Gln Val	
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Glu Asn Leu Ile Pro Leu Cys Glu Glu Gly Leu Leu Cys Gly Ile His	
120 125 130	
ctc gag ggt cct ttc atc aac gca tgc cgt tgt ggt gct caa aac ccg	547
Leu Glu Gly Pro Phe Ile Asn Ala Cys Arg Cys Gly Ala Gln Asn Pro	
135 140 145	
gat ttt att ttt ccc ggc aac cca aca gat ctt gcc cag gtg atc cat	595
Asp Phe Ile Phe Pro Gly Asn Pro Thr Asp Leu Ala Gln Val Ile His	
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gcg gga aaa ggt tgg atc aaa tcg atc aca gta gcg ccg gaa act gac	643
Ala Gly Lys Gly Trp Ile Lys Ser Ile Thr Val Ala Pro Glu Thr Asp	
170 175 180	
aat ctt act gag ctt ctc gat ctc tgc gca gcg cac cac atc att gct	691
Asn Leu Thr Glu Leu Leu Asp Leu Cys Ala Ala His His Ile Ile Ala	
185 190 195	
tcc ttc ggg cac act gat gca gat ttt gat acc act acc agc gca att	739
Ser Phe Gly His Thr Asp Ala Asp Phe Asp Thr Thr Thr Ser Ala Ile	
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gcc ttg gct aaa gag aaa aat gtg acg gtc acg gct acg cat ttg ttc	787
Ala Leu Ala Lys Glu Lys Asn Val Thr Val Thr Ala Thr His Leu Phe	
215 220 225	

aat gcg atg cct ccg ctg cat cat agg gat ccc ggc agc gtg ggc gct 835
 Asn Ala Met Pro Pro Leu His His Arg Asp Pro Gly Ser Val Gly Ala
 230 235 240 245

 ttg ctt gct gcg gca cgt gcc ggg gac gca tat gtt gag ttg atc gcc 883
 Leu Leu Ala Ala Ala Arg Ala Gly Asp Ala Tyr Val Glu Leu Ile Ala
 250 255 260

 gac ggc gtg cat ttg gcc gat gga acg gtc gat cta gct cgt tcc aac 931
 Asp Gly Val His Leu Ala Asp Gly Thr Val Asp Leu Ala Arg Ser Asn
 265 270 275

 aac gcc ttt ttc atc acg gac gcc atg gaa gcc gcc gga atg cca gac 979
 Asn Ala Phe Phe Ile Thr Asp Ala Met Glu Ala Ala Gly Met Pro Asp
 280 285 290

 ggt gag tac att ttg ggc gtt ttg aac gtc acc gtc acc gat ggc gtc 1027
 Gly Glu Tyr Ile Leu Gly Val Leu Asn Val Thr Val Thr Asp Gly Val
 295 300 305

 gcc cgt ctg cgc gat ggc gcc gcc atc gcc ggg ggt acc agc aca cta 1075
 Ala Arg Leu Arg Asp Gly Gly Ala Ile Ala Gly Gly Thr Ser Thr Leu
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 gcg agt cag ttc gtg cac cac gtg cgc agg ggt atg acg ctt atc gac 1123
 Ala Ser Gln Phe Val His His Val Arg Arg Gly Met Thr Leu Ile Asp
 330 335 340

 gcg acc ctc cac acc tca acc gtc gcc gcc aaa att ctc gga ctt agc 1171
 Ala Thr Leu His Thr Ser Thr Val Ala Ala Lys Ile Leu Gly Leu Ser
 345 350 355

 gat cac gaa atc gtt aaa tcc aac cct gta aat ttt gtg gtc ttt gac 1219
 Asp His Glu Ile Val Lys Ser Asn Pro Val Asn Phe Val Val Phe Asp
 360 365 370

 tca aac ggc cag tta caa cag gtc cat tta gac cat caa gta att 1264
 Ser Asn Gly Gln Leu Gln Gln Val His Leu Asp His Gln Val Ile
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<210> 414

<211> 388

<212> PRT

<213> Corynebacterium glutamicum

<400> 414

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 35 40 45

 Pro Lys Asn Ala Gly Phe His Pro Glu Leu Pro Thr Ile Val Pro Ser
 50 55 60

Phe Ile Asp Leu His Asn His Gly Gly Asn Gly Gly Ala Phe Pro Thr
 65 70 75 80
 Gly Thr Gln Asp Gln Ala Arg Asn Ala Ala Gln Tyr His Arg Glu His
 85 90 95
 Gly Thr Thr Val Met Leu Ala Ser Met Val Ser Ala Pro Ala Asp Ala
 100 105 110
 Leu Ala Ala Gln Val Glu Asn Leu Ile Pro Leu Cys Glu Glu Gly Leu
 115 120 125
 Leu Cys Gly Ile His Leu Glu Gly Pro Phe Ile Asn Ala Cys Arg Cys
 130 135 140
 Gly Ala Gln Asn Pro Asp Phe Ile Phe Pro Gly Asn Pro Thr Asp Leu
 145 150 155 160
 Ala Gln Val Ile His Ala Gly Lys Gly Trp Ile Lys Ser Ile Thr Val
 165 170 175
 Ala Pro Glu Thr Asp Asn Leu Thr Glu Leu Leu Asp Leu Cys Ala Ala
 180 185 190
 His His Ile Ile Ala Ser Phe Gly His Thr Asp Ala Asp Phe Asp Thr
 195 200 205
 Thr Thr Ser Ala Ile Ala Leu Ala Lys Glu Lys Asn Val Thr Val Thr
 210 215 220
 Ala Thr His Leu Phe Asn Ala Met Pro Pro Leu His His Arg Asp Pro
 225 230 235 240
 Gly Ser Val Gly Ala Leu Leu Ala Ala Ala Arg Ala Gly Asp Ala Tyr
 245 250 255
 Val Glu Leu Ile Ala Asp Gly Val His Leu Ala Asp Gly Thr Val Asp
 260 265 270
 Leu Ala Arg Ser Asn Asn Ala Phe Phe Ile Thr Asp Ala Met Glu Ala
 275 280 285
 Ala Gly Met Pro Asp Gly Glu Tyr Ile Leu Gly Val Leu Asn Val Thr
 290 295 300
 Val Thr Asp Gly Val Ala Arg Leu Arg Asp Gly Gly Ala Ile Ala Gly
 305 310 315 320
 Gly Thr Ser Thr Leu Ala Ser Gln Phe Val His His Val Arg Arg Gly
 325 330 335
 Met Thr Leu Ile Asp Ala Thr Leu His Thr Ser Thr Val Ala Ala Lys
 340 345 350
 Ile Leu Gly Leu Ser Asp His Glu Ile Val Lys Ser Asn Pro Val Asn
 355 360 365
 Phe Val Val Phe Asp Ser Asn Gly Gln Leu Gln Gln Val His Leu Asp
 370 375 380
 His Gln Val Ile

Ala Gly Lys Gly Trp Ile Lys Ser Ile Thr Val Ala Pro Glu Thr Asp
170 175 180

aat ctt act gag ctt ctc gat ctc tgc gca gcg cac cac atc att gct 691
Asn Leu Thr Glu Leu Leu Asp Leu Cys Ala Ala His His Ile Ile Ala
185 190 195

tcc ttc ggg cac act gat gca gat ttt gat acc act acc agc gca att 739
Ser Phe Gly His Thr Asp Ala Asp Phe Asp Thr Thr Thr Ser Ala Ile
200 205 210

gcc ttg gct aaa gag aaa aat gtg acg gtc acg gct acg cat ttg ttc 787
Ala Leu Ala Lys Glu Lys Asn Val Thr Val Thr Ala Thr His Leu Phe
215 220 225

aat gcg atg cct ccg ctg cat cat agg gat ccc ggc agc gtg ggc gct 835
Asn Ala Met Pro Pro Leu His His Arg Asp Pro Gly Ser Val Gly Ala
230 235 240 245

ttg ctt gct gcg gca cgt gcc ggg gac gca tat gtt gag ttg atc gcc 883
Leu Leu Ala Ala Arg Ala Gly Asp Ala Tyr Val Glu Leu Ile Ala
250 255 260

gac ggc gtg cat ttg gcc gat gga acg gtc gat cta gct cgt tcc aac 931
Asp Gly Val His Leu Ala Asp Gly Thr Val Asp Leu Ala Arg Ser Asn
265 270 275

aac gcc ttt ttc atc acg gac gcc atg gaa gcc gcc gga atg cca gac 979
Asn Ala Phe Phe Ile Thr Asp Ala Met Glu Ala Ala Gly Met Pro Asp
280 285 290

ggt gag tac att ttg ggc gtt ttg aac gtc acc gtc acc gat ggc gtc 1027
Gly Glu Tyr Ile Leu Gly Val Leu Asn Val Thr Val Thr Asp Gly Val
295 300 305

gcc cgt ctg cgc gat ggc ggc gcc atc gcc ggg ggt acc agc aca cta 1075
Ala Arg Leu Arg Asp Gly Gly Ala Ile Ala Gly Gly Thr Ser Thr Leu
310 315 320 325

gcg agt cag ttc gtg cac cac gtg cgc agg ggt atg acg ctt atc gac 1123
Ala Ser Gln Phe Val His His Val Arg Arg Gly Met Thr Leu Ile Asp
330 335 340

gcg acc ctc cac acc tca acc gtc gcc gcc aaa att ctc gga ctt agc 1171
Ala Thr Leu His Thr Ser Thr Val Ala Ala Lys Ile Leu Gly Leu Ser
345 350 355

gat cac gaa atc gtt aaa tcc aac cct gta aat ttt gtg gtc ttt gac 1219
Asp His Glu Ile Val Lys Ser Asn Pro Val Asn Phe Val Val Phe Asp
360 365 370

tca aac ggc cag tta caa cag gtc cat tta gac cat caa gta att 1264
Ser Asn Gly Gln Leu Gln Gln Val His Leu Asp His Gln Val Ile
375 380 385

taaatacgag caaaactttc ctg 1287

<210> 416

<211> 388

<212> PRT

<213> Corynebacterium glutamicum

<400> 416

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Leu Gln Leu Glu Asn Gly Ile Ile Thr Glu Leu Ser Gly Glu Pro Ala
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Pro Lys Asn Ala Gly Phe His Pro Glu Leu Pro Thr Ile Val Pro Ser
      50          55          60

Phe Ile Asp Leu His Asn His Gly Gly Asn Gly Gly Ala Phe Pro Thr
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Gly Thr Gln Asp Gln Ala Arg Asn Ala Ala Gln Tyr His Arg Glu His
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Gly Thr Thr Val Met Leu Ala Ser Met Val Ser Ala Pro Ala Asp Ala
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Leu Ala Ala Gln Val Glu Asn Leu Ile Pro Leu Cys Glu Glu Gly Leu
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Leu Cys Gly Ile His Leu Glu Gly Pro Phe Ile Asn Ala Cys Arg Cys
      130          135          140

Gly Ala Gln Asn Pro Asp Phe Ile Phe Pro Gly Asn Pro Thr Asp Leu
      145          150          155          160

Ala Gln Val Ile His Ala Gly Lys Gly Trp Ile Lys Ser Ile Thr Val
          165          170          175

Ala Pro Glu Thr Asp Asn Leu Thr Glu Leu Leu Asp Leu Cys Ala Ala
      180          185          190

His His Ile Ile Ala Ser Phe Gly His Thr Asp Ala Asp Phe Asp Thr
      195          200          205

Thr Thr Ser Ala Ile Ala Leu Ala Lys Glu Lys Asn Val Thr Val Thr
      210          215          220

Ala Thr His Leu Phe Asn Ala Met Pro Pro Leu His His Arg Asp Pro
      225          230          235          240

Gly Ser Val Gly Ala Leu Leu Ala Ala Ala Arg Ala Gly Asp Ala Tyr
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Val Glu Leu Ile Ala Asp Gly Val His Leu Ala Asp Gly Thr Val Asp
          260          265          270

Leu Ala Arg Ser Asn Asn Ala Phe Phe Ile Thr Asp Ala Met Glu Ala
      275          280          285

Ala Gly Met Pro Asp Gly Glu Tyr Ile Leu Gly Val Leu Asn Val Thr
      290          295          300

Val Thr Asp Gly Val Ala Arg Leu Arg Asp Gly Gly Ala Ile Ala Gly

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Ile	Leu	Gly	Leu	Ser	Asp	His	Glu	Ile	Val	Lys	Ser	Asn	Pro	Val	Asn
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Phe	Val	Val	Phe	Asp	Ser	Asn	Gly	Gln	Leu	Gln	Gln	Val	His	Leu	Asp
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Met Met Glu Gln Asp 5															
ctc agc tac cgt gaa att ctt ccc ctc aac gcg agt gag gag aag aaa 163															
Leu Ser Tyr Arg Glu Ile Leu Pro Leu Asn Ala Ser Glu Glu Lys Lys 20															
aag gct gca ctg att gat gcc att gaa ggg tta agg gtg cgc gat ccg 211															
Lys Ala Ala Leu Ile Asp Ala Ile Glu Gly Leu Arg Val Arg Asp Pro 35															
cta ctc tct gcc tcg att gca ttt act aga ggg cag aaa gtc gcc ttc 259															
Leu Leu Ser Ala Ser Ile Ala Phe Thr Arg Gly Gln Lys Val Ala Phe 50															
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Ile Ala Val Val Val Gly Phe Ile Leu Met Leu Ile Phe Ala Arg Gln 65															
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Ala Ala Leu Ile Gly Leu Ser Ala Thr Cys Thr Phe Met Tyr Leu Ile 85															
aca ttg ttg gac aga ttt atc atg ttt tcc aga ggt atc cgc gcg gaa 403															
Thr Leu Leu Asp Arg Phe Ile Met Phe Ser Arg Gly Ile Arg Ala Glu 100															
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Ser Ile Ile Gln Val Ser Asp Glu Asp Ala Leu Ala Phe Pro Glu Asp															

105										110					115					
aag	ctg	aaa	acc	tac	acg	gtg	ttg	gtg	ccc	gcc	tat	ggc	gaa	cct	gag	499				
Lys	Leu	Lys	Thr	Tyr	Thr	Val	Leu	Val	Pro	Ala	Tyr	Gly	Glu	Pro	Glu					
		120					125					130								
gtg	att	gcg	cag	ctg	ctg	gca	tcc	atg	cac	gct	ttt	gat	tac	ccc	aag	547				
Val	Ile	Ala	Gln	Leu	Leu	Ala	Ser	Met	His	Ala	Phe	Asp	Tyr	Pro	Lys					
	135					140					145									
cat	ctt	ctg	cag	gta	ttg	ctc	atg	ttg	gag	gaa	gat	gat	ctg	ccc	acg	595				
His	Leu	Leu	Gln	Val	Leu	Leu	Met	Leu	Glu	Glu	Asp	Asp	Leu	Pro	Thr					
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atc	gcc	gcg	gca	gag	gca	gcg	gga	gtg	gat	cag	gtg	gca	acg	atc	att	643				
Ile	Ala	Ala	Ala	Glu	Ala	Ala	Gly	Val	Asp	Gln	Val	Ala	Thr	Ile	Ile					
				170					175					180						
aag	gtg	ccg	cca	gcg	cag	ccc	cgc	acc	aag	ccg	aag	gcc	tgt	aac	tat	691				
Lys	Val	Pro	Pro	Ala	Gln	Pro	Arg	Thr	Lys	Pro	Lys	Ala	Cys	Asn	Tyr					
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Gly	Leu	His	Phe	Ala	Thr	Gly	Glu	Ile	Val	Thr	Ile	Phe	Asp	Ala	Glu					
	200					205						210								
gac	atg	cca	gat	ccc	ctc	caa	ctg	cgt	cgc	gtg	gtg	gtg	gca	ttt	gaa	787				
Asp	Met	Pro	Asp	Pro	Leu	Gln	Leu	Arg	Arg	Val	Val	Val	Ala	Phe	Glu					
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cgc	tcg	gct	tcc	aat	acg	gtg	tgc	gtc	cag	tca	agg	ttg	tcg	tat	cga	835				
Arg	Ser	Ala	Ser	Asn	Thr	Val	Cys	Val	Gln	Ser	Arg	Leu	Ser	Tyr	Arg					
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Asn	Ala	Arg	Gln	Asn	Leu	Leu	Thr	Ala	Trp	Phe	Thr	Ile	Glu	Tyr	Asp					
			250					255					260							
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Val	Trp	Phe	Asn	Phe	Leu	Leu	Pro	Gly	Val	Met	Arg	Met	Asn	Ala	Pro					
		265					270					275								
gtc	cca	ttg	ggc	ggt	acc	tcc	aac	cat	ctg	ctc	acg	ggt	gtc	ctg	aaa	979				
Val	Pro	Leu	Gly	Gly	Thr	Ser	Asn	His	Leu	Leu	Thr	Gly	Val	Leu	Lys					
	280					285						290								
gat	ctc	ggc	gcg	tgg	gat	cct	ttc	aat	gtc	aca	gaa	aat	gcc	gac	ctc	1027				
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Val	Thr	Trp	Glu	Glu	Ala	Asn	Ser	Asp	Thr	Ile	Asn	Trp	Leu	Arg	Gln					
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cgt	tct	cgc	tgg	tac	aag	ggc	tat	ctg	caa	aca	tgg	ctt	gtg	tat	atg	1171				
Arg	Ser	Arg	Trp	Tyr	Lys	Gly	Tyr	Leu	Gln	Thr	Trp	Leu	Val	Tyr	Met					
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 Arg Arg Pro Lys Trp Leu Val Gln Glu Leu Gly Ile Ile Pro Ala Val
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 cgt ttt acc ttc ctc atg gca ggc acc ccg atc att gcg gtg ctc aat 1267
 Arg Phe Thr Phe Leu Met Ala Gly Thr Pro Ile Ile Ala Val Leu Asn
 375 380 385
 ctg ctc ttt tgg tac ttg tgc ctc acg tgg att ctg ggc cag ccc ggc 1315
 Leu Leu Phe Trp Tyr Leu Ser Leu Thr Trp Ile Leu Gly Gln Pro Gly
 390 395 400 405
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 Thr Ile Glu Gln Met Phe Pro Pro Ala Val Tyr Tyr Pro Ala Leu Val
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 Pro Leu Tyr Trp Leu Leu Met Ser Ile Ala Ala Leu Lys Gly Thr Trp
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<210> 418

<211> 487

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 418

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 Gln Lys Val Ala Phe Ile Ala Val Val Val Gly Phe Ile Leu Met Leu
 50 55 60
 Ile Phe Ala Arg Gln Ala Ala Leu Ile Gly Leu Ser Ala Thr Cys Thr
 65 70 75 80
 Phe Met Tyr Leu Ile Thr Leu Leu Asp Arg Phe Ile Met Phe Ser Arg
 85 90 95

Gly Ile Arg Ala Glu Ser Ile Ile Gln Val Ser Asp Glu Asp Ala Leu
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 Ala Phe Pro Glu Asp Lys Leu Lys Thr Tyr Thr Val Leu Val Pro Ala
 115 120 125
 Tyr Gly Glu Pro Glu Val Ile Ala Gln Leu Leu Ala Ser Met His Ala
 130 135 140
 Phe Asp Tyr Pro Lys His Leu Leu Gln Val Leu Leu Met Leu Glu Glu
 145 150 155 160
 Asp Asp Leu Pro Thr Ile Ala Ala Ala Glu Ala Ala Gly Val Asp Gln
 165 170 175
 Val Ala Thr Ile Ile Lys Val Pro Pro Ala Gln Pro Arg Thr Lys Pro
 180 185 190
 Lys Ala Cys Asn Tyr Gly Leu His Phe Ala Thr Gly Glu Ile Val Thr
 195 200 205
 Ile Phe Asp Ala Glu Asp Met Pro Asp Pro Leu Gln Leu Arg Arg Val
 210 215 220
 Val Val Ala Phe Glu Arg Ser Ala Ser Asn Thr Val Cys Val Gln Ser
 225 230 235 240
 Arg Leu Ser Tyr Arg Asn Ala Arg Gln Asn Leu Leu Thr Ala Trp Phe
 245 250 255
 Thr Ile Glu Tyr Asp Val Trp Phe Asn Phe Leu Leu Pro Gly Val Met
 260 265 270
 Arg Met Asn Ala Pro Val Pro Leu Gly Gly Thr Ser Asn His Leu Leu
 275 280 285
 Thr Gly Val Leu Lys Asp Leu Gly Ala Trp Asp Pro Phe Asn Val Thr
 290 295 300
 Glu Asn Ala Asp Leu Gly Val Pro Ile Ala Ala Lys Gly Tyr Ser Thr
 305 310 315 320
 Ala Val Leu Asp Ser Val Thr Trp Glu Glu Ala Asn Ser Asp Thr Ile
 325 330 335
 Asn Trp Leu Arg Gln Arg Ser Arg Trp Tyr Lys Gly Tyr Leu Gln Thr
 340 345 350
 Trp Leu Val Tyr Met Arg Arg Pro Lys Trp Leu Val Gln Glu Leu Gly
 355 360 365
 Ile Ile Pro Ala Val Arg Phe Thr Phe Leu Met Ala Gly Thr Pro Ile
 370 375 380
 Ile Ala Val Leu Asn Leu Leu Phe Trp Tyr Leu Ser Leu Thr Trp Ile
 385 390 395 400
 Leu Gly Gln Pro Gly Thr Ile Glu Gln Met Phe Pro Pro Ala Val Tyr
 405 410 415

Tyr Pro Ala Leu Val Cys Leu Val Val Ala Asn Ala Ala Thr Ile Phe
 420 425 430
 Met Asn Leu Ile Gly Cys Arg Glu Gly Arg Asp Pro Leu Leu Leu Ile
 435 440 445
 Ala Val Leu Thr Phe Pro Leu Tyr Trp Leu Leu Met Ser Ile Ala Ala
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 465 470 475 480
 Thr Ala His Gly Leu Glu Ala
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<210> 419
 <211> 689
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
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 <222> (19)..(666)
 <223> FRXA01839

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 Thr Ser Asn His Leu Leu Thr Gly Val Leu Lys Asp Leu Gly Ala Trp
 15 20 25
 gat cct ttc aat gtc aca gaa gat gcg gac ctc ggc gta cgc atc gcg 147
 Asp Pro Phe Asn Val Thr Glu Asp Ala Asp Leu Gly Val Arg Ile Ala
 30 35 40
 gca aag gga tat tcc acc gcg gtg ttg gat tcg gtg acg tgg gag gaa 195
 Ala Lys Gly Tyr Ser Thr Ala Val Leu Asp Ser Val Thr Trp Glu Glu
 45 50 55
 gca aac tcc gac acc atc aac tgg ttg cgc cag cgt tct cgc tgg tac 243
 Ala Asn Ser Asp Thr Ile Asn Trp Leu Arg Gln Arg Ser Arg Trp Tyr
 60 65 70 75
 aag ggc tat ctg caa aca tgg ctt gtg tat atg cgc agg cca aag tgg 291
 Lys Gly Tyr Leu Gln Thr Trp Leu Val Tyr Met Arg Arg Pro Lys Trp
 80 85 90
 tta gtc caa gag ctt ggc atc att cct gct gtg cgt ttt acc ttc ctc 339
 Leu Val Gln Glu Leu Gly Ile Ile Pro Ala Val Arg Phe Thr Phe Leu
 95 100 105
 atg gca ggc acc ccg atc att gcg gtg ctc aat ctg ctc ttt tgg tac 387
 Met Ala Gly Thr Pro Ile Ile Ala Val Leu Asn Leu Phe Trp Tyr
 110 115 120
 ttg tcg ctc acg tgg att ctg ggc cag ccc ggc acc att gag cag atg 435
 Leu Ser Leu Thr Trp Ile Leu Gly Gln Pro Gly Thr Ile Glu Gln Met

125	130	135	
ttc cca cct gcg gtg tac tac cca gcg ttg gtg tgt ttg gtg gtg gcc			483
Phe Pro Pro Ala Val Tyr Tyr Pro Ala Leu Val Cys Leu Val Val Ala			
140	145	150	155
aat gct gcg acc atc ttt atg aat ctc att ggc tgc cgg gaa ggc cgc			531
Asn Ala Ala Thr Ile Phe Met Asn Leu Ile Gly Cys Arg Glu Gly Arg			
	160	165	170
gac ccc ttg ctg ctc atc gcg gtt ctc acg ttc ccg ctg tat tgg ctg			579
Asp Pro Leu Leu Leu Ile Ala Val Leu Thr Phe Pro Leu Tyr Trp Leu			
	175	180	185
ctc atg agc att gca gcg ttg aaa ggc acg tgg caa ttg atc acg cga			627
Leu Met Ser Ile Ala Ala Leu Lys Gly Thr Trp Gln Leu Ile Thr Arg			
	190	195	200
cca tcc tat tgg gag aaa act gcc cac gga ttg gag gcg taagcgggtgc			676
Pro Ser Tyr Trp Glu Lys Thr Ala His Gly Leu Glu Ala			
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Leu Thr Gly Val Leu Lys Asp Leu Gly Ala Trp Asp Pro Phe Asn Val			
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Thr Glu Asp Ala Asp Leu Gly Val Arg Ile Ala Ala Lys Gly Tyr Ser			
	35	40	45
Thr Ala Val Leu Asp Ser Val Thr Trp Glu Glu Ala Asn Ser Asp Thr			
	50	55	60
Ile Asn Trp Leu Arg Gln Arg Ser Arg Trp Tyr Lys Gly Tyr Leu Gln			
	65	70	75
Thr Trp Leu Val Tyr Met Arg Arg Pro Lys Trp Leu Val Gln Glu Leu			
	85	90	95
Gly Ile Ile Pro Ala Val Arg Phe Thr Phe Leu Met Ala Gly Thr Pro			
	100	105	110
Ile Ile Ala Val Leu Asn Leu Leu Phe Trp Tyr Leu Ser Leu Thr Trp			
	115	120	125
Ile Leu Gly Gln Pro Gly Thr Ile Glu Gln Met Phe Pro Pro Ala Val			
	130	135	140
Tyr Tyr Pro Ala Leu Val Cys Leu Val Val Ala Asn Ala Ala Thr Ile			
145	150	155	160

Phe Met Asn Leu Ile Gly Cys Arg Glu Gly Arg Asp Pro Leu Leu Leu
 165 170 175

Ile Ala Val Leu Thr Phe Pro Leu Tyr Trp Leu Leu Met Ser Ile Ala
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Ala Leu Lys Gly Thr Trp Gln Leu Ile Thr Arg Pro Ser Tyr Trp Glu
 195 200 205

Lys Thr Ala His Gly Leu Glu Ala
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<220>
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 <223> RXA01859

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 Met Lys Lys Lys Ser
 1 5

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 Phe Pro Ile Ala Arg Val Ile Gly Ile Gly Val Leu Gly Ile Ala Gly
 10 15 20

atg gga ata ttg ttg cta tgg ctt gca gtt acc ctg tct gat cca gca 211
 Met Gly Ile Leu Leu Leu Trp Leu Ala Val Thr Leu Ser Asp Pro Ala
 25 30 35

tca ccg ggt gcc aaa gaa acc gaa gtc ttt gat agg tgg aaa gtg ctc 259
 Ser Pro Gly Ala Lys Glu Thr Glu Val Phe Asp Arg Trp Lys Val Leu
 40 45 50

ttt gat gac tat att cca cca gtc agg gta ttg gtt gct gcg att atc 307
 Phe Asp Asp Tyr Ile Pro Pro Val Arg Val Leu Val Ala Ala Ile Ile
 55 60 65

gtt gca tta att ttc gtc ttt atc gct gcc aca gtg gaa cga acc gta 355
 Val Ala Leu Ile Phe Val Phe Ile Ala Ala Thr Val Glu Arg Thr Val
 70 75 80 85

acc aac cgc tac cga agc tcc gta gac ggc gaa aga gtg cca tta gcg 403
 Thr Asn Arg Tyr Arg Ser Ser Val Asp Gly Glu Arg Val Pro Leu Ala
 90 95 100

ccg aag att gtg atg gca gaa acc cga ggg gta ttt cat gga ccg att 451
 Pro Lys Ile Val Met Ala Glu Thr Arg Gly Val Phe His Gly Pro Ile
 105 110 115

acc att aac gtg ctc gtg cca gca cac aat gag gcg gaa aga att act 499
 Thr Ile Asn Val Leu Val Pro Ala His Asn Glu Ala Glu Arg Ile Thr
 120 125 130

gga aca att cag gca ttg aaa tca caa cat gag cct cca gaa cgc atc 547
 Gly Thr Ile Gln Ala Leu Lys Ser Gln His Glu Pro Pro Glu Arg Ile
 135 140 145
 gtt gta gtt gcc gat aat tgc act gat gaa act acg gaa tta gcc cgt 595
 Val Val Val Ala Asp Asn Cys Thr Asp Glu Thr Thr Glu Leu Ala Arg
 150 155 160 165
 gct gag gga gtg gag gtc ttg gaa aca gtc aat aat aag ttt aag aag 643
 Ala Glu Gly Val Glu Val Leu Glu Thr Val Asn Asn Lys Phe Lys Lys
 170 175 180
 gcc gga gga ctc aat cag gct ttg agc cgg atg ctt ccc aca ttg ggg 691
 Ala Gly Gly Leu Asn Gln Ala Leu Ser Arg Met Leu Pro Thr Leu Gly
 185 190 195
 gag aat gac att gtg atg atc gtt gac gct gat aca gca ctt gat caa 739
 Glu Asn Asp Ile Val Met Ile Val Asp Ala Asp Thr Ala Leu Asp Gln
 200 205 210
 ggt ttc ctc aag gaa gca cgg cgc cgc ttt gag tct gat cgc gct cta 787
 Gly Phe Leu Lys Glu Ala Arg Arg Arg Phe Glu Ser Asp Arg Ala Leu
 215 220 225
 atg gcc gtg ggc gga ttg ttc tac ggt gag tca ggc tcc gga tgg ctt 835
 Met Ala Val Gly Gly Leu Phe Tyr Gly Glu Ser Gly Ser Gly Trp Leu
 230 235 240 245
 ggc caa tat cag cgc aac gaa tac acc cgt tat agc cgt gac atc tat 883
 Gly Gln Tyr Gln Arg Asn Glu Tyr Thr Arg Tyr Ser Arg Asp Ile Tyr
 250 255 260
 cga cgc cgc gga cgt gtg ttt gtt ttg act gga aca gcg tcg gct ttt 931
 Arg Arg Arg Gly Arg Val Phe Val Leu Thr Gly Thr Ala Ser Ala Phe
 265 270 275
 cgg cca cgc ggc ctg cgg aca gta gcg gaa tca cgc ggg aca ttg atc 979
 Arg Pro Arg Gly Leu Arg Thr Val Ala Glu Ser Arg Gly Thr Leu Ile
 280 285 290
 ccc gga cgt aaa gcc gat gtt tat gac acc gcg ggc gtt gac cga aga 1027
 Pro Gly Arg Lys Ala Asp Val Tyr Asp Thr Ala Gly Val Asp Arg Arg
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 taatgagttg accctggcctt tga 1050

<210> 422

<211> 309

<212> PRT

<213> Corynebacterium glutamicum

<400> 422

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Leu Ser Asp Pro Ala Ser Pro Gly Ala Lys Glu Thr Glu Val Phe Asp

35					40					45									
Arg	Trp	Lys	Val	Leu	Phe	Asp	Asp	Tyr	Ile	Pro	Pro	Val	Arg	Val	Leu				
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Val	Ala	Ala	Ile	Ile	Val	Ala	Leu	Ile	Phe	Val	Phe	Ile	Ala	Ala	Thr				
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Val	Glu	Arg	Thr	Val	Thr	Asn	Arg	Tyr	Arg	Ser	Ser	Val	Asp	Gly	Glu				
85					90					95									
Arg	Val	Pro	Leu	Ala	Pro	Lys	Ile	Val	Met	Ala	Glu	Thr	Arg	Gly	Val				
100					105					110									
Phe	His	Gly	Pro	Ile	Thr	Ile	Asn	Val	Leu	Val	Pro	Ala	His	Asn	Glu				
115					120					125									
Ala	Glu	Arg	Ile	Thr	Gly	Thr	Ile	Gln	Ala	Leu	Lys	Ser	Gln	His	Glu				
130					135					140									
Pro	Pro	Glu	Arg	Ile	Val	Val	Val	Ala	Asp	Asn	Cys	Thr	Asp	Glu	Thr				
145					150					155					160				
Thr	Glu	Leu	Ala	Arg	Ala	Glu	Gly	Val	Glu	Val	Leu	Glu	Thr	Val	Asn				
165					170					175									
Asn	Lys	Phe	Lys	Lys	Ala	Gly	Gly	Leu	Asn	Gln	Ala	Leu	Ser	Arg	Met				
180					185					190									
Leu	Pro	Thr	Leu	Gly	Glu	Asn	Asp	Ile	Val	Met	Ile	Val	Asp	Ala	Asp				
195					200					205									
Thr	Ala	Leu	Asp	Gln	Gly	Phe	Leu	Lys	Glu	Ala	Arg	Arg	Arg	Phe	Glu				
210					215					220									
Ser	Asp	Arg	Ala	Leu	Met	Ala	Val	Gly	Gly	Leu	Phe	Tyr	Gly	Glu	Ser				
225					230					235					240				
Gly	Ser	Gly	Trp	Leu	Gly	Gln	Tyr	Gln	Arg	Asn	Glu	Tyr	Thr	Arg	Tyr				
245					250					255									
Ser	Arg	Asp	Ile	Tyr	Arg	Arg	Arg	Gly	Arg	Val	Phe	Val	Leu	Thr	Gly				
260					265					270									
Thr	Ala	Ser	Ala	Phe	Arg	Pro	Arg	Gly	Leu	Arg	Thr	Val	Ala	Glu	Ser				
275					280					285									
Arg	Gly	Thr	Leu	Ile	Pro	Gly	Arg	Lys	Ala	Asp	Val	Tyr	Asp	Thr	Ala				
290					295					300									
Gly	Val	Asp	Arg	Arg															
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<211> 882

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(859)

<223> RXA00042

<400> 423

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                                         Met Asp Ile Ile Ile
                                         1                               5

tgc aaa gac gag caa gaa gtc ggc aaa gca gcg gca gcc ctg atc gca 163
Cys Lys Asp Glu Gln Glu Val Gly Lys Ala Ala Ala Ala Leu Ile Ala
                        10                        15                        20

ccc ttc gca act aag ggc gga acc ttg ggg ctt gca act gga tgc tca 211
Pro Phe Ala Thr Lys Gly Gly Thr Leu Gly Leu Ala Thr Gly Ser Ser
                        25                        30                        35

cct ttg agc acc tac caa gag ctc att cgc atg tat gaa gct ggg gaa 259
Pro Leu Ser Thr Tyr Gln Glu Leu Ile Arg Met Tyr Glu Ala Gly Glu
                        40                        45                        50

gtg tca ttc aag aac tgc aag gca ttc ttg ttg gat gaa tac gtg gga 307
Val Ser Phe Lys Asn Cys Lys Ala Phe Leu Leu Asp Glu Tyr Val Gly
                        55                        60                        65

tta acg cgc gac gat gaa aac agc tac ttc aaa acc att cgt aaa gag 355
Leu Thr Arg Asp Asp Glu Asn Ser Tyr Phe Lys Thr Ile Arg Lys Glu
                        70                        75                        80                        85

ttc act gac cac atc gac atc gtt gat gaa gag gtc tac agc cca gat 403
Phe Thr Asp His Ile Asp Ile Val Asp Glu Glu Val Tyr Ser Pro Asp
                        90                        95                        100

ggg gca aac cct gat cca tac gaa gca gct gca gag tat gag gca aag 451
Gly Ala Asn Pro Asp Pro Tyr Glu Ala Ala Ala Glu Tyr Glu Ala Lys
                        105                        110                        115

atc gct gca gaa tcc gtt gat gtt caa atc ctt ggc atc ggc gga aac 499
Ile Ala Ala Glu Ser Val Asp Val Gln Ile Leu Gly Ile Gly Gly Asn
                        120                        125                        130

ggc cac atc gct ttc aat gag cca tca tct tct ctg tca gga ctg aca 547
Gly His Ile Ala Phe Asn Glu Pro Ser Ser Ser Leu Ser Gly Leu Thr
                        135                        140                        145

aag gtc cag gcg ctg cac cct aaa act gtg gag gac aac gct cga ttc 595
Lys Val Gln Ala Leu His Pro Lys Thr Val Glu Asp Asn Ala Arg Phe
                        150                        155                        160                        165

ttc aac acc atc gaa gag gtc cca acc cac gcc ctc acc cag ggt ttg 643
Phe Asn Thr Ile Glu Glu Val Pro Thr His Ala Leu Thr Gln Gly Leu
                        170                        175                        180

ggc act ttg tcc cgc gcg caa aac atc gtg ttg gtg gca act ggt gaa 691
Gly Thr Leu Ser Arg Ala Gln Asn Ile Val Leu Val Ala Thr Gly Glu
                        185                        190                        195

gga aaa gcc gac gcc atc cgc gga act gtg gaa gcc cca ctg acc gcc 739
Gly Lys Ala Asp Ala Ile Arg Gly Thr Val Glu Gly Pro Leu Thr Ala
                        200                        205                        210

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atg tgc cca ggt tcc atc ctg cag atg cac aac aat gcc acc atc atc 787
 Met Cys Pro Gly Ser Ile Leu Gln Met His Asn Asn Ala Thr Ile Ile
 215 220 225

gtt gat gaa gca gca gca tcc aag ctg gaa aac gct gat cac tac cgt 835
 Val Asp Glu Ala Ala Ala Ser Lys Leu Glu Asn Ala Asp His Tyr Arg
 230 235 240 245

ctc atg gag caa tta aag ctg cgc tagaaacaaa aaggaaagta gtg 882
 Leu Met Glu Gln Leu Lys Leu Arg
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<210> 424
 <211> 253
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 <213> Corynebacterium glutamicum

<400> 424
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 35 40 45

Tyr Glu Ala Gly Glu Val Ser Phe Lys Asn Cys Lys Ala Phe Leu Leu
 50 55 60

Asp Glu Tyr Val Gly Leu Thr Arg Asp Asp Glu Asn Ser Tyr Phe Lys
 65 70 75 80

Thr Ile Arg Lys Glu Phe Thr Asp His Ile Asp Ile Val Asp Glu Glu
 85 90 95

Val Tyr Ser Pro Asp Gly Ala Asn Pro Asp Pro Tyr Glu Ala Ala Ala
 100 105 110

Glu Tyr Glu Ala Lys Ile Ala Ala Glu Ser Val Asp Val Gln Ile Leu
 115 120 125

Gly Ile Gly Gly Asn Gly His Ile Ala Phe Asn Glu Pro Ser Ser Ser
 130 135 140

Leu Ser Gly Leu Thr Lys Val Gln Ala Leu His Pro Lys Thr Val Glu
 145 150 155 160

Asp Asn Ala Arg Phe Phe Asn Thr Ile Glu Glu Val Pro Thr His Ala
 165 170 175

Leu Thr Gln Gly Leu Gly Thr Leu Ser Arg Ala Gln Asn Ile Val Leu
 180 185 190

Val Ala Thr Gly Glu Gly Lys Ala Asp Ala Ile Arg Gly Thr Val Glu
 195 200 205

Gly Pro Leu Thr Ala Met Cys Pro Gly Ser Ile Leu Gln Met His Asn
 210 215 220

Asn Ala Thr Ile Ile Val Asp Glu Ala Ala Ala Ser Lys Leu Glu Asn
 225 230 235 240

Ala Asp His Tyr Arg Leu Met Glu Gln Leu Lys Leu Arg
 245 250

<210> 425

<211> 1998

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(1975)

<223> RXA01482

<400> 425

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 Met Arg Met Cys Gly
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att gtt gga tat att ggc caa gcg ggc gac tcc cgt gat tac ttt gct 163
 Ile Val Gly Tyr Ile Gly Gln Ala Gly Asp Ser Arg Asp Tyr Phe Ala
 10 15 20

cta gat gta gtt gtt gaa gga cta cgt cgc ctg gaa tac cgc gga tat 211
 Leu Asp Val Val Val Glu Gly Leu Arg Arg Leu Glu Tyr Arg Gly Tyr
 25 30 35

gac tcc gca ggt att gct att cac gcc aat ggt gag att agc tac cga 259
 Asp Ser Ala Gly Ile Ala Ile His Ala Asn Gly Glu Ile Ser Tyr Arg
 40 45 50

aag aag gcc gga aag gtt gct gca cta gat gca gaa atc gct aaa gca 307
 Lys Lys Ala Gly Lys Val Ala Ala Leu Asp Ala Glu Ile Ala Lys Ala
 55 60 65

cct ctt cca gat tct att ttg gga att gga cac acc cgt tgg gca act 355
 Pro Leu Pro Asp Ser Ile Leu Gly Ile Gly His Thr Arg Trp Ala Thr
 70 75 80 85

cat ggt ggc cca acc gat gtc aac gct cac ccc cac gtt gtt tcc aat 403
 His Gly Gly Pro Thr Asp Val Asn Ala His Pro His Val Val Ser Asn
 90 95 100

ggc aag ctt gcc gta gta cac aac ggc atc atc gaa aac ttt gcg gaa 451
 Gly Lys Leu Ala Val Val His Asn Gly Ile Ile Glu Asn Phe Ala Glu
 105 110 115

ctg cgc tct gag ctt tcc gct aag ggc tac aac ttt gta tcc gat acc 499
 Leu Arg Ser Glu Leu Ser Ala Lys Gly Tyr Asn Phe Val Ser Asp Thr
 120 125 130

gat acc gaa gtt gct gct tct ttg ctt gct gaa att tac aat act cag 547
 Asp Thr Glu Val Ala Ala Ser Leu Leu Ala Glu Ile Tyr Asn Thr Gln
 135 140 145

gca aac ggt gac ctc acc ctt gct atg cag ctg acc ggt cag cgc ctt	595
Ala Asn Gly Asp Leu Thr Leu Ala Met Gln Leu Thr Gly Gln Arg Leu	
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Glu Gly Ala Phe Thr Leu Leu Ala Ile His Ala Asp His Asp Asp Arg	
170 175 180	
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Ile Val Ala Ala Arg Arg Asn Ser Pro Leu Val Ile Gly Val Gly Glu	
185 190 195	
ggc gag aac ttc ctc gga tct gac gtt tct ggc ttt att gat tac acc	739
Gly Glu Asn Phe Leu Gly Ser Asp Val Ser Gly Phe Ile Asp Tyr Thr	
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cgc aag gct gta gag ctg gct aat gac cag gtt gtt acc atc acc gct	787
Arg Lys Ala Val Glu Leu Ala Asn Asp Gln Val Val Thr Ile Thr Ala	
215 220 225	
gat gat tac gcc atc acc aac ttt gat gga tca gaa gca gtt ggc aag	835
Asp Asp Tyr Ala Ile Thr Asn Phe Asp Gly Ser Glu Ala Val Gly Lys	
230 235 240 245	
cct ttc gac gtg gag tgg gac gct gca gct gct gaa aag ggt ggc ttc	883
Pro Phe Asp Val Glu Trp Asp Ala Ala Ala Glu Lys Gly Gly Phe	
250 255 260	
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Gly Ser Phe Met Glu Lys Glu Ile His Asp Gln Pro Ala Ala Val Arg	
265 270 275	
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Asp Thr Leu Met Gly Arg Leu Asp Glu Asp Gly Lys Leu Val Leu Asp	
280 285 290	
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Glu Leu Arg Ile Asp Glu Ala Ile Leu Arg Ser Val Asp Lys Ile Val	
295 300 305	
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Ile Val Ala Cys Gly Thr Ala Ala Tyr Ala Gly Gln Val Ala Arg Tyr	
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Ala Ile Glu His Trp Cys Arg Ile Pro Thr Glu Val Glu Leu Ala His	
330 335 340	
gag ttc cgt tac cgc gac cca atc ctc aac gag aag acc ctt gtt gtg	1171
Glu Phe Arg Tyr Arg Asp Pro Ile Leu Asn Glu Lys Thr Leu Val Val	
345 350 355	
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Ala Leu Ser Gln Ser Gly Glu Thr Met Asp Thr Leu Met Ala Val Arg	
360 365 370	
cac gca cgt gag cag ggt gcc aag gtt gtt gct att tgt aac act gtt	1267
His Ala Arg Glu Gln Gly Ala Lys Val Val Ala Ile Cys Asn Thr Val	
375 380 385	
gga tcc act ctt cca cgt gaa gca gat gcg tcc ctg tac acc tac gct	1315

Gly	Ser	Thr	Leu	Pro	Arg	Glu	Ala	Asp	Ala	Ser	Leu	Tyr	Thr	Tyr	Ala		
390					395					400					405		
ggc	cct	gag	atc	gct	gtg	gcg	tcc	acc	aag	gcg	ttc	ttg	gct	cag	atc		1363
Gly	Pro	Glu	Ile	Ala	Val	Ala	Ser	Thr	Lys	Ala	Phe	Leu	Ala	Gln	Ile		
				410					415					420			
act	gct	tct	tac	ttg	ctt	ggc	ctg	tac	ttg	gct	cag	ctg	cgc	ggc	aac		1411
Thr	Ala	Ser	Tyr	Leu	Leu	Gly	Leu	Tyr	Leu	Ala	Gln	Leu	Arg	Gly	Asn		
			425					430					435				
aag	ttc	gct	gat	gag	gtt	tct	tcc	att	ctg	gac	agc	ctg	cgt	gag	atg		1459
Lys	Phe	Ala	Asp	Glu	Val	Ser	Ser	Ile	Leu	Asp	Ser	Leu	Arg	Glu	Met		
		440					445					450					
cct	gag	aag	att	cag	cag	gtc	atc	gat	gca	gaa	gag	cag	atc	aag	aag		1507
Pro	Glu	Lys	Ile	Gln	Gln	Val	Ile	Asp	Ala	Glu	Glu	Gln	Ile	Lys	Lys		
	455					460					465						
ctt	ggc	caa	gat	atg	gca	gat	gct	aag	tct	gtg	ctg	ttc	ctg	ggc	cgc		1555
Leu	Gly	Gln	Asp	Met	Ala	Asp	Ala	Lys	Ser	Val	Leu	Phe	Leu	Gly	Arg		
470					475					480					485		
cac	gtt	ggt	ttc	cca	gtt	gcg	ctt	gag	ggt	gcg	ttg	aag	ctc	aag	gag		1603
His	Val	Gly	Phe	Pro	Val	Ala	Leu	Glu	Gly	Ala	Leu	Lys	Leu	Lys	Glu		
				490					495					500			
atc	gca	tac	ctg	cac	gct	gaa	ggt	ttc	gct	gca	ggc	gag	ctc	aag	cac		1651
Ile	Ala	Tyr	Leu	His	Ala	Glu	Gly	Phe	Ala	Ala	Gly	Glu	Leu	Lys	His		
			505					510					515				
ggc	cca	att	gct	ttg	gtt	gag	gaa	ggc	cag	ccg	atc	ttc	gtt	atc	gtg		1699
Gly	Pro	Ile	Ala	Leu	Val	Glu	Glu	Gly	Gln	Pro	Ile	Phe	Val	Ile	Val		
		520					525					530					
cct	tca	cct	cgt	ggt	cgc	gat	tcc	ctg	cac	tcc	aag	gtt	gtc	tcc	aac		1747
Pro	Ser	Pro	Arg	Gly	Arg	Asp	Ser	Leu	His	Ser	Lys	Val	Val	Ser	Asn		
	535					540					545						
att	cag	gag	atc	cgt	gca	cgt	ggc	gct	gtc	acc	atc	gtg	att	gca	gag		1795
Ile	Gln	Glu	Ile	Arg	Ala	Arg	Gly	Ala	Val	Thr	Ile	Val	Ile	Ala	Glu		
550					555					560					565		
gaa	ggc	gat	gag	gct	gtc	aac	gat	tac	gcc	aac	ttc	atc	atc	cgc	att		1843
Glu	Gly	Asp	Glu	Ala	Val	Asn	Asp	Tyr	Ala	Asn	Phe	Ile	Ile	Arg	Ile		
				570					575					580			
cct	cag	gcc	cca	acc	ctg	atg	cag	cct	ctg	ctg	tcc	acc	gtg	cct	ctg		1891
Pro	Gln	Ala	Pro	Thr	Leu	Met	Gln	Pro	Leu	Leu	Ser	Thr	Val	Pro	Leu		
			585					590					595				
cag	atc	ttt	gcg	tgc	gct	gtg	gca	acc	gca	aag	ggc	tac	aac	gtg	gat		1939
Gln	Ile	Phe	Ala	Cys	Ala	Val	Ala	Thr	Ala	Lys	Gly	Tyr	Asn	Val	Asp		
		600					605					610					
cag	cct	cgt	aac	ctg	gca	aag	tct	gtc	acc	gtc	gaa	taaaaagatt					1985
Gln	Pro	Arg	Asn	Leu	Ala	Lys	Ser	Val	Thr	Val	Glu						
	615					620					625						
tcgcttctcg	acg																1998

<210> 426

<211> 625

<212> PRT

<213> Corynebacterium glutamicum

<400> 426

Met Arg Met Cys Gly Ile Val Gly Tyr Ile Gly Gln Ala Gly Asp Ser
 1 5 10 15

Arg Asp Tyr Phe Ala Leu Asp Val Val Val Glu Gly Leu Arg Arg Leu
 20 25 30

Glu Tyr Arg Gly Tyr Asp Ser Ala Gly Ile Ala Ile His Ala Asn Gly
 35 40 45

Glu Ile Ser Tyr Arg Lys Lys Ala Gly Lys Val Ala Ala Leu Asp Ala
 50 55 60

Glu Ile Ala Lys Ala Pro Leu Pro Asp Ser Ile Leu Gly Ile Gly His
 65 70 75 80

Thr Arg Trp Ala Thr His Gly Gly Pro Thr Asp Val Asn Ala His Pro
 85 90 95

His Val Val Ser Asn Gly Lys Leu Ala Val Val His Asn Gly Ile Ile
 100 105 110

Glu Asn Phe Ala Glu Leu Arg Ser Glu Leu Ser Ala Lys Gly Tyr Asn
 115 120 125

Phe Val Ser Asp Thr Asp Thr Glu Val Ala Ala Ser Leu Leu Ala Glu
 130 135 140

Ile Tyr Asn Thr Gln Ala Asn Gly Asp Leu Thr Leu Ala Met Gln Leu
 145 150 155 160

Thr Gly Gln Arg Leu Glu Gly Ala Phe Thr Leu Leu Ala Ile His Ala
 165 170 175

Asp His Asp Asp Arg Ile Val Ala Ala Arg Arg Asn Ser Pro Leu Val
 180 185 190

Ile Gly Val Gly Glu Gly Glu Asn Phe Leu Gly Ser Asp Val Ser Gly
 195 200 205

Phe Ile Asp Tyr Thr Arg Lys Ala Val Glu Leu Ala Asn Asp Gln Val
 210 215 220

Val Thr Ile Thr Ala Asp Asp Tyr Ala Ile Thr Asn Phe Asp Gly Ser
 225 230 235 240

Glu Ala Val Gly Lys Pro Phe Asp Val Glu Trp Asp Ala Ala Ala Ala
 245 250 255

Glu Lys Gly Gly Phe Gly Ser Phe Met Glu Lys Glu Ile His Asp Gln
 260 265 270

Pro Ala Ala Val Arg Asp Thr Leu Met Gly Arg Leu Asp Glu Asp Gly
 275 280 285

Lys Leu Val Leu Asp Glu Leu Arg Ile Asp Glu Ala Ile Leu Arg Ser
 290 295 300
 Val Asp Lys Ile Val Ile Val Ala Cys Gly Thr Ala Ala Tyr Ala Gly
 305 310 315 320
 Gln Val Ala Arg Tyr Ala Ile Glu His Trp Cys Arg Ile Pro Thr Glu
 325 330 335
 Val Glu Leu Ala His Glu Phe Arg Tyr Arg Asp Pro Ile Leu Asn Glu
 340 345 350
 Lys Thr Leu Val Val Ala Leu Ser Gln Ser Gly Glu Thr Met Asp Thr
 355 360 365
 Leu Met Ala Val Arg His Ala Arg Glu Gln Gly Ala Lys Val Val Ala
 370 375 380
 Ile Cys Asn Thr Val Gly Ser Thr Leu Pro Arg Glu Ala Asp Ala Ser
 385 390 395 400
 Leu Tyr Thr Tyr Ala Gly Pro Glu Ile Ala Val Ala Ser Thr Lys Ala
 405 410 415
 Phe Leu Ala Gln Ile Thr Ala Ser Tyr Leu Leu Gly Leu Tyr Leu Ala
 420 425 430
 Gln Leu Arg Gly Asn Lys Phe Ala Asp Glu Val Ser Ser Ile Leu Asp
 435 440 445
 Ser Leu Arg Glu Met Pro Glu Lys Ile Gln Gln Val Ile Asp Ala Glu
 450 455 460
 Glu Gln Ile Lys Lys Leu Gly Gln Asp Met Ala Asp Ala Lys Ser Val
 465 470 475 480
 Leu Phe Leu Gly Arg His Val Gly Phe Pro Val Ala Leu Glu Gly Ala
 485 490 495
 Leu Lys Leu Lys Glu Ile Ala Tyr Leu His Ala Glu Gly Phe Ala Ala
 500 505 510
 Gly Glu Leu Lys His Gly Pro Ile Ala Leu Val Glu Glu Gly Gln Pro
 515 520 525
 Ile Phe Val Ile Val Pro Ser Pro Arg Gly Arg Asp Ser Leu His Ser
 530 535 540
 Lys Val Val Ser Asn Ile Gln Glu Ile Arg Ala Arg Gly Ala Val Thr
 545 550 555 560
 Ile Val Ile Ala Glu Glu Gly Asp Glu Ala Val Asn Asp Tyr Ala Asn
 565 570 575
 Phe Ile Ile Arg Ile Pro Gln Ala Pro Thr Leu Met Gln Pro Leu Leu
 580 585 590
 Ser Thr Val Pro Leu Gln Ile Phe Ala Cys Ala Val Ala Thr Ala Lys
 595 600 605
 Gly Tyr Asn Val Asp Gln Pro Arg Asn Leu Ala Lys Ser Val Thr Val

610 615 620

Glu
625

<210> 427
<211> 666
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (1)..(666)
<223> RXN03179

<400> 427

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Ala Arg Glu Ala Trp Arg Ile Phe Met Ser His Trp Asp Leu Tyr Ala	
1 5 10 15	
gga acc gca act ggc tac tgg gtg gag cag gaa ttt gag cac gtt ttc	96
Gly Thr Ala Thr Gly Tyr Trp Val Glu Gln Glu Phe Glu His Val Phe	
20 25 30	
ggc atc aac gcg gag cgc ctg aat gtt ggc acc cca gaa cat gct gac	144
Gly Ile Asn Ala Glu Arg Leu Asn Val Gly Thr Pro Glu His Ala Asp	
35 40 45	
gcc atc ttt gat gag ctg acc gat att ctt gcc aag cca gat ttc cga	192
Ala Ile Phe Asp Glu Leu Thr Asp Ile Leu Ala Lys Pro Asp Phe Arg	
50 55 60	
cca cgc gca ctg gct gag cag ttc aac ttg gaa gtt cta gcc acc acc	240
Pro Arg Ala Leu Ala Glu Gln Phe Asn Leu Glu Val Leu Ala Thr Thr	
65 70 75 80	
gac gat ccg ctc gat gac ctg gca gat cac aag gca ctg gca gat gat	288
Asp Asp Pro Leu Asp Asp Leu Ala Asp His Lys Ala Leu Ala Asp Asp	
85 90 95	
cca acc ttc tcc cct cgt gtg ctc cct acc ttc cgc cca gac gca tac	336
Pro Thr Phe Ser Pro Arg Val Leu Pro Thr Phe Arg Pro Asp Ala Tyr	
100 105 110	
acc aag atg tac aac gct ggt tgg gca gaa aaa acc acc aag ctt atc	384
Thr Lys Met Tyr Asn Ala Gly Trp Ala Glu Lys Thr Thr Lys Leu Ile	
115 120 125	
gat acc gca ggt gac ggc aag gca ggc tgg gag ggt tac ctt cag gca	432
Asp Thr Ala Gly Asp Gly Lys Ala Gly Trp Glu Gly Tyr Leu Gln Ala	
130 135 140	
atg cgc aac cgc cgc cag tac ttc atc aat cac ggt gca acc tcc gcg	480
Met Arg Asn Arg Arg Gln Tyr Phe Ile Asn His Gly Ala Thr Ser Ala	
145 150 155 160	
gac cac ggt ctc cac gac acc gac acc acc cca ctg agc cac aaa gat	528
Asp His Gly Leu His Asp Thr Asp Thr Thr Pro Leu Ser His Lys Asp	
165 170 175	

gcc cag aag atc ttg gac aag ggt ctc gct ggc aca gca acc ttg gct 576
 Ala Gln Lys Ile Leu Asp Lys Gly Leu Ala Gly Thr Ala Thr Leu Ala
 180 185 190

gaa atg cat gcc ttc gaa gcc aac acc acc tac cgt tcg cgg aaa tgt 624
 Glu Met His Ala Phe Glu Ala Asn Thr Thr Tyr Arg Ser Arg Lys Cys
 195 200 205

cca aga aga cgg ctg gtc atg acc atc cac cag gtg tgt acc 666
 Pro Arg Arg Arg Leu Val Met Thr Ile His Gln Val Cys Thr
 210 215 220

<210> 428

<211> 222

<212> PRT

<213> Corynebacterium glutamicum

<400> 428

Ala Arg Glu Ala Trp Arg Ile Phe Met Ser His Trp Asp Leu Tyr Ala
 1 5 10 15

Gly Thr Ala Thr Gly Tyr Trp Val Glu Gln Glu Phe Glu His Val Phe
 20 25 30

Gly Ile Asn Ala Glu Arg Leu Asn Val Gly Thr Pro Glu His Ala Asp
 35 40 45

Ala Ile Phe Asp Glu Leu Thr Asp Ile Leu Ala Lys Pro Asp Phe Arg
 50 55 60

Pro Arg Ala Leu Ala Glu Gln Phe Asn Leu Glu Val Leu Ala Thr Thr
 65 70 75 80

Asp Asp Pro Leu Asp Asp Leu Ala Asp His Lys Ala Leu Ala Asp Asp
 85 90 95

Pro Thr Phe Ser Pro Arg Val Leu Pro Thr Phe Arg Pro Asp Ala Tyr
 100 105 110

Thr Lys Met Tyr Asn Ala Gly Trp Ala Glu Lys Thr Thr Lys Leu Ile
 115 120 125

Asp Thr Ala Gly Asp Gly Lys Ala Gly Trp Glu Gly Tyr Leu Gln Ala
 130 135 140

Met Arg Asn Arg Arg Gln Tyr Phe Ile Asn His Gly Ala Thr Ser Ala
 145 150 155 160

Asp His Gly Leu His Asp Thr Asp Thr Thr Pro Leu Ser His Lys Asp
 165 170 175

Ala Gln Lys Ile Leu Asp Lys Gly Leu Ala Gly Thr Ala Thr Leu Ala
 180 185 190

Glu Met His Ala Phe Glu Ala Asn Thr Thr Tyr Arg Ser Arg Lys Cys
 195 200 205

Pro Arg Arg Arg Leu Val Met Thr Ile His Gln Val Cys Thr
 210 215 220

<210> 429
 <211> 672
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (1)..(672)
 <223> FRXA02872

<400> 429
 gct cgt gag gca tgg cgc att ttc atg tcc cac tgg gat ctc tac gca 48
 Ala Arg Glu Ala Trp Arg Ile Phe Met Ser His Trp Asp Leu Tyr Ala
 1 5 10 15
 gga acc gca act ggc tac tgg gtg gag cag gaa ttt gag cac gtt ttc 96
 Gly Thr Ala Thr Gly Tyr Trp Val Glu Gln Glu Phe Glu His Val Phe
 20 25 30
 ggc atc aac gcg gag cgc ctg aat gtt ggc acc cca gaa cat gct gac 144
 Gly Ile Asn Ala Glu Arg Leu Asn Val Gly Thr Pro Glu His Ala Asp
 35 40 45
 gcc atc ttt gat gag ctg acc gat att ctt gcc aag cca gat ttc cga 192
 Ala Ile Phe Asp Glu Leu Thr Asp Ile Leu Ala Lys Pro Asp Phe Arg
 50 55 60
 cca cgc gca ctg gct gag cag ttc aac ttg gaa gtt cta gcc acc acc 240
 Pro Arg Ala Leu Ala Glu Gln Phe Asn Leu Glu Val Leu Ala Thr Thr
 65 70 75 80
 gac gat ccg ctc gat gac ctg gca gat cac aag gca ctg gca gat gat 288
 Asp Asp Pro Leu Asp Asp Leu Ala Asp His Lys Ala Leu Ala Asp Asp
 85 90 95
 cca acc ttc tcc cct cgt gtg ctc cct acc ttc cgc cca gac gca tac 336
 Pro Thr Phe Ser Pro Arg Val Leu Pro Thr Phe Arg Pro Asp Ala Tyr
 100 105 110
 acc aag atg tac aac gct ggt tgg gca gaa aaa acc acc aag ctt atc 384
 Thr Lys Met Tyr Asn Ala Gly Trp Ala Glu Lys Thr Thr Lys Leu Ile
 115 120 125
 gat acc gca ggt gac ggc aag gca ggc tgg gag ggt tac ctt cag gca 432
 Asp Thr Ala Gly Asp Gly Lys Ala Gly Trp Glu Gly Tyr Leu Gln Ala
 130 135 140
 atg cgc aac cgc cgc cag tac ttc atc aat cac ggt gca acc tcc gcg 480
 Met Arg Asn Arg Arg Gln Tyr Phe Ile Asn His Gly Ala Thr Ser Ala
 145 150 155 160
 gac cac ggt ctc cac gac acc gac acc acc cca ctg agc cac aaa gat 528
 Asp His Gly Leu His Asp Thr Asp Thr Thr Pro Leu Ser His Lys Asp
 165 170 175
 gcc cag aag atc ttg gac aag ggt ctc gct ggc aca gca acc ttg gct 576
 Ala Gln Lys Ile Leu Asp Lys Gly Leu Ala Gly Thr Ala Thr Leu Ala
 180 185 190
 gaa atg cat gcc ttc gaa gcc aac acc acc tac cgt ttc gcg gaa atg 624

Glu Met His Ala Phe Glu Ala Asn Thr Thr Tyr Arg Phe Ala Glu Met
 195 200 205

tcc caa gaa gac ggc ctg gtc atg acc atc cac cca ggt gtg tac cgc 672
 Ser Gln Glu Asp Gly Leu Val Met Thr Ile His Pro Gly Val Tyr Arg
 210 215 220

<210> 430

<211> 224

<212> PRT

<213> Corynebacterium glutamicum

<400> 430

Ala Arg Glu Ala Trp Arg Ile Phe Met Ser His Trp Asp Leu Tyr Ala
 1 5 10 15

Gly Thr Ala Thr Gly Tyr Trp Val Glu Gln Glu Phe Glu His Val Phe
 20 25 30

Gly Ile Asn Ala Glu Arg Leu Asn Val Gly Thr Pro Glu His Ala Asp
 35 40 45

Ala Ile Phe Asp Glu Leu Thr Asp Ile Leu Ala Lys Pro Asp Phe Arg
 50 55 60

Pro Arg Ala Leu Ala Glu Gln Phe Asn Leu Glu Val Leu Ala Thr Thr
 65 70 75 80

Asp Asp Pro Leu Asp Asp Leu Ala Asp His Lys Ala Leu Ala Asp Asp
 85 90 95

Pro Thr Phe Ser Pro Arg Val Leu Pro Thr Phe Arg Pro Asp Ala Tyr
 100 105 110

Thr Lys Met Tyr Asn Ala Gly Trp Ala Glu Lys Thr Thr Lys Leu Ile
 115 120 125

Asp Thr Ala Gly Asp Gly Lys Ala Gly Trp Glu Gly Tyr Leu Gln Ala
 130 135 140

Met Arg Asn Arg Arg Gln Tyr Phe Ile Asn His Gly Ala Thr Ser Ala
 145 150 155 160

Asp His Gly Leu His Asp Thr Asp Thr Thr Pro Leu Ser His Lys Asp
 165 170 175

Ala Gln Lys Ile Leu Asp Lys Gly Leu Ala Gly Thr Ala Thr Leu Ala
 180 185 190

Glu Met His Ala Phe Glu Ala Asn Thr Thr Tyr Arg Phe Ala Glu Met
 195 200 205

Ser Gln Glu Asp Gly Leu Val Met Thr Ile His Pro Gly Val Tyr Arg
 210 215 220

<210> 431

<211> 533
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (1)..(510)
 <223> RXN03180

<400> 431
 ttc ggt gag aac aaa gat ctc atc tct gac agc agt ttc aac cgc tgg 48
 Phe Gly Glu Asn Lys Asp Leu Ile Ser Asp Ser Ser Phe Asn Arg Trp
 1 5 10 15
 ctg cgt acg gtt tcc ctc gga tcg acc cag gat gcc gat atg gct gca 96
 Leu Arg Thr Val Ser Leu Gly Ser Thr Gln Asp Ala Asp Met Ala Ala
 20 25 30
 gct tcc aac ttg gca gcc aat tct aaa atg gcc cgc cag aac acc cgc 144
 Ala Ser Asn Leu Ala Ala Asn Ser Lys Met Ala Arg Gln Asn Thr Arg
 35 40 45
 gat atc ctc gac gca gtc tct gat ggt ggc gtc atg ctc ggc cga aac 192
 Asp Ile Leu Asp Ala Val Ser Asp Gly Gly Val Met Leu Gly Arg Asn
 50 55 60
 ggt gcc cta gtg ttg gga cct gtg gtt gga act ctc cac att aaa ttc 240
 Gly Ala Leu Val Leu Gly Pro Val Val Gly Thr Leu His Ile Lys Phe
 65 70 75 80
 att gcg cct ttg aac aag cgt gtg gaa aga gtc atg tac aaa act gga 288
 Ile Ala Pro Leu Asn Lys Arg Val Glu Arg Val Met Tyr Lys Thr Gly
 85 90 95
 ctc tca gaa gct gct gca gct gag caa tgt gct ttg gag gat cgt ctc 336
 Leu Ser Glu Ala Ala Ala Glu Gln Cys Ala Leu Glu Asp Arg Leu
 100 105 110
 cgc gaa gag atg gcc cac gct ttg tat caa tgg aat ccg gga cgc gat 384
 Arg Glu Glu Met Ala His Ala Leu Tyr Gln Trp Asn Pro Gly Arg Asp
 115 120 125
 gaa aac tat gac ctc gtg atc aac acc ggt tcg atg aca tac gaa caa 432
 Glu Asn Tyr Asp Leu Val Ile Asn Thr Gly Ser Met Thr Tyr Glu Gln
 130 135 140
 atc gtt gat cta gtt gtg gaa act tac gcc agg aag tat ccg ctc cac 480
 Ile Val Asp Leu Val Val Glu Thr Tyr Ala Arg Lys Tyr Pro Leu His
 145 150 155 160
 gtg aga atc att ccg aac gga aaa gac caa taaacataca gtccccgtga 530
 Val Arg Ile Ile Pro Asn Gly Lys Asp Gln
 165 170
 tgt 533

<210> 432
 <211> 170
 <212> PRT
 <213> Corynebacterium glutamicum

<400> 432

Phe Gly Glu Asn Lys Asp Leu Ile Ser Asp Ser Ser Phe Asn Arg Trp
 1 5 10 15

Leu Arg Thr Val Ser Leu Gly Ser Thr Gln Asp Ala Asp Met Ala Ala
 20 25 30

Ala Ser Asn Leu Ala Ala Asn Ser Lys Met Ala Arg Gln Asn Thr Arg
 35 40 45

Asp Ile Leu Asp Ala Val Ser Asp Gly Gly Val Met Leu Gly Arg Asn
 50 55 60

Gly Ala Leu Val Leu Gly Pro Val Val Gly Thr Leu His Ile Lys Phe
 65 70 75 80

Ile Ala Pro Leu Asn Lys Arg Val Glu Arg Val Met Tyr Lys Thr Gly
 85 90 95

Leu Ser Glu Ala Ala Ala Ala Glu Gln Cys Ala Leu Glu Asp Arg Leu
 100 105 110

Arg Glu Glu Met Ala His Ala Leu Tyr Gln Trp Asn Pro Gly Arg Asp
 115 120 125

Glu Asn Tyr Asp Leu Val Ile Asn Thr Gly Ser Met Thr Tyr Glu Gln
 130 135 140

Ile Val Asp Leu Val Val Glu Thr Tyr Ala Arg Lys Tyr Pro Leu His
 145 150 155 160

Val Arg Ile Ile Pro Asn Gly Lys Asp Gln
 165 170

<210> 433

<211> 533

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (1)..(510)

<223> FRXA02873

<400> 433

ttc ggt gag aac aaa gat ctc atc tct gac agc agt ttc aac cgc tgg 48
 Phe Gly Glu Asn Lys Asp Leu Ile Ser Asp Ser Ser Phe Asn Arg Trp
 1 5 10 15

ctg cgt acg gtt tcc ctc gga tcg acc cag gat gcc gat atg gct gca 96
 Leu Arg Thr Val Ser Leu Gly Ser Thr Gln Asp Ala Asp Met Ala Ala
 20 25 30

gct tcc aac ttg gca gcc aat tct aaa atg gcc cgc cag aac acc cgc 144
 Ala Ser Asn Leu Ala Ala Asn Ser Lys Met Ala Arg Gln Asn Thr Arg
 35 40 45

gat atc ctc gac gca gtc tct gat ggt ggc gtc atg ctc ggc cga aac 192
 Asp Ile Leu Asp Ala Val Ser Asp Gly Gly Val Met Leu Gly Arg Asn

50	55	60	
ggt gcc cta gtg ttg gga cct gtg gtt gga act ctc cac att aaa ttc			240
Gly Ala Leu Val Leu Gly Pro Val Val Gly Thr Leu His Ile Lys Phe			
65	70	75	80
att gcg cct ttg aac aag cgt gtg gaa aga gtc atg tac aaa act gga			288
Ile Ala Pro Leu Asn Lys Arg Val Glu Arg Val Met Tyr Lys Thr Gly			
	85	90	95
ctc tca gaa gct gct gca gct gag caa tgt gct ttg gag gat cgt ctc			336
Leu Ser Glu Ala Ala Ala Ala Glu Gln Cys Ala Leu Glu Asp Arg Leu			
	100	105	110
cgc gaa gag atg gcc cac gct ttg tat caa tgg aat ccg gga cgc gat			384
Arg Glu Glu Met Ala His Ala Leu Tyr Gln Trp Asn Pro Gly Arg Asp			
	115	120	125
gaa aac tat gac ctc gtg atc aac acc ggt tcg atg aca tac gaa caa			432
Glu Asn Tyr Asp Leu Val Ile Asn Thr Gly Ser Met Thr Tyr Glu Gln			
	130	135	140
atc gtt gat cta gtt gtg gaa act tac gcc agg aag tat ccg ctc cac			480
Ile Val Asp Leu Val Val Glu Thr Tyr Ala Arg Lys Tyr Pro Leu His			
	145	150	155
gtg aga atc att ccg aac gga aaa gac caa taaacataca gtccccgtga			530
Val Arg Ile Ile Pro Asn Gly Lys Asp Gln			
	165	170	
tgt			533

<210> 434

<211> 170

<212> PRT

<213> Corynebacterium glutamicum

<400> 434

Phe Gly Glu Asn Lys Asp Leu Ile Ser Asp Ser Ser Phe Asn Arg Trp			
1	5	10	15
Leu Arg Thr Val Ser Leu Gly Ser Thr Gln Asp Ala Asp Met Ala Ala			
	20	25	30
Ala Ser Asn Leu Ala Ala Asn Ser Lys Met Ala Arg Gln Asn Thr Arg			
	35	40	45
Asp Ile Leu Asp Ala Val Ser Asp Gly Gly Val Met Leu Gly Arg Asn			
	50	55	60
Gly Ala Leu Val Leu Gly Pro Val Val Gly Thr Leu His Ile Lys Phe			
	65	70	75
Ile Ala Pro Leu Asn Lys Arg Val Glu Arg Val Met Tyr Lys Thr Gly			
	85	90	95
Leu Ser Glu Ala Ala Ala Ala Glu Gln Cys Ala Leu Glu Asp Arg Leu			
	100	105	110
Arg Glu Glu Met Ala His Ala Leu Tyr Gln Trp Asn Pro Gly Arg Asp			

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115              120              125
Glu Asn Tyr Asp Leu Val Ile Asn Thr Gly Ser Met Thr Tyr Glu Gln
130              135              140

Ile Val Asp Leu Val Val Glu Thr Tyr Ala Arg Lys Tyr Pro Leu His
145              150              155              160

Val Arg Ile Ile Pro Asn Gly Lys Asp Gln
165              170

<210> 435
<211> 798
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(775)
<223> RXA02292

<400> 435
tgcaccacgc cagctgcaac cctgcgcggt ggtctgggaa gttggtggag gggatcgtcg 60

aaaagcgtag gcactaaagt tctcctgcac aatggaggat atg gac aat gac ttt 115
Met Asp Asn Asp Phe
1 5

gaa tct atc gag aaa atg agc agc ggc gat tgg tac gtg gct acc ggc 163
Glu Ser Ile Glu Lys Met Ser Ser Gly Asp Trp Tyr Val Ala Thr Gly
10 15 20

gcg gaa cgt gaa gaa gtg gca caa aaa aca gcg tta ctt ttc cac gaa 211
Ala Glu Arg Glu Glu Val Ala Gln Lys Thr Ala Leu Leu Phe His Glu
25 30 35

tac aac caa att gga cct aca gac ccc gca cga act gcc gaa ata cta 259
Tyr Asn Gln Ile Gly Pro Thr Asp Pro Ala Arg Thr Ala Glu Ile Leu
40 45 50

aga act gta cta aat cct gcc agc gga acc tgc acg atc aaa gcg cca 307
Arg Thr Val Leu Asn Pro Ala Ser Gly Thr Cys Thr Ile Lys Ala Pro
55 60 65

gcc atc att gaa tac ggc ttc aac acc acg atc ggc gag cat gtg ttc 355
Ala Ile Ile Glu Tyr Gly Phe Asn Thr Thr Ile Gly Glu His Val Phe
70 75 80 85

atc aac ttt ggc ctc acc att tta gat atc gca ccg gtt cgc atc ggg 403
Ile Asn Phe Gly Leu Thr Ile Leu Asp Ile Ala Pro Val Arg Ile Gly
90 95 100

gca cgc agc atg ctc ggg cca aac tgt cag ctc ttc acc gca ggt cac 451
Ala Arg Ser Met Leu Gly Pro Asn Cys Gln Leu Phe Thr Ala Gly His
105 110 115

ccg gtc gat gac tgg gaa atg cgc tcc ggt ggg tgg gaa aat ggc gca 499
Pro Val Asp Asp Trp Glu Met Arg Ser Gly Gly Trp Glu Asn Gly Ala
120 125 130

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ccc att tcc att ggc gag gat acg tgg ctg ggt gga aat gtc acc gtc 547
 Pro Ile Ser Ile Gly Glu Asp Thr Trp Leu Gly Gly Asn Val Thr Val
 135 140 145

gtt ggt ggc gtg agc att ggc gat agg tgt gtg att ggc gcg ggg ccc 595
 Val Gly Gly Val Ser Ile Gly Asp Arg Cys Val Ile Gly Ala Gly Pro
 150 155 160 165

gtg gtg acc aag gat att ccg gat gat tct att gct gtg ggc aac cct 643
 Val Val Thr Lys Asp Ile Pro Asp Asp Ser Ile Ala Val Gly Asn Pro
 170 175 180

gcg cga gta gtg cgg aaa cgt gat gat agc cgg ctc gaa cgt tcg cag 691
 Ala Arg Val Val Arg Lys Arg Asp Asp Ser Arg Leu Glu Arg Ser Gln
 185 190 195

ctg cca gaa ggt gct tcc gtg gat gcg ttg ggg att ctt cct aca aaa 739
 Leu Pro Glu Gly Ala Ser Val Asp Ala Leu Gly Ile Leu Pro Thr Lys
 200 205 210

tca cct agg ctg tca gaa aat att gcc gaa aaa tat taaatacgca 785
 Ser Pro Arg Leu Ser Glu Asn Ile Ala Glu Lys Tyr
 215 220 225

ggcactaaga aga 798

<210> 436
 <211> 225
 <212> PRT
 <213> Corynebacterium glutamicum

<400> 436
 Met Asp Asn Asp Phe Glu Ser Ile Glu Lys Met Ser Ser Gly Asp Trp
 1 5 10 15

Tyr Val Ala Thr Gly Ala Glu Arg Glu Glu Val Ala Gln Lys Thr Ala
 20 25 30

Leu Leu Phe His Glu Tyr Asn Gln Ile Gly Pro Thr Asp Pro Ala Arg
 35 40 45

Thr Ala Glu Ile Leu Arg Thr Val Leu Asn Pro Ala Ser Gly Thr Cys
 50 55 60

Thr Ile Lys Ala Pro Ala Ile Ile Glu Tyr Gly Phe Asn Thr Thr Ile
 65 70 75 80

Gly Glu His Val Phe Ile Asn Phe Gly Leu Thr Ile Leu Asp Ile Ala
 85 90 95

Pro Val Arg Ile Gly Ala Arg Ser Met Leu Gly Pro Asn Cys Gln Leu
 100 105 110

Phe Thr Ala Gly His Pro Val Asp Asp Trp Glu Met Arg Ser Gly Gly
 115 120 125

Trp Glu Asn Gly Ala Pro Ile Ser Ile Gly Glu Asp Thr Trp Leu Gly
 130 135 140

Gly Asn Val Thr Val Val Gly Gly Val Ser Ile Gly Asp Arg Cys Val

145									150									155									160
Ile	Gly	Ala	Gly	Pro	Val	Val	Thr	Lys	Asp	Ile	Pro	Asp	Asp	Ser	Ile												
				165					170								175										
Ala	Val	Gly	Asn	Pro	Ala	Arg	Val	Val	Arg	Lys	Arg	Asp	Asp	Ser	Arg												
				180					185								190										
Leu	Glu	Arg	Ser	Gln	Leu	Pro	Glu	Gly	Ala	Ser	Val	Asp	Ala	Leu	Gly												
				195					200								205										
Ile	Leu	Pro	Thr	Lys	Ser	Pro	Arg	Leu	Ser	Glu	Asn	Ile	Ala	Glu	Lys												
				210					215								220										
Tyr																											
225																											

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<210> 437
<211> 891
<212> DNA
<213> Corynebacterium glutamicum
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<220>  
<221> CDS  
<222> (101) .. (868)  
<223> RXA02666
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<400> 437																
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tcttgacgat	ctgagcttcg	acgacgaaga	ttagacgccc	atg	tcg	tct	aca	cga	115							
				Met	Ser	Ser	Thr	Arg								
				1				5								
atc	ccc	gtc	atc	gca	ctc	ctc	gcg	gcg	gcg	ggg	cgc	gga	acc	cgc	ctc	163
Ile	Pro	Val	Ile	Ala	Leu	Leu	Ala	Ala	Ala	Gly	Arg	Gly	Thr	Arg	Leu	
				10				15						20		
ggc	gga	ccc	atc	ccc	aaa	gca	ttc	gtc	acg	ttg	cgt	gaa	cgc	aca	ctt	211
Gly	Gly	Pro	Ile	Pro	Lys	Ala	Phe	Val	Thr	Leu	Arg	Glu	Arg	Thr	Leu	
			25					30					35			
tta	gag	cgc	tcg	ctc	caa	gcc	atg	ctc	acc	tcc	gaa	agc	gtc	gac	gaa	259
Leu	Glu	Arg	Ser	Leu	Gln	Ala	Met	Leu	Thr	Ser	Glu	Ser	Val	Asp	Glu	
		40					45					50				
atc	atc	atc	ctc	gtc	agc	ccc	gac	atg	gaa	acc	tac	gcc	cgc	gat	ttg	307
Ile	Ile	Ile	Leu	Val	Ser	Pro	Asp	Met	Glu	Thr	Tyr	Ala	Arg	Asp	Leu	
		55				60					65					
ctg	cgc	aaa	cgc	ggt	ctt	ttg	aac	gac	ccc	gaa	ggg	gta	cgc	gta	cgg	355
Leu	Arg	Lys	Arg	Gly	Leu	Leu	Asn	Asp	Pro	Glu	Gly	Val	Arg	Val	Arg	
	70				75					80					85	
ctc	gtg	cac	ggc	ggc	ggg	gag	cgc	gcg	gac	tcg	gtc	tgg	gca	ggc	ctt	403
Leu	Val	His	Gly	Gly	Gly	Glu	Arg	Ala	Asp	Ser	Val	Trp	Ala	Gly	Leu	
			90						95					100		
cag	gca	att	tcg	ctt	gac	gac	gcc	acc	ccc	gat	gca	att	gtc	tta	atc	451
Gln	Ala	Ile	Ser	Leu	Asp	Asp	Ala	Thr	Pro	Asp	Ala	Ile	Val	Leu	Ile	

105	110	115	
cac gac agc gcc cga gcg ctc aca cca ccc ggc atg att gcg cgc gtg			499
His Asp Ser Ala Arg Ala Leu Thr Pro Pro Gly Met Ile Ala Arg Val			
120	125	130	
gtg cgc aaa gtc cac gaa ggc gcc acc gca gtc atc cca gta ctg cca			547
Val Arg Lys Val His Glu Gly Ala Thr Ala Val Ile Pro Val Leu Pro			
135	140	145	
gta tcg gac acc atc aaa cga gtg tcc cct gat ggc gga gta gtt gtc			595
Val Ser Asp Thr Ile Lys Arg Val Ser Pro Asp Gly Gly Val Val Val			
150	155	160	165
gac aca ccc aac cgt gca gaa ctt cgc gcc gtc caa acc cca caa ggc			643
Asp Thr Pro Asn Arg Ala Glu Leu Arg Ala Val Gln Thr Pro Gln Gly			
170	175	180	
ttc ctg ctg tcc gaa ctt gtt gca gcg aat gag aaa ttc ttc gcc gac			691
Phe Leu Leu Ser Glu Leu Val Ala Ala Asn Glu Lys Phe Phe Ala Asp			
185	190	195	
ccc aac cca ggc ttc atc cca acc gat gac gcc agc ttg atg gaa tgg			739
Pro Asn Pro Gly Phe Ile Pro Thr Asp Asp Ala Ser Leu Met Glu Trp			
200	205	210	
tac ggc gca gat gta gtc tgc gta caa ggc gac cca atg gcg ttt aaa			787
Tyr Gly Ala Asp Val Val Cys Val Gln Gly Asp Pro Met Ala Phe Lys			
215	220	225	
gta aca acc ccc att gat atg atg ctg gca caa cgc atc acc gac gaa			835
Val Thr Thr Pro Ile Asp Met Met Leu Ala Gln Arg Ile Thr Asp Glu			
230	235	240	245
gcc gaa ccc aca ata ttt gag gta cca ggt gac taacccaatc atccccgcg			888
Ala Glu Pro Thr Ile Phe Glu Val Pro Gly Asp			
250	255		

tag 891

<210> 438

<211> 256

<212> PRT

<213> Corynebacterium glutamicum

<400> 438

Met Ser Ser Thr Arg Ile Pro Val Ile Ala Leu Leu Ala Ala Ala Gly			
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20	25	30	
Arg Glu Arg Thr Leu Leu Glu Arg Ser Leu Gln Ala Met Leu Thr Ser			
35	40	45	
Glu Ser Val Asp Glu Ile Ile Ile Leu Val Ser Pro Asp Met Glu Thr			
50	55	60	
Tyr Ala Arg Asp Leu Leu Arg Lys Arg Gly Leu Leu Asn Asp Pro Glu			
65	70	75	80

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<211> 1065
<212> DNA
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ctt att gct ctg tcc gct tct gtc gtt ttg gct ttc agc ttg tct gct 163
 Leu Ile Ala Leu Ser Ala Ser Val Val Leu Ala Phe Ser Leu Ser Ala
 10 15 20

629

	25	30	35	
ggg tcg atc acc ttg gct ctg tct acc cag acc aac ccg ttc ttt gtg				259
Gly Ser Ile Thr Leu Ala Leu Ser Thr Gln Thr Asn Pro Phe Phe Val				
	40	45	50	
cag ctt cgt gat ggt gcc cag gaa aag gct gat gaa ttg ggc gtg acc				307
Gln Leu Arg Asp Gly Ala Gln Glu Lys Ala Asp Glu Leu Gly Val Thr				
	55	60	65	
ctc aat gtt cag gat gct tcc gat gac gct gca acg cag gcc aac cag				355
Leu Asn Val Gln Asp Ala Ser Asp Asp Ala Ala Thr Gln Ala Asn Gln				
	70	75	80	85
ctc aac aac gct gtc acc acc ggt gct ggc gtg gtg att gtc aac cca				403
Leu Asn Asn Ala Val Thr Thr Gly Ala Gly Val Val Ile Val Asn Pro				
	90		95	100
act gat tct gat gct gtg gtg ccg tcg gtg gaa gct ctc aac cag gct				451
Thr Asp Ser Asp Ala Val Val Pro Ser Val Glu Ala Leu Asn Gln Ala				
	105	110	115	
gac att cct gtt gtg gct gtc gac cgt tcc tcc aat ggt ggc gag gtg				499
Asp Ile Pro Val Val Ala Val Asp Arg Ser Ser Asn Gly Gly Glu Val				
	120	125	130	
gcg tcc ttc gtg gca tct gac aac gtt gct ggc ggc gcg cag gct gct				547
Ala Ser Phe Val Ala Ser Asp Asn Val Ala Gly Gly Ala Gln Ala Ala				
	135	140	145	
gca gcc ctg gca gag gcg atc ggt ggc gaa ggt gaa atc ctc atg ctg				595
Ala Ala Leu Ala Glu Ala Ile Gly Gly Glu Gly Glu Ile Leu Met Leu				
	150	155	160	165
caa ggc att gcg gga tcc tct gca tca cgt gat cgt gga cag gga ttt				643
Gln Gly Ile Ala Gly Ser Ser Ala Ser Arg Asp Arg Gly Gln Gly Phe				
	170	175		180
gaa gag gag atc gct aag cat gag ggc att tcc att gtg gct aag cag				691
Glu Glu Glu Ile Ala Lys His Glu Gly Ile Ser Ile Val Ala Lys Gln				
	185	190	195	
acc gcc aac ttt gac cgc ggt gag ggc ctg gac gtg gca act aac ctg				739
Thr Ala Asn Phe Asp Arg Gly Glu Gly Leu Asp Val Ala Thr Asn Leu				
	200	205	210	
ctg cag gca cac ccc aat gtg aag gcg atc ttc gcg gaa aac gat gag				787
Leu Gln Ala His Pro Asn Val Lys Ala Ile Phe Ala Glu Asn Asp Glu				
	215	220	225	
atg gcg ttg ggc gca atc gaa gcc ctg ggt gct cgt gct ggt gaa gat				835
Met Ala Leu Gly Ala Ile Glu Ala Leu Gly Ala Arg Ala Gly Glu Asp				
	230	235	240	245
gtc atc gtt gtc ggt ttc gat ggc acc aat gat ggt ctg gca gcg gtt				883
Val Ile Val Val Gly Phe Asp Gly Thr Asn Asp Gly Leu Ala Ala Val				
	250	255	260	
gaa gat gga cgc atg ttg gcc acc gtt gct cag cag cca gaa gag ctg				931
Glu Asp Gly Arg Met Leu Ala Thr Val Ala Gln Gln Pro Glu Glu Leu				
	265	270	275	

gga gca aag gct gtg gaa gaa gca gct aag ctc ctg cgc ggt gag gac 979
 Gly Ala Lys Ala Val Glu Glu Ala Ala Lys Leu Leu Arg Gly Glu Asp
 280 285 290

gct gaa aca gag gta cca gtt gag gtt gtc act gtg aag ctc gac aac 1027
 Ala Glu Thr Glu Val Pro Val Glu Val Val Thr Val Lys Leu Asp Asn
 295 300 305

gtc gcg gac ttc aag tagtcggcga tgaaaaagtc cgt 1065
 Val Ala Asp Phe Lys
 310

<210> 440
 <211> 314
 <212> PRT
 <213> Corynebacterium glutamicum

<400> 440
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Phe Ser Leu Ser Ala Cys Asn Arg Glu Ser Ser Gly Thr Ser Ala Asp
 20 25 30

Gly Gly Ser Ala Asp Gly Ser Ile Thr Leu Ala Leu Ser Thr Gln Thr
 35 40 45

Asn Pro Phe Phe Val Gln Leu Arg Asp Gly Ala Gln Glu Lys Ala Asp
 50 55 60

Glu Leu Gly Val Thr Leu Asn Val Gln Asp Ala Ser Asp Asp Ala Ala
 65 70 75 80

Thr Gln Ala Asn Gln Leu Asn Asn Ala Val Thr Thr Gly Ala Gly Val
 85 90 95

Val Ile Val Asn Pro Thr Asp Ser Asp Ala Val Val Pro Ser Val Glu
 100 105 110

Ala Leu Asn Gln Ala Asp Ile Pro Val Val Ala Val Asp Arg Ser Ser
 115 120 125

Asn Gly Gly Glu Val Ala Ser Phe Val Ala Ser Asp Asn Val Ala Gly
 130 135 140

Gly Ala Gln Ala Ala Ala Leu Ala Glu Ala Ile Gly Gly Glu Gly
 145 150 155 160

Glu Ile Leu Met Leu Gln Gly Ile Ala Gly Ser Ser Ala Ser Arg Asp
 165 170 175

Arg Gly Gln Gly Phe Glu Glu Glu Ile Ala Lys His Glu Gly Ile Ser
 180 185 190

Ile Val Ala Lys Gln Thr Ala Asn Phe Asp Arg Gly Glu Gly Leu Asp
 195 200 205

Val Ala Thr Asn Leu Leu Gln Ala His Pro Asn Val Lys Ala Ile Phe
 210 215 220

Ala Glu Asn Asp Glu Met Ala Leu Gly Ala Ile Glu Ala Leu Gly Ala
 225 230 235 240

Arg Ala Gly Glu Asp Val Ile Val Val Gly Phe Asp Gly Thr Asn Asp
 245 250 255

Gly Leu Ala Ala Val Glu Asp Gly Arg Met Leu Ala Thr Val Ala Gln
 260 265 270

Gln Pro Glu Glu Leu Gly Ala Lys Ala Val Glu Glu Ala Ala Lys Leu
 275 280 285

Leu Arg Gly Glu Asp Ala Glu Thr Glu Val Pro Val Glu Val Val Thr
 290 295 300

Val Lys Leu Asp Asn Val Ala Asp Phe Lys
 305 310

<210> 441
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 <212> DNA
 <213> Corynebacterium glutamicum

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 <222> (101)..(940)
 <223> RXA02440

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aggcggagga accgtcgata cgcctcggtt ggttgtcgcg atg gtg agc cac ggc 115
 Met Val Ser His Gly
 1 5

gcg ccg ggc gat act ttt tgg gat ttg gtc cga aaa ggt gct gaa gac 163
 Ala Pro Gly Asp Thr Phe Trp Asp Leu Val Arg Lys Gly Ala Glu Asp
 10 15 20

gcc gcc caa aaa gac aac gtt gaa ctc cgc tat tcc tct aat ccg gaa 211
 Ala Ala Gln Lys Asp Asn Val Glu Leu Arg Tyr Ser Ser Asn Pro Glu
 25 30 35

atc cct gaa caa tcc aac ctc gtg caa aat gcc atc gat tca cgc gtc 259
 Ile Pro Glu Gln Ser Asn Leu Val Gln Asn Ala Ile Asp Ser Arg Val
 40 45 50

gac ggc atc gcc atg acc atg cct aat gct caa tca cta gga ccg gtc 307
 Asp Gly Ile Ala Met Thr Met Pro Asn Ala Gln Ser Leu Gly Pro Val
 55 60 65

gct caa aag gcc gtg gat gcg ggc att cct gtg gtt ggt ctc aac gct 355
 Ala Gln Lys Ala Val Asp Ala Gly Ile Pro Val Val Gly Leu Asn Ala
 70 75 80 85

gga atg aac gaa tac caa gat tat gga atg aca gga ttc ttt ggt caa 403
 Gly Met Asn Glu Tyr Gln Asp Tyr Gly Met Thr Gly Phe Phe Gly Gln
 90 95 100

gat gaa tcc gtc gca gga gca tcc gca gga gcg cgc ctt gcc gag gaa 451
Asp Glu Ser Val Ala Gly Ala Ser Ala Gly Ala Arg Leu Ala Glu Glu
105 110 115

aac gca caa aaa gtt ttg tgt gtg atc cat gaa cag ggc aac tcc tcc 499
Asn Ala Gln Lys Val Leu Cys Val Ile His Glu Gln Gly Asn Ser Ser
120 125 130

cag gaa gct cgc tgt ggt ggc gtg tct gaa ggt ttg ggc aaa caa gta 547
Gln Glu Ala Arg Cys Gly Gly Val Ser Glu Gly Leu Gly Lys Gln Val
135 140 145

gaa acc ctg tat gtc aac ggc atg gat ctc acc tca gtg aac tcc acc 595
Glu Thr Leu Tyr Val Asn Gly Met Asp Leu Thr Ser Val Asn Ser Thr
150 155 160 165

ctg cag gca aaa ctt gct caa gac cgc agc att gat tgg gtt gtg gga 643
Leu Gln Ala Lys Leu Ala Gln Asp Arg Ser Ile Asp Trp Val Val Gly
170 175 180

ctc cag gct ggt gta tca atg gct att tct gat gcg gca gac gct gcg 691
Leu Gln Ala Gly Val Ser Met Ala Ile Ser Asp Ala Ala Asp Ala Ala
185 190 195

aac tca gaa gta aag atc gcc acc ttt gat aca aac gca cag ctc atg 739
Asn Ser Glu Val Lys Ile Ala Thr Phe Asp Thr Asn Ala Gln Leu Met
200 205 210

acc gct att cgt gat ggc aag atc caa ttc gcc att gat cag caa cca 787
Thr Ala Ile Arg Asp Gly Lys Ile Gln Phe Ala Ile Asp Gln Gln Pro
215 220 225

tat ctg cag ggc tac atg gcc gtg gat tcg ctg tgg ttg gcg cac cga 835
Tyr Leu Gln Gly Tyr Met Ala Val Asp Ser Leu Trp Leu Ala His Arg
230 235 240 245

aac ggc acc act gtt ggt ggc gga cga ccc gtg tac aca gga cca gcc 883
Asn Gly Thr Thr Val Gly Gly Gly Arg Pro Val Tyr Thr Gly Pro Ala
250 255 260

att gtg gat gcc acc aac gtt gat gtc att gct gaa gcc gtt ggg gag 931
Ile Val Asp Ala Thr Asn Val Asp Val Ile Ala Glu Ala Val Gly Glu
265 270 275

ggt ctg cga tgacaaaaat caagagtggg gag 963
Gly Leu Arg
280

<210> 442

<211> 280

<212> PRT

<213> Corynebacterium glutamicum

<400> 442

Met Val Ser His Gly Ala Pro Gly Asp Thr Phe Trp Asp Leu Val Arg
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Lys Gly Ala Glu Asp Ala Ala Gln Lys Asp Asn Val Glu Leu Arg Tyr
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<210> 443
<211> 1482
<212> DNA
<213> Corynebacterium glutamicum
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agaacaacgt cgaagctacc tacgctaagc agggacaata atg gaa tac ggt aaa	115
Met Glu Tyr Gly Lys	
1 5	
caa ctc acc tcc cac acc acc gac atc gaa ggc cta ctg gtt ttc gat	163
Gln Leu Thr Ser His Thr Thr Asp Ile Glu Gly Leu Leu Val Phe Asp	
10 15 20	
ttc ccc gtc cac ggc gac aac cgc ggc tgg ttc aag gaa aat tgg cag	211
Phe Pro Val His Gly Asp Asn Arg Gly Trp Phe Lys Glu Asn Trp Gln	
25 30 35	
cgc acc aag atg acc aac ctg ggg ctg ccc gat ttt ggc ccc gtc caa	259
Arg Thr Lys Met Thr Asn Leu Gly Leu Pro Asp Phe Gly Pro Val Gln	
40 45 50	
aac aac atg agt ttc aac gcc acc gcc ggc acg act cgc ggc atg cac	307
Asn Asn Met Ser Phe Asn Ala Thr Ala Gly Thr Thr Arg Gly Met His	
55 60 65	
gct gag ccg tgg gat aaa ttt gtg tcc gtc gcg gtg ggt tcc gtt ttc	355
Ala Glu Pro Trp Asp Lys Phe Val Ser Val Ala Val Gly Ser Val Phe	
70 75 80 85	
gga gct tgg gtg gat ctg cgc gcg ggc tgc agc acg tac ggt aac gtc	403
Gly Ala Trp Val Asp Leu Arg Ala Gly Ser Ser Thr Tyr Gly Asn Val	
90 95 100	
gta acg caa aaa att acc cct gac gtg gga gtt tac gtc ccg cgt ggt	451
Val Thr Gln Lys Ile Thr Pro Asp Val Gly Val Tyr Val Pro Arg Gly	
105 110 115	
gtg gca aac ggc ttc cag gcg ctc gag gac ggc acg ctg tac acc tac	499
Val Ala Asn Gly Phe Gln Ala Leu Glu Asp Gly Thr Leu Tyr Thr Tyr	
120 125 130	
ctc gtc aac gat cat tgg tcc ccc gac gcg cat tac gcc aac gtc aac	547
Leu Val Asn Asp His Trp Ser Pro Asp Ala His Tyr Ala Asn Val Asn	
135 140 145	
ctc aac atg atc gac tgg ccg ctg ccc atc acc gag atc tcc gaa aaa	595
Leu Asn Met Ile Asp Trp Pro Leu Pro Ile Thr Glu Ile Ser Glu Lys	
150 155 160 165	
gat aaa aaa cat cca gcg ctt atc gac gcc acc ccc ctg ccc gcc cgc	643
Asp Lys Lys His Pro Ala Leu Ile Asp Ala Thr Pro Leu Pro Ala Arg	
170 175 180	
aag gtt ctc gtg gtc ggc gcc ggc gga caa ctg gga acc gcg cta cgc	691
Lys Val Leu Val Val Gly Ala Gly Gly Gln Leu Gly Thr Ala Leu Arg	
185 190 195	
gcg cag ttc cca gac gcg gaa ttt gtc acg cgc caa gaa ctc gat atc	739
Ala Gln Phe Pro Asp Ala Glu Phe Val Thr Arg Gln Glu Leu Asp Ile	
200 205 210	
acc tca gat ctc acc gag gct cgc gcg tgg aaa caa tac tcc acc atc	787
Thr Ser Asp Leu Thr Glu Ala Arg Ala Trp Lys Gln Tyr Ser Thr Ile	
215 220 225	

ata aac gcc gcc gcc tac act gcc gtt gac cag gca gaa cac gac cgc 835
 Ile Asn Ala Ala Ala Tyr Thr Ala Val Asp Gln Ala Glu His Asp Arg
 230 235 240 245
 gca gca gcg tgg gac atc aac gca gcg gca gtg gct aac ctc gcg acc 883
 Ala Ala Ala Trp Asp Ile Asn Ala Ala Val Ala Asn Leu Ala Thr
 250 255 260
 atc gcg cgc gac aac aac ctc acc ctc gtg cac gtg tcc tca gat tat 931
 Ile Ala Arg Asp Asn Asn Leu Thr Leu Val His Val Ser Ser Asp Tyr
 265 270 275
 gtc ttc gac ggt gcg gcc gaa tcc tac gat gaa aac gca ccg ttt tcc 979
 Val Phe Asp Gly Ala Ala Glu Ser Tyr Asp Glu Asn Ala Pro Phe Ser
 280 285 290
 cca ctc ggc gtg tac ggc caa tcc aaa gca gcc ggc gac atc gga gac 1027
 Pro Leu Gly Val Tyr Gly Gln Ser Lys Ala Ala Gly Asp Ile Gly Asp
 295 300 305
 acc acc gca ccg cgc cac tac att gtg cgc acc agc tgg gtg att ggc 1075
 Thr Thr Ala Pro Arg His Tyr Ile Val Arg Thr Ser Trp Val Ile Gly
 310 315 320 325
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 Asp Gly Asn Asn Phe Val Arg Thr Met Lys Ser Leu Asp Glu Arg Gly
 330 335 340
 atc gca cca tca gta gtt gat gat caa atc ggc cgc cta tcc ttc acc 1171
 Ile Ala Pro Ser Val Val Asp Asp Gln Ile Gly Arg Leu Ser Phe Thr
 345 350 355
 gaa gac atc gca gcc ggc atc gcg cac ctt ttg gaa gtg ggt gca gca 1219
 Glu Asp Ile Ala Ala Gly Ile Ala His Leu Leu Glu Val Gly Ala Ala
 360 365 370
 tat ggc acc tac aac ctc acc aac acc ggc gaa ccc gca agc tgg gcc 1267
 Tyr Gly Thr Tyr Asn Leu Thr Asn Thr Gly Glu Pro Ala Ser Trp Ala
 375 380 385
 gat gtt gcc cgc gca gta ttt tcc gac ccc acc aaa gtt acc ggc gtg 1315
 Asp Val Ala Arg Ala Val Phe Ser Asp Pro Thr Lys Val Thr Gly Val
 390 395 400 405
 agc acc gcc gag tac ttc gcc aac aaa gac gca gcg ccc cgc cca ctg 1363
 Ser Thr Ala Glu Tyr Phe Ala Asn Lys Asp Ala Ala Pro Arg Pro Leu
 410 415 420
 aac tcc gtt ttg gat ctc ggc aaa atc gaa gcc acc gga ttt agc gca 1411
 Asn Ser Val Leu Asp Leu Gly Lys Ile Glu Ala Thr Gly Phe Ser Ala
 425 430 435
 ccg acc tgg cag acc cgc ctc aac gac tac ctc aag gaa ctc tca aag 1459
 Pro Thr Trp Gln Thr Arg Leu Asn Asp Tyr Leu Lys Glu Leu Ser Lys
 440 445 450
 tgaaaggcat catcctcgca ggt 1482

<210> 444

<211> 453

<212> PRT

<213> Corynebacterium glutamicum

<400> 444

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Leu Leu Val Phe Asp Phe Pro Val His Gly Asp Asn Arg Gly Trp Phe
      20           25           30

Lys Glu Asn Trp Gln Arg Thr Lys Met Thr Asn Leu Gly Leu Pro Asp
      35           40           45

Phe Gly Pro Val Gln Asn Asn Met Ser Phe Asn Ala Thr Ala Gly Thr
      50           55           60

Thr Arg Gly Met His Ala Glu Pro Trp Asp Lys Phe Val Ser Val Ala
      65           70           75           80

Val Gly Ser Val Phe Gly Ala Trp Val Asp Leu Arg Ala Gly Ser Ser
      85           90           95

Thr Tyr Gly Asn Val Val Thr Gln Lys Ile Thr Pro Asp Val Gly Val
      100          105          110

Tyr Val Pro Arg Gly Val Ala Asn Gly Phe Gln Ala Leu Glu Asp Gly
      115          120          125

Thr Leu Tyr Thr Tyr Leu Val Asn Asp His Trp Ser Pro Asp Ala His
      130          135          140

Tyr Ala Asn Val Asn Leu Asn Met Ile Asp Trp Pro Leu Pro Ile Thr
      145          150          155          160

Glu Ile Ser Glu Lys Asp Lys Lys His Pro Ala Leu Ile Asp Ala Thr
      165          170          175

Pro Leu Pro Ala Arg Lys Val Leu Val Val Gly Ala Gly Gly Gln Leu
      180          185          190

Gly Thr Ala Leu Arg Ala Gln Phe Pro Asp Ala Glu Phe Val Thr Arg
      195          200          205

Gln Glu Leu Asp Ile Thr Ser Asp Leu Thr Glu Ala Arg Ala Trp Lys
      210          215          220

Gln Tyr Ser Thr Ile Ile Asn Ala Ala Ala Tyr Thr Ala Val Asp Gln
      225          230          235          240

Ala Glu His Asp Arg Ala Ala Ala Trp Asp Ile Asn Ala Ala Ala Val
      245          250          255

Ala Asn Leu Ala Thr Ile Ala Arg Asp Asn Asn Leu Thr Leu Val His
      260          265          270

Val Ser Ser Asp Tyr Val Phe Asp Gly Ala Ala Glu Ser Tyr Asp Glu
      275          280          285

Asn Ala Pro Phe Ser Pro Leu Gly Val Tyr Gly Gln Ser Lys Ala Ala
      290          295          300

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Gly Asp Ile Gly Asp Thr Thr Ala Pro Arg His Tyr Ile Val Arg Thr
 305 310 315 320
 Ser Trp Val Ile Gly Asp Gly Asn Asn Phe Val Arg Thr Met Lys Ser
 325 330 335
 Leu Asp Glu Arg Gly Ile Ala Pro Ser Val Val Asp Asp Gln Ile Gly
 340 345 350
 Arg Leu Ser Phe Thr Glu Asp Ile Ala Ala Gly Ile Ala His Leu Leu
 355 360 365
 Glu Val Gly Ala Ala Tyr Gly Thr Tyr Asn Leu Thr Asn Thr Gly Glu
 370 375 380
 Pro Ala Ser Trp Ala Asp Val Ala Arg Ala Val Phe Ser Asp Pro Thr
 385 390 395 400
 Lys Val Thr Gly Val Ser Thr Ala Glu Tyr Phe Ala Asn Lys Asp Ala
 405 410 415
 Ala Pro Arg Pro Leu Asn Ser Val Leu Asp Leu Gly Lys Ile Glu Ala
 420 425 430
 Thr Gly Phe Ser Ala Pro Thr Trp Gln Thr Arg Leu Asn Asp Tyr Leu
 435 440 445
 Lys Glu Leu Ser Lys
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<210> 445

<211> 449

<212> DNA

<213> *Corynebacterium glutamicum*

<220>

<221> CDS

<222> (1)..(426)

<223> FRXA01569

<400> 445

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aat aat ttt gtc cgc acc atg aaa tcc ctc gac gaa cgc ggc atc gca	96
Asn Asn Phe Val Arg Thr Met Lys Ser Leu Asp Glu Arg Gly Ile Ala	
20 25 30	
cca tca gta gtt gat gat caa atc ggc cgc cta tcc ttc acc gaa gac	144
Pro Ser Val Val Asp Asp Gln Ile Gly Arg Leu Ser Phe Thr Glu Asp	
35 40 45	
atc gca gcc ggc atc gcg cac ctt ttg gaa gtg ggt gca gca tat ggc	192
Ile Ala Ala Gly Ile Ala His Leu Glu Val Gly Ala Ala Tyr Gly	
50 55 60	
acc tac aac ctc acc aac acc ggc gaa ccc gca agc tgg gcc gat gtt	240
Thr Tyr Asn Leu Thr Asn Thr Gly Glu Pro Ala Ser Trp Ala Asp Val	
65 70 75 80	

gcc cgc gca gta ttt tcc gac ccc acc aaa gtt acc ggc gtg agc acc 288
 Ala Arg Ala Val Phe Ser Asp Pro Thr Lys Val Thr Gly Val Ser Thr
 85 90 95

gcc gag tac ttc gcc aac aaa gac gca gcg ccc cgc cca ctg aac tcc 336
 Ala Glu Tyr Phe Ala Asn Lys Asp Ala Ala Pro Arg Pro Leu Asn Ser
 100 105 110

gtt ttg gat ctc ggc aaa atc gaa gcc acc gga ttt agc gca ccg acc 384
 Val Leu Asp Leu Gly Lys Ile Glu Ala Thr Gly Phe Ser Ala Pro Thr
 115 120 125

tgg cag acc cgc ctc aac gac tac ctc aag gaa ctc tca aag 426
 Trp Gln Thr Arg Leu Asn Asp Tyr Leu Lys Glu Leu Ser Lys
 130 135 140

tgaaaggcat catcctcgca ggt 449

<210> 446
 <211> 142
 <212> PRT
 <213> Corynebacterium glutamicum.

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 20 25 30

Pro Ser Val Val Asp Asp Gln Ile Gly Arg Leu Ser Phe Thr Glu Asp
 35 40 45

Ile Ala Ala Gly Ile Ala His Leu Leu Glu Val Gly Ala Ala Tyr Gly
 50 55 60

Thr Tyr Asn Leu Thr Asn Thr Gly Glu Pro Ala Ser Trp Ala Asp Val
 65 70 75 80

Ala Arg Ala Val Phe Ser Asp Pro Thr Lys Val Thr Gly Val Ser Thr
 85 90 95

Ala Glu Tyr Phe Ala Asn Lys Asp Ala Ala Pro Arg Pro Leu Asn Ser
 100 105 110

Val Leu Asp Leu Gly Lys Ile Glu Ala Thr Gly Phe Ser Ala Pro Thr
 115 120 125

Trp Gln Thr Arg Leu Asn Asp Tyr Leu Lys Glu Leu Ser Lys
 130 135 140

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 <211> 1028
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS

<222> (101)..(1021)

<223> FRXA02055

<400> 447

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agaacaacgt cgaagctacc tacgctaagc agggacaata atg gaa tac ggt aaa 115
                                         Met Glu Tyr Gly Lys
                                         1           5

caa ctc acc tcc cac acc acc gac atc gaa ggc cta ctg gtt ttc gat 163
Gln Leu Thr Ser His Thr Thr Asp Ile Glu Gly Leu Leu Val Phe Asp
                10                15                20

ttc ccc gtc cac ggc gac aac cgc ggc tgg ttc aag gaa aat tgg cag 211
Phe Pro Val His Gly Asp Asn Arg Gly Trp Phe Lys Glu Asn Trp Gln
                25                30                35

cgc acc aag atg acc aac ctg ggg ctg ccc gat ttt ggc ccc gtc caa 259
Arg Thr Lys Met Thr Asn Leu Gly Leu Pro Asp Phe Gly Pro Val Gln
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aac aac atg agt ttc aac gcc acc gcc ggc acg act cgc ggc atg cac 307
Asn Asn Met Ser Phe Asn Ala Thr Ala Gly Thr Thr Arg Gly Met His
                55                60                65

gct gag ccg tgg gat aaa ttt gtg tcc gtc gcg gtg ggt tcc gtt ttc 355
Ala Glu Pro Trp Asp Lys Phe Val Ser Val Ala Val Gly Ser Val Phe
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gga gct tgg gtg gat ctg cgc gcg ggc tcg agc acg tac ggt aac gtc 403
Gly Ala Trp Val Asp Leu Arg Ala Gly Ser Ser Thr Tyr Gly Asn Val
                90                95                100

gta acg caa aaa att acc cct gac gtg gga gtt tac gtc ccg cgt ggt 451
Val Thr Gln Lys Ile Thr Pro Asp Val Gly Val Tyr Val Pro Arg Gly
                105                110                115

gtg gca aac ggc ttc cag gcg ctc gag gac ggc acg ctg tac acc tac 499
Val Ala Asn Gly Phe Gln Ala Leu Glu Asp Gly Thr Leu Tyr Thr Tyr
                120                125                130

ctc gtc aac gat cat tgg tcc ccc gac gcg cat tac gcc aac gtc aac 547
Leu Val Asn Asp His Trp Ser Pro Asp Ala His Tyr Ala Asn Val Asn
                135                140                145

ctc aac atg atc gac tgg ccg ctg ccc atc acc gag atc tcc gaa aaa 595
Leu Asn Met Ile Asp Trp Pro Leu Pro Ile Thr Glu Ile Ser Glu Lys
                150                155                160                165

gat aaa aaa cat cca gcg ctt atc gac gcc acc ccc ctg ccc gcc cgc 643
Asp Lys Lys His Pro Ala Leu Ile Asp Ala Thr Pro Leu Pro Ala Arg
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aag gtt ctc gtg gtc ggc gcc ggc gga caa ctg gga acc gcg cta cgc 691
Lys Val Leu Val Val Gly Ala Gly Gly Gln Leu Gly Thr Ala Leu Arg
                185                190                195

gcg cag ttc cca gac gcg gaa ttt gtc acg cgc caa gaa ctc gat atc 739
Ala Gln Phe Pro Asp Ala Glu Phe Val Thr Arg Gln Glu Leu Asp Ile
                200                205                210

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acc tca gat ctc acc gag gct cgc gcg tgg aaa caa tac tcc acc atc 787
 Thr Ser Asp Leu Thr Glu Ala Arg Ala Trp Lys Gln Tyr Ser Thr Ile
 215 220 225

ata aac gcc gcc gcc tac act gcc gtt gac cag gca gaa cac gac cgc 835
 Ile Asn Ala Ala Ala Tyr Thr Ala Val Asp Gln Ala Glu His Asp Arg
 230 235 240 245

gca gca gcg tgg gac att aac gca gcg gca gtg gct acc tcg cga cca 883
 Ala Ala Ala Trp Asp Ile Asn Ala Ala Ala Val Ala Thr Ser Arg Pro
 250 255 260

tcg cgc gcg aca aca acc tca ccc tcg tgc acg tgt cct cag att atg 931
 Ser Arg Ala Thr Thr Thr Ser Pro Ser Cys Thr Cys Pro Gln Ile Met
 265 270 275

tct tcg acg gtg cgg gcg aat cct acg atg aaa acg cac cgt ttt ccc 979
 Ser Ser Thr Val Arg Ala Asn Pro Thr Met Lys Thr His Arg Phe Pro
 280 285 290

cac tcg gcg tgt acg gcc aat cca aag cag ccg gcg aca tcg 1021
 His Ser Ala Cys Thr Ala Asn Pro Lys Gln Pro Ala Thr Ser
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taagcac 1028

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 <213> Corynebacterium glutamicum

<400> 448
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 20 25 30

Lys Glu Asn Trp Gln Arg Thr Lys Met Thr Asn Leu Gly Leu Pro Asp
 35 40 45

Phe Gly Pro Val Gln Asn Asn Met Ser Phe Asn Ala Thr Ala Gly Thr
 50 55 60

Thr Arg Gly Met His Ala Glu Pro Trp Asp Lys Phe Val Ser Val Ala
 65 70 75 80

Val Gly Ser Val Phe Gly Ala Trp Val Asp Leu Arg Ala Gly Ser Ser
 85 90 95

Thr Tyr Gly Asn Val Val Thr Gln Lys Ile Thr Pro Asp Val Gly Val
 100 105 110

Tyr Val Pro Arg Gly Val Ala Asn Gly Phe Gln Ala Leu Glu Asp Gly
 115 120 125

Thr Leu Tyr Thr Tyr Leu Val Asn Asp His Trp Ser Pro Asp Ala His
 130 135 140

Tyr Ala Asn Val Asn Leu Asn Met Ile Asp Trp Pro Leu Pro Ile Thr
 145 150 155 160
 Glu Ile Ser Glu Lys Asp Lys Lys His Pro Ala Leu Ile Asp Ala Thr
 165 170 175
 Pro Leu Pro Ala Arg Lys Val Leu Val Val Gly Ala Gly Gly Gln Leu
 180 185 190
 Gly Thr Ala Leu Arg Ala Gln Phe Pro Asp Ala Glu Phe Val Thr Arg
 195 200 205
 Gln Glu Leu Asp Ile Thr Ser Asp Leu Thr Glu Ala Arg Ala Trp Lys
 210 215 220
 Gln Tyr Ser Thr Ile Ile Asn Ala Ala Ala Tyr Thr Ala Val Asp Gln
 225 230 235 240
 Ala Glu His Asp Arg Ala Ala Ala Trp Asp Ile Asn Ala Ala Ala Val
 245 250 255
 Ala Thr Ser Arg Pro Ser Arg Ala Thr Thr Thr Ser Pro Ser Cys Thr
 260 265 270
 Cys Pro Gln Ile Met Ser Ser Thr Val Arg Ala Asn Pro Thr Met Lys
 275 280 285
 Thr His Arg Phe Pro His Ser Ala Cys Thr Ala Asn Pro Lys Gln Pro
 290 295 300
 Ala Thr Ser
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 <212> DNA
 <213> *Corynebacterium glutamicum*

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 <221> CDS
 <222> (101)..(1033)
 <223> RXA00825

<400> 449
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 Met Arg Thr Val Val
 1 5
 acc ggc ggt gcc ggc ttc atc gga tcc cat ctc gtt gac ctt ttg atc 163
 Thr Gly Gly Ala Gly Phe Ile Gly Ser His Leu Val Asp Leu Leu Ile
 10 15 20
 aag gaa ggc cac gag gtc gtt gtg atc gat aac ctc tcc cgc gga cgc 211
 Lys Glu Gly His Glu Val Val Val Ile Asp Asn Leu Ser Arg Gly Arg
 25 30 35
 ctg gag aat ctc tcc gat gcg gaa gcc acc gga aaa ctc acc ttt gtg 259
 Leu Glu Asn Leu Ser Asp Ala Glu Ala Thr Gly Lys Leu Thr Phe Val

40	45	50	
gaa gcc gat ctt ctc gac gtt gat ttc aac gag ttt cta gga acc cac Glu Ala Asp Leu Leu Asp Val Asp Phe Asn Glu Phe Leu Gly Thr His 55 60 65			307
aag cct gag gtt att ttc cac ctg gca gcg caa atc gat gtg cgc cac Lys Pro Glu Val Ile Phe His Leu Ala Ala Gln Ile Asp Val Arg His 70 75 80 85			355
tct gtt gta gat cct ctt cac gac gcc gaa acc aac att ttg tcc acc Ser Val Val Asp Pro Leu His Asp Ala Glu Thr Asn Ile Leu Ser Thr 90 95 100			403
atc cgc atc gct gac gct gcc cgc cag cac ggt gtt cgc aag gtt gtc Ile Arg Ile Ala Asp Ala Ala Arg Gln His Gly Val Arg Lys Val Val 105 110 115			451
ttt acc tcc tca ggc ggt tcc att tac ggt gag cct tcg gaa ttc cca Phe Thr Ser Ser Gly Gly Ser Ile Tyr Gly Glu Pro Ser Glu Phe Pro 120 125 130			499
gtt gat gaa acc gtg cca gtg gat cca cat tcc cct tat gcg gca tcc Val Asp Glu Thr Val Pro Val Asp Pro His Ser Pro Tyr Ala Ala Ser 135 140 145			547
aag gtg tcc ggt gaa att tac ctg aac acc ttc cgc cac ctg tac ggc Lys Val Ser Gly Glu Ile Tyr Leu Asn Thr Phe Arg His Leu Tyr Gly 150 155 160 165			595
tta gac tgt tct cac atc gca ccg gca aat gtt tac ggc cca cgc caa Leu Asp Cys Ser His Ile Ala Pro Ala Asn Val Tyr Gly Pro Arg Gln 170 175 180			643
gat cca cac ggt gaa gca gga gtt gtg gcc att ttc gcg ctg cga ctt Asp Pro His Gly Glu Ala Gly Val Val Ala Ile Phe Ala Leu Arg Leu 185 190 195			691
ctg gga ggc ctg gac acc aag gta ttc ggc gac ggc gga aac acc cgc Leu Gly Gly Leu Asp Thr Lys Val Phe Gly Asp Gly Gly Asn Thr Arg 200 205 210			739
gac tac gtc tac gtc ggt gac gta gtt cgt gct ttc tac ctg gct tct Asp Tyr Val Tyr Val Gly Asp Val Val Arg Ala Phe Tyr Leu Ala Ser 215 220 225			787
ggg gaa atc ggt ggg gga gag cgc ttc aac att ggc acc tct gtg gaa Gly Glu Ile Gly Gly Gly Glu Arg Phe Asn Ile Gly Thr Ser Val Glu 230 235 240 245			835
acc tct gac cgc cag ctg cac acc ctc gtg gcc act gcg gca ggt tcc Thr Ser Asp Arg Gln Leu His Thr Leu Val Ala Thr Ala Ala Gly Ser 250 255 260			883
aaa gat gat cct gaa tat gca cct gca cgt ctc ggc gat gtg cca cgc Lys Asp Asp Pro Glu Tyr Ala Pro Ala Arg Leu Gly Asp Val Pro Arg 265 270 275			931
agt gca ctc agc ttc ggc aag gcc aaa gag gtg ctt ggt tgg gag cct Ser Ala Leu Ser Phe Gly Lys Ala Lys Glu Val Leu Gly Trp Glu Pro 280 285 290			979

gag gtg aac atc gaa caa ggt gtg gcc aag act gtg gag tac ttc cgc 1027
Glu Val Asn Ile Glu Gln Gly Val Ala Lys Thr Val Glu Tyr Phe Arg
295 300 305

act cac taggggaaaa tccaccacaa atc 1056
Thr His
310

<210> 450

<211> 311

<212> PRT

<213> Corynebacterium glutamicum

<400> 450

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Val Asp Leu Leu Ile Lys Glu Gly His Glu Val Val Val Ile Asp Asn
20 25 30

Leu Ser Arg Gly Arg Leu Glu Asn Leu Ser Asp Ala Glu Ala Thr Gly
35 40 45

Lys Leu Thr Phe Val Glu Ala Asp Leu Leu Asp Val Asp Phe Asn Glu
50 55 60

Phe Leu Gly Thr His Lys Pro Glu Val Ile Phe His Leu Ala Ala Gln
65 70 75 80

Ile Asp Val Arg His Ser Val Val Asp Pro Leu His Asp Ala Glu Thr
85 90 95

Asn Ile Leu Ser Thr Ile Arg Ile Ala Asp Ala Ala Arg Gln His Gly
100 105 110

Val Arg Lys Val Val Phe Thr Ser Ser Gly Gly Ser Ile Tyr Gly Glu
115 120 125

Pro Ser Glu Phe Pro Val Asp Glu Thr Val Pro Val Asp Pro His Ser
130 135 140

Pro Tyr Ala Ala Ser Lys Val Ser Gly Glu Ile Tyr Leu Asn Thr Phe
145 150 155 160

Arg His Leu Tyr Gly Leu Asp Cys Ser His Ile Ala Pro Ala Asn Val
165 170 175

Tyr Gly Pro Arg Gln Asp Pro His Gly Glu Ala Gly Val Val Ala Ile
180 185 190

Phe Ala Leu Arg Leu Leu Gly Gly Leu Asp Thr Lys Val Phe Gly Asp
195 200 205

Gly Gly Asn Thr Arg Asp Tyr Val Tyr Val Gly Asp Val Val Arg Ala
210 215 220

Phe Tyr Leu Ala Ser Gly Glu Ile Gly Gly Gly Glu Arg Phe Asn Ile
225 230 235 240

<400> 451																
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								Met	Thr	Ser	Leu	Leu				
								1							5	
gtg	acc	gga	ggt	gcc	gga	ttt	atc	ggc	gcc	aac	ttc	gtc	cgc	caa	acc	163
Val	Thr	Gly	Gly	Ala	Gly	Phe	Ile	Gly	Ala	Asn	Phe	Val	Arg	Gln	Thr	
				10					15				20			
gta	gag	cag	cac	cct	gaa	tac	acc	cac	atc	acg	gtg	ctg	gat	aaa	ctc	211
Val	Glu	Gln	His	Pro	Glu	Tyr	Thr	His	Ile	Thr	Val	Leu	Asp	Lys	Leu	
				25					30				35			
acc	tac	gca	gga	aac	gcc	gac	aat	ctc	aaa	ggc	ctc	ccc	gac	agc	aaa	259
Thr	Tyr	Ala	Gly	Asn	Ala	Asp	Asn	Leu	Lys	Gly	Leu	Pro	Asp	Ser	Lys	
			40					45				50				
gta	acc	ctc	atc	gaa	ggc	gat	atc	tgc	gat	gct	gaa	tta	gtc	gac	tcc	307
Val	Thr	Leu	Ile	Glu	Gly	Asp	Ile	Cys	Asp	Ala	Glu	Leu	Val	Asp	Ser	
			55					60				65				
ctg	gtc	aaa	gac	cac	gac	atc	aca	gtc	cac	ttc	gca	gca	gaa	tcc	cac	355
Leu	Val	Lys	Asp	His	Asp	Ile	Thr	Val	His	Phe	Ala	Ala	Glu	Ser	His	
70					75					80				85		
aac	gac	aac	tcc	ctc	aac	gac	ccc	tcc	ccg	ttt	gtt	cac	act	aac	ctc	403
Asn	Asp	Asn	Ser	Leu	Asn	Asp	Pro	Ser	Pro	Phe	Val	His	Thr	Asn	Leu	
				90					95				100			
atc	ggc	acc	ttt	gtc	ctg	cta	gaa	gca	gtc	cgc	aag	cac	aac	aaa	cgc	451
Ile	Gly	Thr	Phe	Val	Leu	Leu	Glu	Ala	Val	Arg	Lys	His	Asn	Lys	Arg	
			105					110				115				

ttc cac cac atc tcc acc gat gaa gtc ttc ggc gat cta gag ctg gat 499
 Phe His His Ile Ser Thr Asp Glu Val Phe Gly Asp Leu Glu Leu Asp
 120 125 130

gat cca aac cgc ttc act gaa acc acc gcc tac aag cca tcg tct cca 547
 Asp Pro Asn Arg Phe Thr Glu Thr Thr Ala Tyr Lys Pro Ser Ser Pro
 135 140 145

tat tct gca acc aag gca ggg tct gat cac ttg gta cac gca tgg atc 595
 Tyr Ser Ala Thr Lys Ala Gly Ser Asp His Leu Val His Ala Trp Ile
 150 155 160 165

cgc tcc ttc gga atc cag gca acc atg tct aac tgc tcc aac aat tac 643
 Arg Ser Phe Gly Ile Gln Ala Thr Met Ser Asn Cys Ser Asn Asn Tyr
 170 175 180

ggt ccc tac cag cac att gaa aag ttc atc ccc cgc cag atc acc aat 691
 Gly Pro Tyr Gln His Ile Glu Lys Phe Ile Pro Arg Gln Ile Thr Asn
 185 190 195

att ctg gcc ggc ctg aca cca aaa ctt tat gga acc ggc gag cag gtc 739
 Ile Leu Ala Gly Leu Thr Pro Lys Leu Tyr Gly Thr Gly Glu Gln Val
 200 205 210

cgc gac tgg atc cac gtc gat gat cac aat gac gcc gtc cac ctg atc 787
 Arg Asp Trp Ile His Val Asp Asp His Asn Asp Ala Val His Leu Ile
 215 220 225

ctg agt aag ggc aag atc ggc gaa acc tac atc atc gcc gcc gac aac 835
 Leu Ser Lys Gly Lys Ile Gly Glu Thr Tyr Ile Ile Gly Ala Asp Asn
 230 235 240 245

gat cat gtg aat aac aag cag gtc atc gag ctt att tgt gaa ctc atg 883
 Asp His Val Asn Asn Lys Gln Val Ile Glu Leu Ile Cys Glu Leu Met
 250 255 260

ggc ctc gac aaa aac gca tac gag cac gtc gca gac cgc ccc ggc cac 931
 Gly Leu Asp Lys Asn Ala Tyr Glu His Val Ala Asp Arg Pro Gly His
 265 270 275

gat atg cgt tac gcc atg gat tcc acc aag ctg cgc acc gag ctc ggc 979
 Asp Met Arg Tyr Ala Met Asp Ser Thr Lys Leu Arg Thr Glu Leu Gly
 280 285 290

tgg gca cct aaa tac acc gac gtt gat tcc ggc atg cgc aaa ggc cta 1027
 Trp Ala Pro Lys Tyr Thr Asp Val Asp Ser Gly Met Arg Lys Gly Leu
 295 300 305

gag cag acc atc gat tgg tac cgc gaa aac gag gcc tgg tgg cgc cct 1075
 Glu Gln Thr Ile Asp Trp Tyr Arg Glu Asn Glu Ala Trp Trp Arg Pro
 310 315 320 325

gcc aag aac aac gtc gaa gct acc tac gct aag cag gga caa 1117
 Ala Lys Asn Asn Val Glu Ala Thr Tyr Ala Lys Gln Gly Gln
 330 335

taatggaata cggtaaacaa ctc 1140

<210> 452

<211> 339

<212> PRT

<213> Corynebacterium glutamicum

<400> 452

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Phe Val Arg Gln Thr Val Glu Gln His Pro Glu Tyr Thr His Ile Thr
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Val Leu Asp Lys Leu Thr Tyr Ala Gly Asn Ala Asp Asn Leu Lys Gly
          35           40           45

Leu Pro Asp Ser Lys Val Thr Leu Ile Glu Gly Asp Ile Cys Asp Ala
          50           55           60

Glu Leu Val Asp Ser Leu Val Lys Asp His Asp Ile Thr Val His Phe
          65           70           75           80

Ala Ala Glu Ser His Asn Asp Asn Ser Leu Asn Asp Pro Ser Pro Phe
          85           90           95

Val His Thr Asn Leu Ile Gly Thr Phe Val Leu Leu Glu Ala Val Arg
          100          105          110

Lys His Asn Lys Arg Phe His His Ile Ser Thr Asp Glu Val Phe Gly
          115          120          125

Asp Leu Glu Leu Asp Asp Pro Asn Arg Phe Thr Glu Thr Thr Ala Tyr
          130          135          140

Lys Pro Ser Ser Pro Tyr Ser Ala Thr Lys Ala Gly Ser Asp His Leu
          145          150          155          160

Val His Ala Trp Ile Arg Ser Phe Gly Ile Gln Ala Thr Met Ser Asn
          165          170          175

Cys Ser Asn Asn Tyr Gly Pro Tyr Gln His Ile Glu Lys Phe Ile Pro
          180          185          190

Arg Gln Ile Thr Asn Ile Leu Ala Gly Leu Thr Pro Lys Leu Tyr Gly
          195          200          205

Thr Gly Glu Gln Val Arg Asp Trp Ile His Val Asp Asp His Asn Asp
          210          215          220

Ala Val His Leu Ile Leu Ser Lys Gly Lys Ile Gly Glu Thr Tyr Ile
          225          230          235          240

Ile Gly Ala Asp Asn Asp His Val Asn Asn Lys Gln Val Ile Glu Leu
          245          250          255

Ile Cys Glu Leu Met Gly Leu Asp Lys Asn Ala Tyr Glu His Val Ala
          260          265          270

Asp Arg Pro Gly His Asp Met Arg Tyr Ala Met Asp Ser Thr Lys Leu
          275          280          285

Arg Thr Glu Leu Gly Trp Ala Pro Lys Tyr Thr Asp Val Asp Ser Gly
          290          295          300

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Met Arg Lys Gly Leu Glu Gln Thr Ile Asp Trp Tyr Arg Glu Asn Glu
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Ala Trp Trp Arg Pro Ala Lys Asn Asn Val Glu Ala Thr Tyr Ala Lys
325 330 335

Gln Gly Gln

<210> 453

<211> 909

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(886)

<223> RXN00427

<400> 453

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Met Gly Arg Ile Leu
1 5

gta ttc tat agt gtc act tta gag gtg gcg gga gac cgt ccc gtt tac 163
Val Phe Tyr Ser Val Thr Leu Glu Val Ala Gly Asp Arg Pro Val Tyr
10 15 20

acg cct tcg cgc acc aat ttg ggc gac ggt ggc ggt ttt gct ttt ggt 211
Thr Pro Ser Arg Thr Asn Leu Gly Asp Gly Gly Gly Phe Ala Phe Gly
25 30 35

ttt ttg acg gcg ttg gcg ctg ggg gcg aac gcg gtg tgg tgc aca gac 259
Phe Leu Thr Ala Leu Ala Leu Gly Ala Asn Ala Val Trp Cys Thr Asp
40 45 50

gat gac ggc cgg ccg gag ggg cca ggg gtg ttg aag acg ctt atc gac 307
Asp Asp Gly Arg Pro Glu Gly Pro Gly Val Leu Lys Thr Leu Ile Asp
55 60 65

gcc gct tct cgg cat aat ctg gag gag gtt tct ccg gtg gta tgc aat 355
Ala Ala Ser Arg His Asn Leu Glu Glu Val Ser Pro Val Val Cys Asn
70 75 80 85

gct gat gat ccg gag cgg ttg gca ttt ccg ctg cgt cgg ggc ttg gag 403
Ala Asp Asp Pro Glu Arg Leu Ala Phe Pro Leu Arg Arg Gly Leu Glu
90 95 100

tgg cgt cgg atg cgc agt gag ttg att gat cca gcc aac ccg gag gat 451
Trp Arg Arg Met Arg Ser Glu Leu Ile Asp Pro Ala Asn Pro Glu Asp
105 110 115

gat ttg ctg ccg ggc atc gcc tcc ttg ttc aat ggt gcc ctg atc agc 499
Asp Leu Leu Pro Gly Ile Ala Ser Leu Phe Asn Gly Ala Leu Ile Ser
120 125 130

gct tat gca atg gag cgc att ggc gtg ccg gac tat cga ctg ttt att 547
Ala Tyr Ala Met Glu Arg Ile Gly Val Pro Asp Tyr Arg Leu Phe Ile

135	140	145	
cgc ggc gat gag gtg gag tat cac cgc cgt ttg gtg cgt tcc ggt ttg			595
Arg Gly Asp Glu Val Glu Tyr His Arg Arg Leu Val Arg Ser Gly Leu			
150	155	160	165
ccg ttt ggt acg tgt ttg acc acg gcg tat ttg cac ccg gat ggt tct			643
Pro Phe Gly Thr Cys Leu Thr Thr Ala Tyr Leu His Pro Asp Gly Ser			
	170	175	180
gat gag ttc aag ccg att ctg ggt ggg cgg atg cat acg cag tat ccg			691
Asp Glu Phe Lys Pro Ile Leu Gly Gly Arg Met His Thr Gln Tyr Pro			
	185	190	195
gat aat gat ttc aag agg ttt ttc acc tac cgc aac cgt ggc tac ctg			739
Asp Asn Asp Phe Lys Arg Phe Phe Thr Tyr Arg Asn Arg Gly Tyr Leu			
	200	205	210
atg agc cag ccg gga atg cgc aag ctt ctc cct cag gaa tat gcg cgc			787
Met Ser Gln Pro Gly Met Arg Lys Leu Leu Pro Gln Glu Tyr Ala Arg			
	215	220	225
ttt gcg tgg ttc ttc ctg gtt cag aaa cgg gat gtg aag gga ttc cgg			835
Phe Ala Trp Phe Phe Leu Val Gln Lys Arg Asp Val Lys Gly Phe Arg			
230	235	240	245
gag tgg ctg cgc ctg cac aaa ctg ggc cgc gac gag aaa ttc aat agg			883
Glu Trp Leu Arg Leu His Lys Leu Gly Arg Asp Glu Lys Phe Asn Arg			
	250	255	260
ccc tagatcagtt ttagtagttc ctc			909
Pro			

<210> 454

<211> 262

<212> PRT

<213> Corynebacterium glutamicum

<400> 454

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20 25 30

Gly Phe Ala Phe Gly Phe Leu Thr Ala Leu Ala Leu Gly Ala Asn Ala
35 40 45

Val Trp Cys Thr Asp Asp Asp Gly Arg Pro Glu Gly Pro Gly Val Leu
50 55 60

Lys Thr Leu Ile Asp Ala Ala Ser Arg His Asn Leu Glu Glu Val Ser
65 70 75 80

Pro Val Val Cys Asn Ala Asp Asp Pro Glu Arg Leu Ala Phe Pro Leu
85 90 95

Arg Arg Gly Leu Glu Trp Arg Arg Met Arg Ser Glu Leu Ile Asp Pro
100 105 110

Ala Asn Pro Glu Asp Asp Leu Leu Pro Gly Ile Ala Ser Leu Phe Asn
 115 120 125

Gly Ala Leu Ile Ser Ala Tyr Ala Met Glu Arg Ile Gly Val Pro Asp
 130 135 140

Tyr Arg Leu Phe Ile Arg Gly Asp Glu Val Glu Tyr His Arg Arg Leu
 145 150 155 160

Val Arg Ser Gly Leu Pro Phe Gly Thr Cys Leu Thr Thr Ala Tyr Leu
 165 170 175

His Pro Asp Gly Ser Asp Glu Phe Lys Pro Ile Leu Gly Gly Arg Met
 180 185 190

His Thr Gln Tyr Pro Asp Asn Asp Phe Lys Arg Phe Phe Thr Tyr Arg
 195 200 205

Asn Arg Gly Tyr Leu Met Ser Gln Pro Gly Met Arg Lys Leu Leu Pro
 210 215 220

Gln Glu Tyr Ala Arg Phe Ala Trp Phe Phe Leu Val Gln Lys Arg Asp
 225 230 235 240

Val Lys Gly Phe Arg Glu Trp Leu Arg Leu His Lys Leu Gly Arg Asp
 245 250 255

Glu Lys Phe Asn Arg Pro
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<210> 455
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 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(532)
 <223> FRXA00427

<400> 455
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 Leu Leu Pro Gly Ile
 1 5

gcc tcc ttg ttc aat ggt gcc ctg atc agc gct tat gca atg gag cgc 163
 Ala Ser Leu Phe Asn Gly Ala Leu Ile Ser Ala Tyr Ala Met Glu Arg
 10 15 20

att ggc gtg ccg gac tat cga ctg ttt att cgc ggc gat gag gtg gag 211
 Ile Gly Val Pro Asp Tyr Arg Leu Phe Ile Arg Gly Asp Glu Val Glu
 25 30 35

tat cac cgc cgt ttg gtg cgt tcc ggt ttg ccg ttt ggt acg tgt ttg 259
 Tyr His Arg Arg Leu Val Arg Ser Gly Leu Pro Phe Gly Thr Cys Leu
 40 45 50

acc acg gcg tat ttg cac ccg gat ggt tct gat gag ttc aag ccg att 307
 Thr Thr Ala Tyr Leu His Pro Asp Gly Ser Asp Glu Phe Lys Pro Ile
 55 60 65

ctg ggt ggg cgg atg cat acg cag tat ccg gat aat gat ttc aag agg 355
 Leu Gly Gly Arg Met His Thr Gln Tyr Pro Asp Asn Asp Phe Lys Arg
 70 75 80 85

ttt ttc acc tac cgc aac cgt ggc tac ctg atg agc cag ccg gga atg 403
 Phe Phe Thr Tyr Arg Asn Arg Gly Tyr Leu Met Ser Gln Pro Gly Met
 90 95 100

cgc aag ctt ctc cct cag gaa tat gcg cgc ttt gcg tgg ttc ttc ctg 451
 Arg Lys Leu Leu Pro Gln Glu Tyr Ala Arg Phe Ala Trp Phe Phe Leu
 105 110 115

gtt cag aaa cgg gat gtg aag gga ttc cgg gag tgg ctg cgc ctg cac 499
 Val Gln Lys Arg Asp Val Lys Gly Phe Arg Glu Trp Leu Arg Leu His
 120 125 130

aaa ctg ggc cgc gac gag aaa ttc aat agg ccc tagatcagtt ttagtagttc 552
 Lys Leu Gly Arg Asp Glu Lys Phe Asn Arg Pro
 135 140

ctc 555

<210> 456
 <211> 144
 <212> PRT
 <213> Corynebacterium glutamicum

<400> 456
 Leu Leu Pro Gly Ile Ala Ser Leu Phe Asn Gly Ala Leu Ile Ser Ala
 1 5 10 15

Tyr Ala Met Glu Arg Ile Gly Val Pro Asp Tyr Arg Leu Phe Ile Arg
 20 25 30

Gly Asp Glu Val Glu Tyr His Arg Arg Leu Val Arg Ser Gly Leu Pro
 35 40 45

Phe Gly Thr Cys Leu Thr Thr Ala Tyr Leu His Pro Asp Gly Ser Asp
 50 55 60

Glu Phe Lys Pro Ile Leu Gly Gly Arg Met His Thr Gln Tyr Pro Asp
 65 70 75 80

Asn Asp Phe Lys Arg Phe Phe Thr Tyr Arg Asn Arg Gly Tyr Leu Met
 85 90 95

Ser Gln Pro Gly Met Arg Lys Leu Leu Pro Gln Glu Tyr Ala Arg Phe
 100 105 110

Ala Trp Phe Phe Leu Val Gln Lys Arg Asp Val Lys Gly Phe Arg Glu
 115 120 125

Trp Leu Arg Leu His Lys Leu Gly Arg Asp Glu Lys Phe Asn Arg Pro
 130 135 140

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<210> 457
<211> 507
<212> DNA
<213> Corynebacterium glutamicum
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<221> CDS  
<222> (101)..(484)  
<223> RXA00327
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<400> 457																	
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ctagggggcc aggcgcggga tgattgggtt tgtcacgccg atg att cag gcg gcg 115																	
Met Ile Gln Ala Ala 1 5																	
ttg tgg atc gtg ctc ttt tta ttc gct gat cgc ctg tcc aat ccg ctg 163																	
Leu Trp Ile Val Leu Phe Leu Phe Ala Asp Arg Leu Ser Asn Pro Leu 10 15 20																	
gtt ttt gtc agc gcc atc atg ttc gcg att tcc ttt agc tcc ccc gtg 211																	
Val Phe Val Ser Ala Ile Met Phe Ala Ile Ser Phe Ser Ser Pro Val 25 30 35																	
gcg aac ttc ggt ttc gat acg atc tgc gaa aaa ctc gac cgc cgc gtc 259																	
Ala Asn Phe Gly Phe Asp Thr Ile Cys Glu Lys Leu Asp Arg Arg Val 40 45 50																	
atg gtc gcc ggc acc ggc atg gcc aac atg agc gcc tac att tgc gcg 307																	
Met Val Ala Gly Thr Gly Met Ala Asn Met Ser Ala Tyr Ile Cys Ala 55 60 65																	
atg ctg gcc aca caa atc atc gga ttt tta ctc gac tgg aac gcc gac 355																	
Met Leu Ala Thr Gln Ile Ile Gly Phe Leu Leu Asp Trp Asn Ala Asp 70 75 80 85																	
ggc cac gcc tac acc tgg tcg aat ttc cag gtg gcg tgg ctt ggt ctg 403																	
Gly His Ala Tyr Thr Trp Ser Asn Phe Gln Val Ala Trp Leu Gly Leu 90 95 100																	
ggc gcg gtg tgg ctg gca ggc atg atc ggg ctt gca gtc tgc ctc ctg 451																	
Gly Ala Val Trp Leu Ala Gly Met Ile Gly Leu Ala Val Cys Leu Leu 105 110 115																	
ctg cag cgt cga aaa aat att gct ttt cga cgc taaaaccgga ccgtaaccgc 504																	
Leu Gln Arg Arg Lys Asn Ile Ala Phe Arg Arg 120 125																	
tag 507																	

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<210> 458
<211> 128
<212> PRT
<213> Corynebacterium glutamicum
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<400> 458

Met Ile Gln Ala Ala Leu Trp Ile Val Leu Phe Leu Phe Ala Asp Arg
 1 5 10 15
 Leu Ser Asn Pro Leu Val Phe Val Ser Ala Ile Met Phe Ala Ile Ser
 20 25 30
 Phe Ser Ser Pro Val Ala Asn Phe Gly Phe Asp Thr Ile Cys Glu Lys
 35 40 45
 Leu Asp Arg Arg Val Met Val Ala Gly Thr Gly Met Ala Asn Met Ser
 50 55 60
 Ala Tyr Ile Cys Ala Met Leu Ala Thr Gln Ile Ile Gly Phe Leu Leu
 65 70 75 80
 Asp Trp Asn Ala Asp Gly His Ala Tyr Thr Trp Ser Asn Phe Gln Val
 85 90 95
 Ala Trp Leu Gly Leu Gly Ala Val Trp Leu Ala Gly Met Ile Gly Leu
 100 105 110
 Ala Val Cys Leu Leu Leu Gln Arg Arg Lys Asn Ile Ala Phe Arg Arg
 115 120 125

<210> 459
 <211> 615
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(592)
 <223> RXA00328

<400> 459
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 attaggtcta ccaaggactt ttaaagatcg ggtaaaacct gtg ggc gtt gaa agg 115
 Val Gly Val Glu Arg
 1 5
 ggc aag gtc tct gcc aag gca cta gtt gtc tgg ttg acg gca atg tgc 163
 Gly Lys Val Ser Ala Lys Ala Leu Val Val Trp Leu Thr Ala Met Cys
 10 15 20
 gtg tac atc gtg gcc att gct ggt cga aca tca ttt ggt gtc gcc gga 211
 Val Tyr Ile Val Ala Ile Ala Gly Arg Thr Ser Phe Gly Val Ala Gly
 25 30 35
 gtg cat gcg atc gat cgc ttt gat atc gac gcc tcc cggttg gcc gtg 259
 Val His Ala Ile Asp Arg Phe Asp Ile Asp Ala Ser Arg Leu Ala Val
 40 45 50
 ttc act tct gtt cag gtt gga gtc tat gtt ctc gcg cag att ccc atg 307
 Phe Thr Ser Val Gln Val Gly Val Tyr Val Leu Ala Gln Ile Pro Met
 55 60 65

ggc atg ctg gtg gac agg ttc gac gcc cgg aaa ctc ttg ctg gct ggc 355
 Gly Met Leu Val Asp Arg Phe Asp Ala Arg Lys Leu Leu Leu Ala Gly
 70 75 80 85

 gct tta att ttg gca gct ggc cag ctc att ttg ggt ttc act gat tct 403
 Ala Leu Ile Leu Ala Ala Gly Gln Leu Ile Leu Gly Phe Thr Asp Ser
 90 95 100

 tat atg atc gcc att ttt gcc cga gtg ctc atc agt gtt ggc gat tct 451
 Tyr Met Ile Ala Ile Phe Ala Arg Val Leu Ile Ser Val Gly Asp Ser
 105 110 115

 tct gca ttt ttg tcc gtg atg cga ctg ttg ccc aac tgg ttc ccg atg 499
 Ser Ala Phe Leu Ser Val Met Arg Leu Leu Pro Asn Trp Phe Pro Met
 120 125 130

 tct tgg aca cct gtg ttg cag cag ctc acg ggc gct ttt ggc ttt gtg 547
 Ser Trp Thr Pro Val Leu Gln Gln Leu Thr Gly Ala Phe Gly Phe Val
 135 140 145

 ggg cag ttt tct ccg cgg tgc cgt ttt tgc aca tac tca aca cct 592
 Gly Gln Phe Ser Pro Arg Cys Arg Phe Cys Thr Tyr Ser Thr Pro
 150 155 160

 taggggtggac aattcctttc gca 615

<210> 460
 <211> 164
 <212> PRT
 <213> Corynebacterium glutamicum

<400> 460
 Val Gly Val Glu Arg Gly Lys Val Ser Ala Lys Ala Leu Val Val Trp
 1 5 10 15

 Leu Thr Ala Met Cys Val Tyr Ile Val Ala Ile Ala Gly Arg Thr Ser
 20 25 30

 Phe Gly Val Ala Gly Val His Ala Ile Asp Arg Phe Asp Ile Asp Ala
 35 40 45

 Ser Arg Leu Ala Val Phe Thr Ser Val Gln Val Gly Val Tyr Val Leu
 50 55 60

 Ala Gln Ile Pro Met Gly Met Leu Val Asp Arg Phe Asp Ala Arg Lys
 65 70 75 80

 Leu Leu Leu Ala Gly Ala Leu Ile Leu Ala Ala Gly Gln Leu Ile Leu
 85 90 95

 Gly Phe Thr Asp Ser Tyr Met Ile Ala Ile Phe Ala Arg Val Leu Ile
 100 105 110

 Ser Val Gly Asp Ser Ser Ala Phe Leu Ser Val Met Arg Leu Leu Pro
 115 120 125

 Asn Trp Phe Pro Met Ser Trp Thr Pro Val Leu Gln Gln Leu Thr Gly
 130 135 140

 Ala Phe Gly Phe Val Gly Gln Phe Ser Pro Arg Cys Arg Phe Cys Thr

655

150	155	160	165	
ggt cgg gat act cca gat cct cag cca aaa cct gtc gaa tca gct cag	643			
Val Arg Asp Thr Pro Asp Pro Gln Pro Lys Pro Val Glu Ser Ala Gln				
170 175 180				
gaa gca gat aaa cca agc ctg cgc gcg agt ttg aag ttg att gtc cgc	691			
Glu Ala Asp Lys Pro Ser Leu Arg Ala Ser Leu Lys Leu Ile Val Arg				
185 190 195				
aat ccg att acg tgg cag ggt ttc ttc att cac tac gta ttg atg gtg	739			
Asn Pro Ile Thr Trp Gln Gly Phe Phe Ile His Tyr Val Leu Met Val				
200 205 210				
tgg cag acc gtg ttc tcc atg atg tgg ggc gtc ccg ctg atg act ttg	787			
Trp Gln Thr Val Phe Ser Met Met Trp Gly Val Pro Leu Met Thr Leu				
215 220 225				
ggc atg gga ctg tct gca acg acg gct ggt ttg gtg ttg agc atc aac	835			
Gly Met Gly Leu Ser Ala Thr Thr Ala Gly Leu Val Leu Ser Ile Asn				
230 235 240 245				
acg ctg tgc atg gtg gta tcg gcg cca atc atc gga ata att tcc gca	883			
Thr Leu Cys Met Val Val Ser Ala Pro Ile Ile Gly Ile Ile Ser Ala				
250 255 260				
cgc ctt ggg tat cgc cgt gac gtg gtc gcc att gcg ctg tcg ttt gtt	931			
Arg Leu Gly Tyr Arg Arg Asp Val Val Ala Ile Ala Leu Ser Phe Val				
265 270 275				
caa tcc gca gta tgg ctg gtg ttc ttg gcc tcc gat gca cct cgt ggt	979			
Gln Ser Ala Val Trp Leu Val Phe Leu Ala Ser Asp Ala Pro Arg Gly				
280 285 290				
ttg atg gct atc atc ttg gtc aac atc gtc atg ggt ctg act act gcg	1027			
Leu Met Ala Ile Ile Leu Val Asn Ile Val Met Gly Leu Thr Thr Ala				
295 300 305				
gct tct ggt tat ggc ttt gac acc att cgt gag cgc cta gat cgc aag	1075			
Ala Ser Gly Tyr Gly Phe Asp Thr Ile Arg Glu Arg Leu Asp Arg Lys				
310 315 320 325				
att ttg gct gcg ggc acg gga ctg gca aac atg ggt gga ttc ttg tca	1123			
Ile Leu Ala Ala Gly Thr Gly Leu Ala Asn Met Gly Gly Phe Leu Ser				
330 335 340				
tcg atg gtt gca gcg cag gtt atg ggg ttc ctt ctt gat cac agc gcg	1171			
Ser Met Val Ala Ala Gln Val Met Gly Phe Leu Leu Asp His Ser Ala				
345 350 355				
cat ggt agc acc tat act tgg gtg gac ttc cgt ttt ggt ttc ctt gcg	1219			
His Gly Ser Thr Tyr Thr Trp Val Asp Phe Arg Phe Gly Phe Leu Ala				
360 365 370				
att ctt gtc aca tgg gcc gtc gga gtc acg gga ttt gtt gta gcc cga	1267			
Ile Leu Val Thr Trp Ala Val Gly Val Thr Gly Phe Val Val Ala Arg				
375 380 385				
ctc aag ggt gga ccg ggc cgc aga tta ctc gcc cag att agg tct acc	1315			
Leu Lys Gly Gly Pro Gly Arg Arg Leu Leu Ala Gln Ile Arg Ser Thr				
390 395 400 405				

aag gac ttt taaagatcgg gtaaaacctg tgg
Lys Asp Phe

1347

<210> 462

<211> 408

<212> PRT

<213> Corynebacterium glutamicum

<400> 462

Met Ala Ala Ile Thr Ser Arg Thr Ser Phe Gly Val Ala Gly Val Glu
1 5 10 15

Ala Ile Asp Arg Phe Gln Val Asp Ala Thr Arg Ile Ala Val Phe Thr
20 25 30

Ser Val Gln Val Gly Val Tyr Ala Phe Ala Gln Ile Pro Met Gly Ile
35 40 45

Leu Ile Asp Lys Phe Gly Pro Arg Lys Leu Leu Ala Ile Gly Ala Leu
50 55 60

Val Met Gly Ile Gly Gln Leu Ile Leu Gly Phe Thr Asp Ser Tyr Ser
65 70 75 80

Ile Ala Ile Ile Ala Arg Val Phe Ile Gly Ala Gly Asp Ala Ser Ile
85 90 95

Phe Leu Ser Val Met Arg Ile Leu Pro Phe Trp Phe Pro Leu Lys His
100 105 110

Thr Pro Ile Phe Thr Gln Leu Thr Thr Cys Leu Gly Gln Leu Gly Gln
115 120 125

Phe Phe Ser Ala Val Pro Phe Met Ala Leu Leu Gly Ala Gln Gly Trp
130 135 140

Pro Val Ala Phe Val Ser Leu Gly Ser Val Val Ala Leu Ile Ala Ile
145 150 155 160

Ala Ala Leu Val Ala Val Arg Asp Thr Pro Asp Pro Gln Pro Lys Pro
165 170 175

Val Glu Ser Ala Gln Glu Ala Asp Lys Pro Ser Leu Arg Ala Ser Leu
180 185 190

Lys Leu Ile Val Arg Asn Pro Ile Thr Trp Gln Gly Phe Phe Ile His
195 200 205

Tyr Val Leu Met Val Trp Gln Thr Val Phe Ser Met Met Trp Gly Val
210 215 220

Pro Leu Met Thr Leu Gly Met Gly Leu Ser Ala Thr Thr Ala Gly Leu
225 230 235 240

Val Leu Ser Ile Asn Thr Leu Cys Met Val Val Ser Ala Pro Ile Ile
245 250 255

Gly Ile Ile Ser Ala Arg Leu Gly Tyr Arg Arg Asp Val Val Ala Ile

260	265	270	
Ala Leu Ser Phe Val Gln Ser	Ala Val Trp Leu Val	Phe Leu Ala Ser	
275	280	285	
Asp Ala Pro Arg Gly Leu Met	Ala Ile Ile Leu Val	Asn Ile Val Met	
290	295	300	
Gly Leu Thr Thr Ala Ala Ser	Gly Tyr Gly Phe Asp Thr	Ile Arg Glu	
305	310	315	320
Arg Leu Asp Arg Lys Ile Leu	Ala Ala Gly Thr Gly Leu	Ala Asn Met	
	325	330	335
Gly Gly Phe Leu Ser Ser Met	Val Ala Ala Gln Val Met	Gly Phe Leu	
	340	345	350
Leu Asp His Ser Ala His Gly	Ser Thr Tyr Thr Trp Val	Asp Phe Arg	
	355	360	365
Phe Gly Phe Leu Ala Ile Leu	Val Thr Trp Ala Val Gly	Val Thr Gly	
	370	375	380
Phe Val Val Ala Arg Leu Lys	Gly Gly Pro Gly Arg Arg	Leu Leu Ala	
385	390	395	400
Gln Ile Arg Ser Thr Lys Asp	Phe		
	405		
<210> 463			
<211> 2265			
<212> DNA			
<213> Corynebacterium glutamicum			
<220>			
<221> CDS			
<222> (101)..(2242)			
<223> RXN01554			
<400> 463			
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tagacgtata aacaagtttg aaaaaggaag gttatccatc ttg aaa aag cat gtg 115			
Leu Lys Lys His Val			
1 5			
acc tca gcc gtt acc gcc gtg gtg acg gct ttt tca acg gct gcg ctt 163			
Thr Ser Ala Val Thr Ala Val Val Thr Ala Phe Ser Thr Ala Ala Leu			
10 15 20			
ggg tta agt att gcc gtt tct cct gct gtt gcc caa gtg gct aat cca 211			
Gly Leu Ser Ile Ala Val Ser Pro Ala Val Ala Gln Val Ala Asn Pro			
25 30 35			
gct cca gat ctt tct gcg ccg tat aca tgg gtg gaa gag ttt gat tcc 259			
Ala Pro Asp Leu Ser Ala Pro Tyr Thr Trp Val Glu Glu Phe Asp Ser			
40 45 50			
gag gat gct ctc aaa ggg tgg aac att ttc cgc cag cca gat tat ggc 307			
Glu Asp Ala Leu Lys Gly Trp Asn Ile Phe Arg Gln Pro Asp Tyr Gly			

55	60	65	
agc gac aaa gtt ctc tat Ser Asp Lys Val Leu Tyr 70	acc gaa gat gct tta agt atc Thr Glu Asp Ala Leu Ser Ile 75	gaa gat ggc Glu Asp Gly 80	355
aag ctc acc atc acc act Lys Leu Thr Ile Thr Thr 90	cag cgc cac tgc gtt gac Gln Arg His Cys Val Asp 95	gaa gac ttc gcg Glu Asp Phe Ala 100	403
atc agt gat cct gtc aac cgc Ile Ser Asp Pro Val Asn Arg 105	gga aag ctc aat gac agc Gly Lys Leu Asn Asp 110	acc gcg caa Ser Thr Ala Gln 115	451
gtt gaa cct tgt gct cca ggt Val Glu Pro Cys Ala Pro Gly 120	cag ttt gaa aag ttc acc Gln Phe Glu Lys Phe Thr 125	agc gcg cgc Ser Ala Arg 130	499
atc gtc act ccg aaa att gct Ile Val Thr Pro Lys Ile 135	cgt gga gag ttc gac ctt Ala Arg Gly Glu Phe Asp 140	tct gtc act Leu Ser Val Thr 145	547
gca act ctt aac acc ggt ggc Ala Thr Leu Asn Thr Gly 150	gtc gaa ggt gtc cga agt Val Glu Gly Val Arg Ser 155	gcc att tgg Ala Ile Trp 160	595
atg caa aac ggt gaa cag gcg Met Gln Asn Gly Glu Gln 170	tgt tcc tca gca acc aac Ala Cys Ser Ser Ala Thr 175	aat ggc ctc Asn Asn Gly Leu 180	643
tac gga gaa cta gac ctg gta Tyr Gly Glu Leu Asp Leu 185	gag cac ttt tct tac gat Glu His Phe Ser Tyr Asp 190	ctt cgc tcg Leu Arg Ser 195	691
cca tgg tct cca tca aac acc Pro Trp Ser Pro Ser Asn Thr 200	cac ttg ggt tgt gat cct His Leu Gly Cys Asp Pro 205	gaa agt gtc Glu Ser Val 210	739
aac ggc acc aac cgt gca cct Asn Gly Thr Asn Arg Ala 215	cgt gaa ctt aaa cta gat Arg Glu Leu Lys Leu Asp 220	gag tca ctc Glu Ser Leu 225	787
gat ggc gtg gag cac acc Asp Gly Val Glu His Thr 230	tgg act gtg agc acc acc Trp Thr Val Ser Thr Thr 235	cgc gac ggc gtt Arg Asp Gly Val 240	835
gag tac ttc att gat gat Glu Tyr Phe Ile Asp Asp 250	gag gcg att aac cgc cag Glu Ala Ile Asn Arg Gln 255	tca tgg cgc aac Ser Trp Arg Asn 260	883
gat gtc act ttg ggg cat gcc Asp Val Thr Leu Gly His 265	gaa att gat gat ttc ggg Glu Ile Asp Asp Phe Gly 270	atc tcc gcg Ile Ser Ala 275	931
cag acg ttt gat gag atc gtc Gln Thr Phe Asp Glu Ile 280	gac cgc gaa tgg act ctc Asp Arg Glu Trp Thr Leu 285	act ctt aat Thr Leu Asn 290	979
caa aag gta gaa agc gcc gac Gln Lys Val Glu Ser Ala 295	tgg gca aaa cca cgt tcc Trp Ala Lys Pro Arg Ser 300	tct gag gaa Ser Ser Glu Glu 305	1027

gat ttc cca gtc cgg tcc atg gtg att gac cgc atc gag gtc acc gga	1075
Asp Phe Pro Val Arg Ser Met Val Ile Asp Arg Ile Glu Val Thr Gly	
310 315 320 325	
tct ccc gca gta tct gaa gac acc ccc atg cca gat acc acc cag ctt	1123
Ser Pro Ala Val Ser Glu Asp Thr Pro Met Pro Asp Thr Thr Gln Leu	
330 335 340	
ttg acc caa gac act ctg gaa tac ctc ggt cgc atg cca gtg ctg gaa	1171
Leu Thr Gln Asp Thr Leu Glu Tyr Leu Gly Arg Met Pro Val Leu Glu	
345 350 355	
cgc tac gag cca gca agt gct gat ttt gcc gat ggc cgc agg cct tcc	1219
Arg Tyr Glu Pro Ala Ser Ala Asp Phe Ala Asp Gly Arg Arg Pro Ser	
360 365 370	
tgg aac tac ttc aat ttg aag gaa tcg tgg cag aat cca gaa ctc gag	1267
Trp Asn Tyr Phe Asn Leu Lys Glu Ser Trp Gln Asn Pro Glu Leu Glu	
375 380 385	
caa cgc cca gaa gct gtc gaa ttc gtt gat gga cgc atg gat atc gtg	1315
Gln Arg Pro Glu Ala Val Glu Phe Val Asp Gly Arg Met Asp Ile Val	
390 395 400 405	
acc cgt cgc cac tgt ctg gcc acc act gat gac atc gcc act ccg gaa	1363
Thr Arg Arg His Cys Leu Ala Thr Thr Asp Ile Ala Thr Pro Glu	
410 415 420	
aac gca cag gag gaa ccg tgc gcg ccg ggt gag gtg aca cgc tac agc	1411
Asn Ala Gln Glu Glu Pro Cys Ala Pro Gly Glu Val Thr Arg Tyr Ser	
425 430 435	
tca gcg cgt gtc cac ctt cca gag atc ccc gcc ggc aac ttc cgg ctc	1459
Ser Ala Arg Val His Leu Pro Glu Ile Pro Ala Gly Asn Phe Arg Leu	
440 445 450	
acc gtg cgc gca cgg gcg cag tcc gaa gag ctt gtc gac ggc gtc cgc	1507
Thr Val Arg Ala Arg Ala Gln Ser Glu Glu Leu Val Asp Gly Val Arg	
455 460 465	
ccc gct atc tgg atg cag aac aat acc aac ttc tgt gct gac aac gat	1555
Pro Ala Ile Trp Met Gln Asn Asn Thr Asn Phe Cys Ala Asp Asn Asp	
470 475 480 485	
gga cgc cct tat ggt gaa ctg gat att act gag ttc tac agc tct cgt	1603
Gly Arg Pro Tyr Gly Glu Leu Asp Ile Thr Glu Phe Tyr Ser Ser Arg	
490 495 500	
gtg aac acc cag tac tcg gca gta cac ctt gga tgt gct ggc aac cgc	1651
Val Asn Thr Gln Tyr Ser Ala Val His Leu Gly Cys Ala Gly Asn Arg	
505 510 515	
cca gag atg aag ctt cgc caa atg gaa atg gaa gag tcc atg ttt ggg	1699
Pro Glu Met Lys Leu Arg Gln Met Glu Met Glu Glu Ser Met Phe Gly	
520 525 530	
gat tgg cat gac tgg ggc gtc gaa gtc ttc gac ggc cag atc gta ttc	1747
Asp Trp His Asp Trp Gly Val Glu Val Phe Asp Gly Gln Ile Val Phe	
535 540 545	

acc att gac ggc aag gca gta act tcc tct ggc aaa gat gtc ttt ggc 1795
 Thr Ile Asp Gly Lys Ala Val Thr Ser Ser Gly Lys Asp Val Phe Gly
 550 555 560 565

 aac tct gtt acc cca gcc gct gca cct ctt cgc ccc gcg cac ttc aag 1843
 Asn Ser Val Thr Pro Ala Ala Ala Pro Leu Arg Pro Ala His Phe Lys
 570 575 580

 ttg tcg gaa gag gaa tac cgt gaa gtc atc ggg cag cct tgg cac ctt 1891
 Leu Ser Glu Glu Glu Tyr Arg Glu Val Ile Gly Gln Pro Trp His Leu
 585 590 595

 att ttg aac acc atg gtg gag cag tct ggc aaa gac agc tgg att aca 1939
 Ile Leu Asn Thr Met Val Glu Gln Ser Gly Lys Asp Ser Trp Ile Thr
 600 605 610

 gcg gtc gac aat aac gag gcg ttc cca gaa cac cgc ttc caa att gac 1987
 Ala Val Asp Asn Asn Glu Ala Phe Pro Glu His Arg Phe Gln Ile Asp
 615 620 625

 cat gtg gca gta gat atc gag tct gac tct gtg gac aat gta tgg cct 2035
 His Val Ala Val Asp Ile Glu Ser Asp Ser Val Asp Asn Val Trp Pro
 630 635 640 645

 gac gct gcg aat gaa atc cca gac aat gtt ggt att gaa gac tct gat 2083
 Asp Ala Ala Asn Glu Ile Pro Asp Asn Val Gly Ile Glu Asp Ser Asp
 650 655 660

 gat ggc agc gac ctg gag gtt ggt tcg acc gga agc tct aca gct gag 2131
 Asp Gly Ser Asp Leu Glu Val Gly Ser Thr Gly Ser Ser Thr Ala Glu
 665 670 675

 acc gtg agc tgg atc tcg ttg ttc acc gcg ttg agc tcg ctg gtc ttc 2179
 Thr Val Ser Trp Ile Ser Leu Phe Thr Ala Leu Ser Ser Leu Val Phe
 680 685 690

 aca ctg gct ctc aat caa gaa gca ttg cag aat ttg att aat cag ttc 2227
 Thr Leu Ala Leu Asn Gln Glu Ala Leu Gln Asn Leu Ile Asn Gln Phe
 695 700 705

 atg aga cag ttc aag taatccttgt gggcgctttg tct 2265
 Met Arg Gln Phe Lys
 710

<210> 464

<211> 714

<212> PRT

<213> Corynebacterium glutamicum

<400> 464

Leu Lys Lys His Val Thr Ser Ala Val Thr Ala Val Val Thr Ala Phe
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Ser Thr Ala Ala Leu Gly Leu Ser Ile Ala Val Ser Pro Ala Val Ala
 20 25 30

Gln Val Ala Asn Pro Ala Pro Asp Leu Ser Ala Pro Tyr Thr Trp Val
 35 40 45

Glu Glu Phe Asp Ser Glu Asp Ala Leu Lys Gly Trp Asn Ile Phe Arg

50	55	60
Gln Pro Asp Tyr Gly Ser Asp Lys Val Leu Tyr Thr Glu Asp Ala Leu		
65	70	75
Ser Ile Glu Asp Gly Lys Leu Thr Ile Thr Thr Gln Arg His Cys Val		
	85	90
Asp Glu Asp Phe Ala Ile Ser Asp Pro Val Asn Arg Gly Lys Leu Asn		
	100	105
Asp Ser Thr Ala Gln Val Glu Pro Cys Ala Pro Gly Gln Phe Glu Lys		
	115	120
Phe Thr Ser Ala Arg Ile Val Thr Pro Lys Ile Ala Arg Gly Glu Phe		
	130	135
Asp Leu Ser Val Thr Ala Thr Leu Asn Thr Gly Gly Val Glu Gly Val		
	145	150
Arg Ser Ala Ile Trp Met Gln Asn Gly Glu Gln Ala Cys Ser Ser Ala		
	165	170
Thr Asn Asn Gly Leu Tyr Gly Glu Leu Asp Leu Val Glu His Phe Ser		
	180	185
Tyr Asp Leu Arg Ser Pro Trp Ser Pro Ser Asn Thr His Leu Gly Cys		
	195	200
Asp Pro Glu Ser Val Asn Gly Thr Asn Arg Ala Pro Arg Glu Leu Lys		
	210	215
Leu Asp Glu Ser Leu Asp Gly Val Glu His Thr Trp Thr Val Ser Thr		
	225	230
Thr Arg Asp Gly Val Glu Tyr Phe Ile Asp Asp Glu Ala Ile Asn Arg		
	245	250
Gln Ser Trp Arg Asn Asp Val Thr Leu Gly His Ala Glu Ile Asp Asp		
	260	265
Phe Gly Ile Ser Ala Gln Thr Phe Asp Glu Ile Val Asp Arg Glu Trp		
	275	280
Thr Leu Thr Leu Asn Gln Lys Val Glu Ser Ala Asp Trp Ala Lys Pro		
	290	295
Arg Ser Ser Glu Glu Asp Phe Pro Val Arg Ser Met Val Ile Asp Arg		
	305	310
Ile Glu Val Thr Gly Ser Pro Ala Val Ser Glu Asp Thr Pro Met Pro		
	325	330
Asp Thr Thr Gln Leu Leu Thr Gln Asp Thr Leu Glu Tyr Leu Gly Arg		
	340	345
Met Pro Val Leu Glu Arg Tyr Glu Pro Ala Ser Ala Asp Phe Ala Asp		
	355	360
Gly Arg Arg Pro Ser Trp Asn Tyr Phe Asn Leu Lys Glu Ser Trp Gln		
	370	375
		380

Asn Pro Glu Leu Glu Gln Arg Pro Glu Ala Val Glu Phe Val Asp Gly
 385 390 395 400
 Arg Met Asp Ile Val Thr Arg Arg His Cys Leu Ala Thr Thr Asp Asp
 405 410 415
 Ile Ala Thr Pro Glu Asn Ala Gln Glu Glu Pro Cys Ala Pro Gly Glu
 420 425 430
 Val Thr Arg Tyr Ser Ser Ala Arg Val His Leu Pro Glu Ile Pro Ala
 435 440 445
 Gly Asn Phe Arg Leu Thr Val Arg Ala Arg Ala Gln Ser Glu Glu Leu
 450 455 460
 Val Asp Gly Val Arg Pro Ala Ile Trp Met Gln Asn Asn Thr Asn Phe
 465 470 475 480
 Cys Ala Asp Asn Asp Gly Arg Pro Tyr Gly Glu Leu Asp Ile Thr Glu
 485 490 495
 Phe Tyr Ser Ser Arg Val Asn Thr Gln Tyr Ser Ala Val His Leu Gly
 500 505 510
 Cys Ala Gly Asn Arg Pro Glu Met Lys Leu Arg Gln Met Glu Met Glu
 515 520 525
 Glu Ser Met Phe Gly Asp Trp His Asp Trp Gly Val Glu Val Phe Asp
 530 535 540
 Gly Gln Ile Val Phe Thr Ile Asp Gly Lys Ala Val Thr Ser Ser Gly
 545 550 555 560
 Lys Asp Val Phe Gly Asn Ser Val Thr Pro Ala Ala Ala Pro Leu Arg
 565 570 575
 Pro Ala His Phe Lys Leu Ser Glu Glu Glu Tyr Arg Glu Val Ile Gly
 580 585 590
 Gln Pro Trp His Leu Ile Leu Asn Thr Met Val Glu Gln Ser Gly Lys
 595 600 605
 Asp Ser Trp Ile Thr Ala Val Asp Asn Asn Glu Ala Phe Pro Glu His
 610 615 620
 Arg Phe Gln Ile Asp His Val Ala Val Asp Ile Glu Ser Asp Ser Val
 625 630 635 640
 Asp Asn Val Trp Pro Asp Ala Ala Asn Glu Ile Pro Asp Asn Val Gly
 645 650 655
 Ile Glu Asp Ser Asp Asp Gly Ser Asp Leu Glu Val Gly Ser Thr Gly
 660 665 670
 Ser Ser Thr Ala Glu Thr Val Ser Trp Ile Ser Leu Phe Thr Ala Leu
 675 680 685
 Ser Ser Leu Val Phe Thr Leu Ala Leu Asn Gln Glu Ala Leu Gln Asn
 690 695 700

Leu Ile Asn Gln Phe Met Arg Gln Phe Lys
705 710

<210> 465
<211> 389
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(382)
<223> RXN03015

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gattatgcgg aggctgcggc tttcgcgag gtgcatttct ttg ggc gtg ggt act . 115
Leu Gly Val Gly Thr
1 5
cct cag cag aag ggt act tat gcg gcg gat ctg acg tat gtt cgt cag 163
Pro Gln Gln Lys Gly Thr Tyr Ala Ala Asp Leu Thr Tyr Val Arg Gln
10 15 20
gtt gtt gag gat ttg gtg ccg ctg ctt gag ggc gag cac att att ttc 211
Val Val Glu Asp Leu Val Pro Leu Leu Glu Gly Glu His Ile Ile Phe
25 30 35
ggc aag tct acg gtt ccg gtt ggt act gct gag cag ttg cag gag ctt 259
Gly Lys Ser Thr Val Pro Val Gly Thr Ala Glu Gln Leu Gln Glu Leu
40 45 50
gct gat tct ctg gtc aag cct ggt tcg cac gtg gag atc gcg tgg aat 307
Ala Asp Ser Leu Val Lys Pro Gly Ser His Val Glu Ile Ala Trp Asn
55 60 65
ccg gag ttc ttg cgt gag ggc tac gcg gtc aaa gac acc atc act ccg 355
Pro Glu Phe Leu Arg Glu Gly Tyr Ala Val Lys Asp Thr Ile Thr Pro
70 75 80 85
gac cgc atc gtg gtg ggt gtg cgt gaa taagaca 389
Asp Arg Ile Val Val Gly Val Arg Glu
90

<210> 466
<211> 94
<212> PRT
<213> Corynebacterium glutamicum

<400> 466
Leu Gly Val Gly Thr Pro Gln Gln Lys Gly Thr Tyr Ala Ala Asp Leu
1 5 10 15
Thr Tyr Val Arg Gln Val Val Glu Asp Leu Val Pro Leu Leu Glu Gly
20 25 30
Glu His Ile Ile Phe Gly Lys Ser Thr Val Pro Val Gly Thr Ala Glu
35 40 45

Gln Leu Gln Glu Leu Ala Asp Ser Leu Val Lys Pro Gly Ser His Val
50 55 60

Glu Ile Ala Trp Asn Pro Glu Phe Leu Arg Glu Gly Tyr Ala Val Lys
65 70 75 80

Asp Thr Ile Thr Pro Asp Arg Ile Val Val Gly Val Arg Glu
85 90

<210> 467

<211> 801

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(778)

<223> RXN03056

<400> 467

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ttaataaaact gaagaacagc tcgcggaagc taaagccaaa ttg gat gcc gca gga 115
Leu Asp Ala Ala Gly
1 5

att tca ctt tca gcc gtt gga tcc gac ttc ggc aag atc aac atc acc 163
Ile Ser Leu Ser Ala Val Gly Ser Asp Phe Gly Lys Ile Asn Ile Thr
10 15 20

gat cct ttt gaa gat cac ttg gag cgc gca cgc cac ggt gtt gag gtc 211
Asp Pro Phe Glu Asp His Leu Glu Arg Ala Arg His Gly Val Glu Val
25 30 35

gct aag ctc ttc ggc gcg aaa tac atc cgc atg ttc tcc ttc ttt att 259
Ala Lys Leu Phe Gly Ala Lys Tyr Ile Arg Met Phe Ser Phe Phe Ile
40 45 50

gca gaa ggc gac aac cct gaa agc ttc cgc aaa gaa gta ctc tcc cgc 307
Ala Glu Gly Asp Asn Pro Glu Ser Phe Arg Lys Glu Val Leu Ser Arg
55 60 65

acc cac gca atg gtc gaa ctc gca gaa gcc ggc ggc atc acc ctc ctc 355
Thr His Ala Met Val Glu Leu Ala Glu Ala Gly Gly Ile Thr Leu Leu
70 75 80 85

cac gaa aat gaa aag gga atc tat ggc gac tcc ccg cag cgc gtg aag 403
His Glu Asn Glu Lys Gly Ile Tyr Gly Asp Ser Pro Gln Arg Val Lys
90 95 100

gat tta atc acc agc atc gac tcc cct aac tac cgc gca atc tac gac 451
Asp Leu Ile Thr Ser Ile Asp Ser Pro Asn Tyr Arg Ala Ile Tyr Asp
105 110 115

gca gct aac tac gtg caa acc gga ttc aag cct ttt gat gag gca tgg 499
Ala Ala Asn Tyr Val Gln Thr Gly Phe Lys Pro Phe Asp Glu Ala Trp
120 125 130

ccg atc gtt aag gac tac gtc gac tac gtc cac atc aag gac gcg acc 547
Pro Ile Val Lys Asp Tyr Val Asp Tyr Val His Ile Lys Asp Ala Thr

135	140	145	
att cca gat gca gag cac	ccc atc gga atc atc	aag cca gca gga caa	595
Ile Pro Asp Ala Glu His	Pro Ile Gly Ile Ile Lys	Pro Ala Gly Gln	
150	155	160 165	
ggc gac ggc caa tac cca	gag ctc ctt gcc gcg cta	aac gcc gac ggt	643
Gly Asp Gly Gln Tyr Pro	Glu Leu Leu Ala Ala Leu	Asn Ala Asp Gly	
170	175	180	
tac aac gga ttc gtc tcc	atc gag cct cac ctg ggt	gac ttc gat gaa	691
Tyr Asn Gly Phe Val Ser	Ile Glu Pro His Leu Gly	Asp Phe Asp Glu	
185	190	195	
ttc ggc gga ctc tgc gga	cct gac ctg tgg acc agc	gca tgc gac gct	739
Phe Gly Gly Leu Cys Gly	Pro Asp Leu Trp Thr Ser	Ala Cys Asp Ala	
200	205	210	
ctc gca gga atc ctg aac	aac atc aac gcc gag tac	aac taaggacaac	788
Leu Ala Gly Ile Leu Asn	Asn Ile Asn Ala Glu Tyr	Asn	
215	220	225	
tgataatgac aaa			801

<210> 468

<211> 226

<212> PRT

<213> Corynebacterium glutamicum

<400> 468

Leu Asp Ala Ala Gly Ile Ser Leu Ser Ala Val Gly Ser Asp Phe Gly	
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Lys Ile Asn Ile Thr Asp Pro Phe Glu Asp His Leu Glu Arg Ala Arg	
20 25 30	
His Gly Val Glu Val Ala Lys Leu Phe Gly Ala Lys Tyr Ile Arg Met	
35 40 45	
Phe Ser Phe Phe Ile Ala Glu Gly Asp Asn Pro Glu Ser Phe Arg Lys	
50 55 60	
Glu Val Leu Ser Arg Thr His Ala Met Val Glu Leu Ala Glu Ala Gly	
65 70 75 80	
Gly Ile Thr Leu Leu His Glu Asn Glu Lys Gly Ile Tyr Gly Asp Ser	
85 90 95	
Pro Gln Arg Val Lys Asp Leu Ile Thr Ser Ile Asp Ser Pro Asn Tyr	
100 105 110	
Arg Ala Ile Tyr Asp Ala Ala Asn Tyr Val Gln Thr Gly Phe Lys Pro	
115 120 125	
Phe Asp Glu Ala Trp Pro Ile Val Lys Asp Tyr Val Asp Tyr Val His	
130 135 140	
Ile Lys Asp Ala Thr Ile Pro Asp Ala Glu His Pro Ile Gly Ile Ile	
145 150 155 160	

Lys Pro Ala Gly Gln Gly Asp Gly Gln Tyr Pro Glu Leu Leu Ala Ala
 165 170 175
 Leu Asn Ala Asp Gly Tyr Asn Gly Phe Val Ser Ile Glu Pro His Leu
 180 185 190
 Gly Asp Phe Asp Glu Phe Gly Gly Leu Cys Gly Pro Asp Leu Trp Thr
 195 200 205
 Ser Ala Cys Asp Ala Leu Ala Gly Ile Leu Asn Asn Ile Asn Ala Glu
 210 215 220
 Tyr Asn
 225

<210> 469

<211> 687

<212> DNA

<213> *Corynebacterium glutamicum*

<220>

<221> CDS

<222> (101)..(664)

<223> RXN03030

<400> 469

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cagcttgatt ccgtcacctt gctgcgtaac aaccccatcc gtg ctg cca ctg gat 115
 Val Leu Pro Leu Asp
 1 5

cct gca gca agc ctg aag atc tac cca ttg gtt act ggc cgt acc aag 163
 Pro Ala Ala Ser Leu Lys Ile Tyr Pro Leu Val Thr Gly Arg Thr Lys
 10 15 20

atc gac gag gtt caa cta cag ctg gaa gca gcc att cgc gca gaa ctc 211
 Ile Asp Glu Val Gln Leu Gln Leu Glu Ala Ala Ile Arg Ala Glu Leu
 25 30 35

cca ggg gta acc ttg gtg tct tcc gag tca gaa gca gat ctt gca atc 259
 Pro Gly Val Thr Leu Val Ser Ser Glu Ser Glu Ala Asp Leu Ala Ile
 40 45 50

gtg tgg gct cgc cct gaa att gca ctg ttt gaa gat gac ctc gaa ggt 307
 Val Trp Ala Arg Pro Glu Ile Ala Leu Phe Glu Asp Asp Leu Glu Gly
 55 60 65

gtt tcc ctc tct gtt gac cct cgt gcc aat ggt gtc gat gtg gaa cgc 355
 Val Ser Leu Ser Val Asp Pro Arg Ala Asn Gly Val Asp Val Glu Arg
 70 75 80 85

gtt cag gct gtg gaa gct gca gtc cca acc atc ttg gct gtg aac ttc 403
 Val Gln Ala Val Glu Ala Ala Val Pro Thr Ile Leu Ala Val Asn Phe
 90 95 100

acc aac cct tgg gtg ctg tct gag atc gag cct ggt gcc gct gcc gtg 451
 Thr Asn Pro Trp Val Leu Ser Glu Ile Glu Pro Gly Ala Ala Val
 105 110 115

gtg ggc act ttt gag atc aag cca gag ttc ctt ctc aag gct ttg act 499
 Val Gly Thr Phe Glu Ile Lys Pro Glu Phe Leu Leu Lys Ala Leu Thr
 120 125 130

ggt caa gag gga gga cca aag ggc aag ctg cca ttg act gtt cct gct 547
 Gly Gln Glu Gly Gly Pro Lys Gly Lys Leu Pro Leu Thr Val Pro Ala
 135 140 145

tcc atg cag gcg att gct gat tcc cct cgc gat atc cca ggc aag ttc 595
 Ser Met Gln Ala Ile Ala Asp Ser Pro Arg Asp Ile Pro Gly Lys Phe
 150 155 160 165

ctc gat gag tct tac acc tac gtg gac tcc gca ggg atg gcc tac aag 643
 Leu Asp Glu Ser Tyr Thr Tyr Val Asp Ser Ala Gly Met Ala Tyr Lys
 170 175 180

tac ggt cac gga ctt aat ttc tagattgtag gtagtctcgt ggg 687
 Tyr Gly His Gly Leu Asn Phe
 185

<210> 470
 <211> 188
 <212> PRT
 <213> Corynebacterium glutamicum

<400> 470
 Val Leu Pro Leu Asp Pro Ala Ala Ser Leu Lys Ile Tyr Pro Leu Val
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Thr Gly Arg Thr Lys Ile Asp Glu Val Gln Leu Gln Leu Glu Ala Ala
 20 25 30

Ile Arg Ala Glu Leu Pro Gly Val Thr Leu Val Ser Ser Glu Ser Glu
 35 40 45

Ala Asp Leu Ala Ile Val Trp Ala Arg Pro Glu Ile Ala Leu Phe Glu
 50 55 60

Asp Asp Leu Glu Gly Val Ser Leu Ser Val Asp Pro Arg Ala Asn Gly
 65 70 75 80

Val Asp Val Glu Arg Val Gln Ala Val Glu Ala Ala Val Pro Thr Ile
 85 90 95

Leu Ala Val Asn Phe Thr Asn Pro Trp Val Leu Ser Glu Ile Glu Pro
 100 105 110

Gly Ala Ala Ala Val Val Gly Thr Phe Glu Ile Lys Pro Glu Phe Leu
 115 120 125

Leu Lys Ala Leu Thr Gly Gln Glu Gly Gly Pro Lys Gly Lys Leu Pro
 130 135 140

Leu Thr Val Pro Ala Ser Met Gln Ala Ile Ala Asp Ser Pro Arg Asp
 145 150 155 160

Ile Pro Gly Lys Phe Leu Asp Glu Ser Tyr Thr Tyr Val Asp Ser Ala
 165 170 175

Gly Met Ala Tyr Lys Tyr Gly His Gly Leu Asn Phe

Phe Ile Gly Phe Lys Asp Gly Thr Gly Asn Ile Glu His Leu Ala Lys
 170 175 180
 atc acc acg cta tgc gga gat cgc ctg ttc tac ctc ggt gga ctt ccc 691
 Ile Thr Thr Leu Cys Gly Asp Arg Leu Phe Tyr Leu Gly Gly Leu Pro
 185 190 195
 acc gct gag acc ttt gca cta cca ctg ctt cag atg ggc atg agc acc 739
 Thr Ala Glu Thr Phe Ala Leu Pro Leu Leu Gln Met Gly Met Ser Thr
 200 205 210
 tac tcc tct gca atg ttc aac ttc att cca gat ttc gca ctg agc ttc 787
 Tyr Ser Ser Ala Met Phe Asn Phe Ile Pro Asp Phe Ala Leu Ser Phe
 215 220 225
 tac gcc gat gtt cgt gcg cag gac agc gca gca gta aag cag aag ctg 835
 Tyr Ala Asp Val Arg Ala Gln Asp Ser Ala Ala Val Lys Gln Lys Leu
 230 235 240 245
 agc gat ttt gtg ctc ccc tac ttg gat atc cgc gat cgc gca caa ggc 883
 Ser Asp Phe Val Leu Pro Tyr Leu Asp Ile Arg Asp Arg Ala Gln Gly
 250 255 260
 tac ggt gtc tcc att ggt aag ggc gga ctc aag gct gtt ggc cgc aac 931
 Tyr Gly Val Ser Ile Gly Lys Gly Gly Leu Lys Ala Val Gly Arg Asn
 265 270 275
 gct ggc ggc gtt cgc cca cca ctg cgt aac ctt tcc gag caa gat atc 979
 Ala Gly Gly Val Arg Pro Pro Leu Arg Asn Leu Ser Glu Gln Asp Ile
 280 285 290
 gcg gac ctg tcg gat ttg ctt gcc acc tct ggc gca ggt tcc tac cgc 1027
 Ala Asp Leu Ser Asp Leu Leu Ala Thr Ser Gly Ala Gly Ser Tyr Arg
 295 300 305
 ctt cag ttg agg tgaaagcatg atcaccgcaa ccg 1062
 Leu Gln Leu Arg
 310

<210> 472

<211> 313

<212> PRT

<213> Corynebacterium glutamicum

<400> 472

Met Ala Arg Phe Ser Pro Gln Asp Leu Ala Asp His Leu Lys Asp Gly
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 Leu Leu Ser Phe Pro Ala Thr Ala Phe Gln Asp Asp Leu Glu Val Asp
 20 25 30
 Glu Ala Ala Tyr Val Glu His Ile Glu Trp Gln Ser Ser Tyr Pro Val
 35 40 45
 Ala Gly Leu Phe Ala Ala Gly Gly Thr Gly Glu Gly Phe Ser Leu Thr
 50 55 60
 Val Glu Glu Asn His Arg Val Thr Gln Leu Ala Val Gln Ala Ser Ser
 65 70 75 80

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<210> 473
<211> 924
<212> DNA
<213> Corynebacterium glutamicum
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<400> 473
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gaatatccat ttatgctgct gtagtcggct atgtggacgc atg gtg gca acc tct 115
Met Val Ala Thr Ser

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	1	5	
cag ttt atc gat gac agc gag gct gcc cag gcg gta cgc gca gct att			163
Gln Phe Ile Asp Asp Ser Glu Ala Ala Gln Ala Val Arg Ala Ala Ile			
	10	15	20
gtt gca gga tac cga aac att gat act gcc cta gcg tat gga aac gag			211
Val Ala Gly Tyr Arg Asn Ile Asp Thr Ala Leu Ala Tyr Gly Asn Glu			
	25	30	35
cgc ggc gtt ggc gaa ggc att cgc acc gct gga gtg ccc cgc gag gag			259
Arg Gly Val Gly Glu Gly Ile Arg Thr Ala Gly Val Pro Arg Glu Glu			
	40	45	50
ctc ttt att tcc acc aag cta gct gca gaa atc aaa gat tac gat gga			307
Leu Phe Ile Ser Thr Lys Leu Ala Ala Glu Ile Lys Asp Tyr Asp Gly			
	55	60	65
gca gtc gcc gcg att gat gag tct ttg gcg aaa att ggc ttg gat tat			355
Ala Val Ala Ala Ile Asp Glu Ser Leu Ala Lys Ile Gly Leu Asp Tyr			
	70	75	80
gtc gat ctg atg ctc att cac tcc cca caa cca tgg agt gat ttc cgt			403
Val Asp Leu Met Leu Ile His Ser Pro Gln Pro Trp Ser Asp Phe Arg			
	90	95	100
ggt ggg gac tat tca gag gga aac cgt gaa gcg tgg cgc gcg ctg gaa			451
Gly Gly Asp Tyr Ser Glu Gly Asn Arg Glu Ala Trp Arg Ala Leu Glu			
	105	110	115
gat gcc tac aaa gcc gga aag att cga tcc att ggt gtc tcg aac ttc			499
Asp Ala Tyr Lys Ala Gly Lys Ile Arg Ser Ile Gly Val Ser Asn Phe			
	120	125	130
ctg gag gcc gat ctg gag aat atc tta gac tcc gcg acg gtt gct cct			547
Leu Glu Ala Asp Leu Glu Asn Ile Leu Asp Ser Ala Thr Val Ala Pro			
	135	140	145
cac gtt aat cag ctt ctt gtg cat gtt gga aac acc cca agc gag tta			595
His Val Asn Gln Leu Leu Val His Val Gly Asn Thr Pro Ser Glu Leu			
	150	155	160
atc agt ttc tgc gat tcc aag ggc att ctg gtc gaa gca tat tca ccc			643
Ile Ser Phe Cys Asp Ser Lys Gly Ile Leu Val Glu Ala Tyr Ser Pro			
	170	175	180
atc gcc cac gga gag atg ctg aag aac cag cag gtc aag gcg att gct			691
Ile Ala His Gly Glu Met Leu Lys Asn Gln Gln Val Lys Ala Ile Ala			
	185	190	195
gac aag tac aac gtg agc att ccg cag cta tgc att cgg tac aca att			739
Asp Lys Tyr Asn Val Ser Ile Pro Gln Leu Cys Ile Arg Tyr Thr Ile			
	200	205	210
caa ctg gga acg gtg tct ttg cca aag act gcc aac cca gat cat atg			787
Gln Leu Gly Thr Val Ser Leu Pro Lys Thr Ala Asn Pro Asp His Met			
	215	220	225
agc tcc aat gcg cag atc gac ttt gaa att tcc gag gaa gac atg gcg			835
Ser Ser Asn Ala Gln Ile Asp Phe Glu Ile Ser Glu Glu Asp Met Ala			
	230	235	240
			245

gca ctt caa gaa gtg acc gcc cgc gat tat ggc gag cac agc ggt ttt 883
 Ala Leu Gln Glu Val Thr Ala Arg Asp Tyr Gly Glu His Ser Gly Phe
 250 255 260

cct gtg tat tcc ggc aag tagaaagatt tttatcatgg gac 924
 Pro Val Tyr Ser Gly Lys
 265

<210> 474

<211> 267

<212> PRT

<213> Corynebacterium glutamicum

<400> 474

Met Val Ala Thr Ser Gln Phe Ile Asp Asp Ser Glu Ala Ala Gln Ala
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Val Arg Ala Ala Ile Val Ala Gly Tyr Arg Asn Ile Asp Thr Ala Leu
 20 25 30

Ala Tyr Gly Asn Glu Arg Gly Val Gly Glu Gly Ile Arg Thr Ala Gly
 35 40 45

Val Pro Arg Glu Glu Leu Phe Ile Ser Thr Lys Leu Ala Ala Glu Ile
 50 55 60

Lys Asp Tyr Asp Gly Ala Val Ala Ala Ile Asp Glu Ser Leu Ala Lys
 65 70 75 80

Ile Gly Leu Asp Tyr Val Asp Leu Met Leu Ile His Ser Pro Gln Pro
 85 90 95

Trp Ser Asp Phe Arg Gly Gly Asp Tyr Ser Glu Gly Asn Arg Glu Ala
 100 105 110

Trp Arg Ala Leu Glu Asp Ala Tyr Lys Ala Gly Lys Ile Arg Ser Ile
 115 120 125

Gly Val Ser Asn Phe Leu Glu Ala Asp Leu Glu Asn Ile Leu Asp Ser
 130 135 140

Ala Thr Val Ala Pro His Val Asn Gln Leu Leu Val His Val Gly Asn
 145 150 155 160

Thr Pro Ser Glu Leu Ile Ser Phe Cys Asp Ser Lys Gly Ile Leu Val
 165 170 175

Glu Ala Tyr Ser Pro Ile Ala His Gly Glu Met Leu Lys Asn Gln Gln
 180 185 190

Val Lys Ala Ile Ala Asp Lys Tyr Asn Val Ser Ile Pro Gln Leu Cys
 195 200 205

Ile Arg Tyr Thr Ile Gln Leu Gly Thr Val Ser Leu Pro Lys Thr Ala
 210 215 220

Asn Pro Asp His Met Ser Ser Asn Ala Gln Ile Asp Phe Glu Ile Ser
 225 230 235 240

Glu Glu Asp Met Ala Ala Leu Gln Glu Val Thr Ala Arg Asp Tyr Gly
245 250 255

Glu His Ser Gly Phe Pro Val Tyr Ser Gly Lys
260 265

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<211> 3561
<212> DNA
<213> Corynebacterium glutamicum
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<220>  
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<222> (101)..(3538)  
<223> RXN00200
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acgcacaatg agtaattcct caccaaacga cccaagccct atg cgc caa gtc ggt 115
Met Arg Gln Val Gly
1 5

ggt aat ggg ggc cat caa cta gac tcg atc aac gtg tca gat gta gtt 163
Gly Asn Gly Gly His Gln Leu Asp Ser Ile Asn Val Ser Asp Val Val
10 15 20

gag tcg aag aaa cta aag ggt tct gcg caa gaa ccc ccg cag gtt gcc 211
Glu Ser Lys Lys Leu Lys Gly Ser Ala Gln Glu Pro Pro Gln Val Ala
25 30 35

ccg ggc tgg ctg aag aaa ctg gct atc tca tca ggt ctg ctt ggc ctg 259
Pro Gly Trp Leu Lys Lys Leu Ala Ile Ser Ser Gly Leu Leu Gly Leu
40 45 50

ttg atg ttt gtg ctg ttg cct ttc ctg cca gtg aac cag gtg cag tct 307
Leu Met Phe Val Leu Leu Pro Phe Leu Pro Val Asn Gln Val Gln Ser
55 60 65

tcg ctg tca tgg cca caa aat ggt gag ctt tcc agc gtt aac gcc ccg 355
Ser Leu Ser Trp Pro Gln Asn Gly Glu Leu Ser Ser Val Asn Ala Pro
70 75 80 85

ctg att tcc tac gca ccg cag tcg atg gat gcg tcc atc cct gtg tcc 403
Leu Ile Ser Tyr Ala Pro Gln Ser Met Asp Ala Ser Ile Pro Val Ser
90 95 100

gcg ctg gac agt ctc aat gac aat cag tcg ttg gtg atg ggc acg ttg 451
Ala Leu Asp Ser Leu Asn Asp Asn Gln Ser Leu Val Met Gly Thr Leu
105 110 115

cct ctg gac agt acg gac gcc acc aac cgt ggt ctg ttt gtg cgc acc 499
Pro Leu Asp Ser Thr Asp Ala Thr Asn Arg Gly Leu Phe Val Arg Thr
120 125 130

atc gac ggt aac ctt gac gtg att gtt cgc ggt gag gtg ctg ttg gat 547
Ile Asp Gly Asn Leu Asp Val Ile Val Arg Gly Glu Val Leu Leu Asp
135 140 145

ctt tca cca aca gag gtg aac cgt ctg cca gat gat gcg atc cta gag 595

Leu Ser Pro Thr Glu Val Asn Arg Leu Pro Asp Asp Ala Ile Leu Glu 150 155 160 165	
att tcc tcc acc gag gaa acc acc agc gcg gaa atc acc ggc acg gca Ile Ser Ser Thr Glu Glu Thr Thr Ser Ala Glu Ile Thr Gly Thr Ala 170 175 180	643
ttc agc ggc gag acc gaa ggc gat gag cgg cct cag gtc acc ggc gtt Phe Ser Gly Glu Thr Glu Gly Asp Glu Arg Pro Gln Val Thr Gly Val 185 190 195	691
tac acc gag ctt gtc gac gac ccc tcc acc gca tcg gcc ctg gcc tca Tyr Thr Glu Leu Val Asp Asp Pro Ser Thr Ala Ser Ala Leu Ala Ser 200 205 210	739
gcg ggc tta aac gtt gat att gag atc aac tcc cgc ttc act tca tcc Ala Gly Leu Asn Val Asp Ile Glu Ile Asn Ser Arg Phe Thr Ser Ser 215 220 225	787
ccc agc ctt cta aag tac gca gcc atc ttc att ggc ctt gcg tct gtg Pro Ser Leu Leu Lys Tyr Ala Ala Ile Phe Ile Gly Leu Ala Ser Val 230 235 240 245	835
ttg gtc tcc ctg tgg aca ctg cac cgc atg gat att ttg gat ggt cga Leu Val Ser Leu Trp Thr Leu His Arg Met Asp Ile Leu Asp Gly Arg 250 255 260	883
aaa gca cac cgc ttc ctg cct gcc aac tgg tac aag ctg aag cca ctt Lys Ala His Arg Phe Leu Pro Ala Asn Trp Tyr Lys Leu Lys Pro Leu 265 270 275	931
gat ggt gtt gtc gta gcg att ttg gtg ttc tgg cac ttc ctt ggc gcc Asp Gly Val Val Val Ala Ile Leu Val Phe Trp His Phe Leu Gly Ala 280 285 290	979
aac acc tct gac gac ggc ttc atc atg acc atg gcc cgc gtg tcc cag Asn Thr Ser Asp Asp Gly Phe Ile Met Thr Met Ala Arg Val Ser Gln 295 300 305	1027
aac gcg gat tat atg gcc aac tac tac cgc tgg ttc ggt gtc cca gaa Asn Ala Asp Tyr Met Ala Asn Tyr Tyr Arg Trp Phe Gly Val Pro Glu 310 315 320 325	1075
tca cca ttc ggc gca cca tat tac gac ttg ctg gct ctg atg gcc tac Ser Pro Phe Gly Ala Pro Tyr Tyr Asp Leu Leu Ala Leu Met Ala Tyr 330 335 340	1123
atc tca acc tca tca atc tgg ctt cgt cta ccc gca ttg ctc gct gga Ile Ser Thr Ser Ser Ile Trp Leu Arg Leu Pro Ala Leu Leu Ala Gly 345 350 355	1171
ctg atc atg tgg ttc gtg atc acc aga gag gtc atg cca cgg ttt ggc Leu Ile Met Trp Phe Val Ile Thr Arg Glu Val Met Pro Arg Phe Gly 360 365 370	1219
tca ttg gtt aac ggt cgc cgc gtt gcg cac tgg tct gca gcc atg gtg Ser Leu Val Asn Gly Arg Arg Val Ala His Trp Ser Ala Ala Met Val 375 380 385	1267
ttc ctg gcg ttc tgg ctt cca tac aac aac ggc act cgc cca gag cca Phe Leu Ala Phe Trp Leu Pro Tyr Asn Asn Gly Thr Arg Pro Glu Pro	1315

390	395	400	405	
atc atc gcg atg gga gct cta ctt gcg tgg gtt tcc ttc gag cgc gct				1363
Ile Ile Ala Met Gly Ala Leu Leu Ala Trp Val Ser Phe Glu Arg Ala	410	415	420	
atc gct acc tcc agg ttg ttg ccc gct gcc att ggt gtc att atc gcc				1411
Ile Ala Thr Ser Arg Leu Leu Pro Ala Ala Ile Gly Val Ile Ile Ala	425	430	435	
acc att tcc ctg gca tca ggc ccc acc ggt cta atg gca gtt gct gcg				1459
Thr Ile Ser Leu Ala Ser Gly Thr Gly Leu Met Ala Val Ala Ala	440	445	450	
ttg ctg gtc agt ttg tcc gcg ttg att cgc att ctt tat agg cgc ttg				1507
Leu Leu Val Ser Leu Ser Ala Leu Ile Arg Ile Leu Tyr Arg Arg Leu	455	460	465	
ccg ctt att ggg gcg tcg agg ggg gcg tcg aaa agc aaa gtc ttt ggc				1555
Pro Leu Ile Gly Ala Ser Arg Gly Ala Ser Lys Ser Lys Val Phe Gly	470	475	480	485
gct tcg atg gct atg ctt gcc cca ttc ctt gcg tct ggc acc gcg att				1603
Ala Ser Met Ala Met Leu Ala Pro Phe Leu Ala Ser Gly Thr Ala Ile	490	495	500	
ctc atc gcc gtt ttt ggc gat cag act ctg tca acc gtc atg gaa tcc				1651
Leu Ile Ala Val Phe Gly Asp Gln Thr Leu Ser Thr Val Met Glu Ser	505	510	515	
atc agc gtg cgc tcc gcg aag ggc ccg gca ctg acc tgg tac cac gaa				1699
Ile Ser Val Arg Ser Ala Lys Gly Pro Ala Leu Thr Trp Tyr His Glu	520	525	530	
tat gtg cgc tac caa acc gtc atg gaa caa acc gtt gat ggt tcc ttc				1747
Tyr Val Arg Tyr Gln Thr Val Met Glu Gln Thr Val Asp Gly Ser Phe	535	540	545	
acc cgc cgt ttt gct gtg ctg atg ctc atg gcg tgt ctg gct att gtg				1795
Thr Arg Arg Phe Ala Val Leu Met Leu Met Ala Cys Leu Ala Ile Val	550	555	560	565
gtc atc gcg atc ctg cgt tac ggc cgc att cca ggc gct gcg aag gga				1843
Val Ile Ala Ile Leu Arg Tyr Gly Arg Ile Pro Gly Ala Ala Lys Gly	570	575	580	
cca tca ctg cgt ttg atg atg gtc att ttc ggc acc atg ttc ttc atg				1891
Pro Ser Leu Arg Leu Met Met Val Ile Phe Gly Thr Met Phe Phe Met	585	590	595	
atg ttc acc cca acc aag tgg act cac cac ttc ggt gtc tac gca gga				1939
Met Phe Thr Pro Thr Lys Trp Thr His His Phe Gly Val Tyr Ala Gly	600	605	610	
ctt gcc ggc gca ttg gcc gga ctt gct gcc gtg ggg ctg tcc tat gtt				1987
Leu Ala Gly Ala Leu Ala Gly Leu Ala Ala Val Gly Leu Ser Tyr Val	615	620	625	
gcg gtg aaa tca cca cgc atg cgc acc att tcc atc ggt gcg ttc ctc				2035
Ala Val Lys Ser Pro Arg Met Arg Thr Ile Ser Ile Gly Ala Phe Leu	630	635	640	645

ttc ctg ctg gcg ctg gct ctc gca ggc gtg aac gga ttc tgg tac acc	2083
Phe Leu Leu Ala Leu Ala Leu Ala Gly Val Asn Gly Phe Trp Tyr Thr	
650 655 660	
tcc agc tac gcc gtg cca tgg tgg gat aaa acc atc cag atc aag ggc	2131
Ser Ser Tyr Ala Val Pro Trp Trp Asp Lys Thr Ile Gln Ile Lys Gly	
665 670 675	
atc gaa gca tcc acc gta gtg ctc gtg atc gcc gtg atc gtg ctg atc	2179
Ile Glu Ala Ser Thr Val Val Leu Val Ile Ala Val Ile Val Leu Ile	
680 685 690	
atc ggt gtt att caa tcc ttt gtc cac gat gtg aaa acc gcg caa gcc	2227
Ile Gly Val Ile Gln Ser Phe Val His Asp Val Lys Thr Ala Gln Ala	
695 700 705	
gaa acc aat cac tcc atg ggc gaa ctc gtg gcg gaa gat gaa gca aag	2275
Glu Thr Asn His Ser Met Gly Glu Leu Val Ala Glu Asp Glu Ala Lys	
710 715 720 725	
cgc gag cgt gcc tcc agg ttc acc ggc ctt gcg gcc tcc cct atc gca	2323
Arg Glu Arg Ala Ser Arg Phe Thr Gly Leu Ala Ala Ser Pro Ile Ala	
730 735 740	
gga gtg tcc gcc ctc gtt gtg ctg att acc tgc gca tcc atg ggc aaa	2371
Gly Val Ser Ala Leu Val Val Leu Ile Thr Cys Ala Ser Met Gly Lys	
745 750 755	
ggc ttt gtg gac caa tac ccc gcg tac tcc gtg ggt ctt ggc aac ctc	2419
Gly Phe Val Asp Gln Tyr Pro Ala Tyr Ser Val Gly Leu Gly Asn Leu	
760 765 770	
cgc tcc ctg acc ggc aac aca tgt ggc ctt gcc tcc gac gcc atg ctg	2467
Arg Ser Leu Thr Gly Asn Thr Cys Gly Leu Ala Ser Asp Ala Met Leu	
775 780 785	
gaa acc aac tcc aac gat tcc ttc ctc act cca gtg aac tcc aca ctt	2515
Glu Thr Asn Ser Asn Asp Ser Phe Leu Thr Pro Val Asn Ser Thr Leu	
790 795 800 805	
ggc gag tcc ctg gaa tcc gaa gat att cgc ggc ttt agt gct gcc ggc	2563
Gly Glu Ser Leu Glu Ser Glu Asp Ile Arg Gly Phe Ser Ala Ala Gly	
810 815 820	
atc cca cca tca atc agc cag gac caa gca gac ctg tct gct gtt ggt	2611
Ile Pro Pro Ser Ile Ser Gln Asp Gln Ala Asp Leu Ser Ala Val Gly	
825 830 835	
gcc att gcc aac act gac gac tcc acc gaa acc ggc gga tcc gac gaa	2659
Ala Ile Ala Asn Thr Asp Asp Ser Thr Glu Thr Gly Gly Ser Asp Glu	
840 845 850	
tca tcc gga caa tcc acc ggc aac acc ggc ggt gtc cga ggc tcc gaa	2707
Ser Ser Gly Gln Ser Thr Gly Asn Thr Gly Gly Val Arg Gly Ser Glu	
855 860 865	
ggc atc aac ggc tcc aac gcc cgc ctg cca ttc aac ctg gac tac acc	2755
Gly Ile Asn Gly Ser Asn Ala Arg Leu Pro Phe Asn Leu Asp Tyr Thr	
870 875 880 885	

caa gtt cca gtc gtc ggc tcc tgg tcc gct ggc acc caa aac cca gca	2803
Gln Val Pro Val Val Gly Ser Trp Ser Ala Gly Thr Gln Asn Pro Ala	
890 895 900	
aac atc acc acc gac tgg tac gaa atc cca gaa gcc acc gaa gaa gca	2851
Asn Ile Thr Thr Asp Trp Tyr Glu Ile Pro Glu Ala Thr Glu Glu Ala	
905 910 915	
ccc atc atc gtg gta tct gca gca ggt cgc atc gaa cac tac gac atc	2899
Pro Ile Ile Val Val Ser Ala Ala Gly Arg Ile Glu His Tyr Asp Ile	
920 925 930	
aac ggc gtc cgc caa tcc gga caa tcc gtc atg ctc gaa tac ggt cgc	2947
Asn Gly Val Arg Gln Ser Gly Gln Ser Val Met Leu Glu Tyr Gly Arg	
935 940 945	
ctt cgc gat aac ggc gac gtt gaa gac ctc ggc gaa gcc atg atg tac	2995
Leu Arg Asp Asn Gly Asp Val Glu Asp Leu Gly Glu Ala Met Met Tyr	
950 955 960 965	
gac atc ggc ccc gag cca tcc tgg cgc aac ctc cgc tac cca ctt gac	3043
Asp Ile Gly Pro Glu Pro Ser Trp Arg Asn Leu Arg Tyr Pro Leu Asp	
970 975 980	
caa ctc cca gaa gaa gcg gac gtc gtg cgc atc gtc gcc acc gac gtc	3091
Gln Leu Pro Glu Glu Ala Asp Val Val Arg Ile Val Ala Thr Asp Val	
985 990 995	
aac ctc gac gaa gac caa tgg gta gca ctg acg cca cca cgc gta cct	3139
Asn Leu Asp Glu Asp Gln Trp Val Ala Leu Thr Pro Pro Arg Val Pro	
1000 1005 1010	
aac cta gat tct ctg aac aac gtc atc gga tcc gaa acc cca gga ctc	3187
Asn Leu Asp Ser Leu Asn Asn Val Ile Gly Ser Glu Thr Pro Gly Leu	
1015 1020 1025	
ctc gac tgg gca gtt ggc ctg caa ttc cca tgc caa cgc acc ttc gac	3235
Leu Asp Trp Ala Val Gly Leu Gln Phe Pro Cys Gln Arg Thr Phe Asp	
1030 1035 1040 1045	
cac tac gcc gga gtc acc gag att cct gaa tac cga atc tcc cca gac	3283
His Tyr Ala Gly Val Thr Glu Ile Pro Glu Tyr Arg Ile Ser Pro Asp	
1050 1055 1060	
cac ggc gga aaa tcc acc ctc tcc cca ttc caa gac tgg gca ggc ggc	3331
His Gly Gly Lys Ser Thr Leu Ser Pro Phe Gln Asp Trp Ala Gly Gly	
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gga tcc atg ggc acg gcc gaa gca gta aac aac gcc tac gaa atc ccg	3379
Gly Ser Met Gly Thr Ala Glu Ala Val Asn Asn Ala Tyr Glu Ile Pro	
1080 1085 1090	
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Ser Tyr Leu Arg Asn Asp Trp Gly Arg Asp Trp Gly Ser Ile Glu Arg	
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Tyr Ser Leu Arg Thr Asn Ser Asn Gly Asp Ala Pro Lys Val Ala Asp	
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atc aac ctt gaa acc atc caa cgt tcc gga ctc tgg aat cca ggg cat	3523

Ile Asn Leu Glu Thr Ile Gln Arg Ser Gly Leu Trp Asn Pro Gly His
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 Met Lys Val Asp Glu
 1145

<210> 476

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<212> PRT

<213> Corynebacterium glutamicum

<400> 476

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 20 25 30

Pro Pro Gln Val Ala Pro Gly Trp Leu Lys Lys Leu Ala Ile Ser Ser
 35 40 45

Gly Leu Leu Gly Leu Leu Met Phe Val Leu Leu Pro Phe Leu Pro Val
 50 55 60

Asn Gln Val Gln Ser Ser Leu Ser Trp Pro Gln Asn Gly Glu Leu Ser
 65 70 75 80

Ser Val Asn Ala Pro Leu Ile Ser Tyr Ala Pro Gln Ser Met Asp Ala
 85 90 95

Ser Ile Pro Val Ser Ala Leu Asp Ser Leu Asn Asp Asn Gln Ser Leu
 100 105 110

Val Met Gly Thr Leu Pro Leu Asp Ser Thr Asp Ala Thr Asn Arg Gly
 115 120 125

Leu Phe Val Arg Thr Ile Asp Gly Asn Leu Asp Val Ile Val Arg Gly
 130 135 140

Glu Val Leu Leu Asp Leu Ser Pro Thr Glu Val Asn Arg Leu Pro Asp
 145 150 155 160

Asp Ala Ile Leu Glu Ile Ser Ser Thr Glu Glu Thr Thr Ser Ala Glu
 165 170 175

Ile Thr Gly Thr Ala Phe Ser Gly Glu Thr Glu Gly Asp Glu Arg Pro
 180 185 190

Gln Val Thr Gly Val Tyr Thr Glu Leu Val Asp Asp Pro Ser Thr Ala
 195 200 205

Ser Ala Leu Ala Ser Ala Gly Leu Asn Val Asp Ile Glu Ile Asn Ser
 210 215 220

Arg Phe Thr Ser Ser Pro Ser Leu Leu Lys Tyr Ala Ala Ile Phe Ile
 225 230 235 240

Gly Leu Ala Ser Val Leu Val Ser Leu Trp Thr Leu His Arg Met Asp
 245 250 255

Ile Leu Asp Gly Arg Lys Ala His Arg Phe Leu Pro Ala Asn Trp Tyr
 260 265 270
 Lys Leu Lys Pro Leu Asp Gly Val Val Val Ala Ile Leu Val Phe Trp
 275 280 285
 His Phe Leu Gly Ala Asn Thr Ser Asp Asp Gly Phe Ile Met Thr Met
 290 295 300
 Ala Arg Val Ser Gln Asn Ala Asp Tyr Met Ala Asn Tyr Tyr Arg Trp
 305 310 315 320
 Phe Gly Val Pro Glu Ser Pro Phe Gly Ala Pro Tyr Tyr Asp Leu Leu
 325 330 335
 Ala Leu Met Ala Tyr Ile Ser Thr Ser Ser Ile Trp Leu Arg Leu Pro
 340 345 350
 Ala Leu Leu Ala Gly Leu Ile Met Trp Phe Val Ile Thr Arg Glu Val
 355 360 365
 Met Pro Arg Phe Gly Ser Leu Val Asn Gly Arg Arg Val Ala His Trp
 370 375 380
 Ser Ala Ala Met Val Phe Leu Ala Phe Trp Leu Pro Tyr Asn Asn Gly
 385 390 395 400
 Thr Arg Pro Glu Pro Ile Ile Ala Met Gly Ala Leu Leu Ala Trp Val
 405 410 415
 Ser Phe Glu Arg Ala Ile Ala Thr Ser Arg Leu Leu Pro Ala Ala Ile
 420 425 430
 Gly Val Ile Ile Ala Thr Ile Ser Leu Ala Ser Gly Pro Thr Gly Leu
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 Met Ala Val Ala Ala Leu Leu Val Ser Leu Ser Ala Leu Ile Arg Ile
 450 455 460
 Leu Tyr Arg Arg Leu Pro Leu Ile Gly Ala Ser Arg Gly Ala Ser Lys
 465 470 475 480
 Ser Lys Val Phe Gly Ala Ser Met Ala Met Leu Ala Pro Phe Leu Ala
 485 490 495
 Ser Gly Thr Ala Ile Leu Ile Ala Val Phe Gly Asp Gln Thr Leu Ser
 500 505 510
 Thr Val Met Glu Ser Ile Ser Val Arg Ser Ala Lys Gly Pro Ala Leu
 515 520 525
 Thr Trp Tyr His Glu Tyr Val Arg Tyr Gln Thr Val Met Glu Gln Thr
 530 535 540
 Val Asp Gly Ser Phe Thr Arg Arg Phe Ala Val Leu Met Leu Met Ala
 545 550 555 560
 Cys Leu Ala Ile Val Val Ile Ala Ile Leu Arg Tyr Gly Arg Ile Pro
 565 570 575

Gly Ala Ala Lys Gly Pro Ser Leu Arg Leu Met Met Val Ile Phe Gly
 580 585 590
 Thr Met Phe Phe Met Met Phe Thr Pro Thr Lys Trp Thr His His Phe
 595 600 605
 Gly Val Tyr Ala Gly Leu Ala Gly Ala Leu Ala Gly Leu Ala Ala Val
 610 615 620
 Gly Leu Ser Tyr Val Ala Val Lys Ser Pro Arg Met Arg Thr Ile Ser
 625 630 635 640
 Ile Gly Ala Phe Leu Phe Leu Leu Ala Leu Ala Leu Ala Gly Val Asn
 645 650 655
 Gly Phe Trp Tyr Thr Ser Ser Tyr Ala Val Pro Trp Trp Asp Lys Thr
 660 665 670
 Ile Gln Ile Lys Gly Ile Glu Ala Ser Thr Val Val Leu Val Ile Ala
 675 680 685
 Val Ile Val Leu Ile Ile Gly Val Ile Gln Ser Phe Val His Asp Val
 690 695 700
 Lys Thr Ala Gln Ala Glu Thr Asn His Ser Met Gly Glu Leu Val Ala
 705 710 715 720
 Glu Asp Glu Ala Lys Arg Glu Arg Ala Ser Arg Phe Thr Gly Leu Ala
 725 730 735
 Ala Ser Pro Ile Ala Gly Val Ser Ala Leu Val Val Leu Ile Thr Cys
 740 745 750
 Ala Ser Met Gly Lys Gly Phe Val Asp Gln Tyr Pro Ala Tyr Ser Val
 755 760 765
 Gly Leu Gly Asn Leu Arg Ser Leu Thr Gly Asn Thr Cys Gly Leu Ala
 770 775 780
 Ser Asp Ala Met Leu Glu Thr Asn Ser Asn Asp Ser Phe Leu Thr Pro
 785 790 795 800
 Val Asn Ser Thr Leu Gly Glu Ser Leu Glu Ser Glu Asp Ile Arg Gly
 805 810 815
 Phe Ser Ala Ala Gly Ile Pro Pro Ser Ile Ser Gln Asp Gln Ala Asp
 820 825 830
 Leu Ser Ala Val Gly Ala Ile Ala Asn Thr Asp Asp Ser Thr Glu Thr
 835 840 845
 Gly Gly Ser Asp Glu Ser Ser Gly Gln Ser Thr Gly Asn Thr Gly Gly
 850 855 860
 Val Arg Gly Ser Glu Gly Ile Asn Gly Ser Asn Ala Arg Leu Pro Phe
 865 870 875 880
 Asn Leu Asp Tyr Thr Gln Val Pro Val Val Gly Ser Trp Ser Ala Gly
 885 890 895
 Thr Gln Asn Pro Ala Asn Ile Thr Thr Asp Trp Tyr Glu Ile Pro Glu

900										905										910									
Ala Thr Glu Glu Ala Pro Ile Ile Val Val Ser Ala Ala Gly Arg Ile	915	920	925																										
Glu His Tyr Asp Ile Asn Gly Val Arg Gln Ser Gly Gln Ser Val Met	930	935	940																										
Leu Glu Tyr Gly Arg Leu Arg Asp Asn Gly Asp Val Glu Asp Leu Gly	945	950	955																										
Glu Ala Met Met Tyr Asp Ile Gly Pro Glu Pro Ser Trp Arg Asn Leu	965	970	975																										
Arg Tyr Pro Leu Asp Gln Leu Pro Glu Glu Ala Asp Val Val Arg Ile	980	985	990																										
Val Ala Thr Asp Val Asn Leu Asp Glu Asp Gln Trp Val Ala Leu Thr	995	1000	1005																										
Pro Pro Arg Val Pro Asn Leu Asp Ser Leu Asn Asn Val Ile Gly Ser	1010	1015	1020																										
Glu Thr Pro Gly Leu Leu Asp Trp Ala Val Gly Leu Gln Phe Pro Cys	1025	1030	1035																1040										
Gln Arg Thr Phe Asp His Tyr Ala Gly Val Thr Glu Ile Pro Glu Tyr	1045	1050	1055																										
Arg Ile Ser Pro Asp His Gly Gly Lys Ser Thr Leu Ser Pro Phe Gln	1060	1065	1070																										
Asp Trp Ala Gly Gly Gly Ser Met Gly Thr Ala Glu Ala Val Asn Asn	1075	1080	1085																										
Ala Tyr Glu Ile Pro Ser Tyr Leu Arg Asn Asp Trp Gly Arg Asp Trp	1090	1095	1100																										
Gly Ser Ile Glu Arg Tyr Ser Leu Arg Thr Asn Ser Asn Gly Asp Ala	1105	1110	1115																1120										
Pro Lys Val Ala Asp Ile Asn Leu Glu Thr Ile Gln Arg Ser Gly Leu	1125	1130	1135																										
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<211> 1509

<212> DNA

<213> Corynebacterium glutamicum

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<221> CDS

<222> (101)..(1486)

<223> RXN01175

<400> 477

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	Val Ser Trp Thr Val	5
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gat atc cct aaa gaa gtt ctc cct gat ttg cca cca ttg cca gaa ggc		163
Asp Ile Pro Lys Glu Val Leu Pro Asp Leu Pro Pro Leu Pro Glu Gly		
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atg cag cag cag ttc gag gac acc att tcc cgt gac gct aag cag caa		211
Met Gln Gln Gln Phe Glu Asp Thr Ile Ser Arg Asp Ala Lys Gln Gln		
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cct acg tgg gat cgt gca cag gca gaa aac gtg cgc aag atc ctt gag		259
Pro Thr Trp Asp Arg Ala Gln Ala Glu Asn Val Arg Lys Ile Leu Glu		
	40 45 50	
tcg gtt cct cca atc gtt gtt gcc cct gag gta ctt gag ctg aag cag		307
Ser Val Pro Pro Ile Val Val Ala Pro Glu Val Leu Glu Leu Lys Gln		
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aag ctt gct gat gtt gcc aac ggt aag gcc ttc ctc ttg cag ggt ggt		355
Lys Leu Ala Asp Val Ala Asn Gly Lys Ala Phe Leu Leu Gln Gly Gly		
	70 75 80 85	
gac tgt gcg gaa act ttc gag tca aac act gag ccg cac att cgc gcc		403
Asp Cys Ala Glu Thr Phe Glu Ser Asn Thr Glu Pro His Ile Arg Ala		
	90 95 100	
aac gta aag act ctg ctg cag atg gca gtt gtt ttg acc tac ggt gca		451
Asn Val Lys Thr Leu Leu Gln Met Ala Val Val Leu Thr Tyr Gly Ala		
	105 110 115	
tcc act cct gtg atc aag atg gct cgt att gct ggt cag tac gca aag		499
Ser Thr Pro Val Ile Lys Met Ala Arg Ile Ala Gly Gln Tyr Ala Lys		
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cct cgc tct tct gat ctg gat gga aat ggt ctg cca aac tac cgt ggc		547
Pro Arg Ser Ser Asp Leu Asp Gly Asn Gly Leu Pro Asn Tyr Arg Gly		
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gat atc gtc aac ggt gtg gag gca acc cca gag gct cgt cgc cac gat		595
Asp Ile Val Asn Gly Val Glu Ala Thr Pro Glu Ala Arg Arg His Asp		
	150 155 160 165	
cct gcc cgc atg atc cgt gct tac gct aac gct tct gct gcg atg aac		643
Pro Ala Arg Met Ile Arg Ala Tyr Ala Asn Ala Ser Ala Ala Met Asn		
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ttg gtg cgc gcg ctc acc agc tct ggc acc gct gat ctt tac cgt ctc		691
Leu Val Arg Ala Leu Thr Ser Ser Gly Thr Ala Asp Leu Tyr Arg Leu		
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agc gag tgg aac cgc gag ttc gtt gcg aac tcc cca gct ggt gca cgc		739
Ser Glu Trp Asn Arg Glu Phe Val Ala Asn Ser Pro Ala Gly Ala Arg		
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tac gag gct ctt gct cgt gag atc gac tcc ggt ctg cgc ttc atg gaa		787
Tyr Glu Ala Leu Ala Arg Glu Ile Asp Ser Gly Leu Arg Phe Met Glu		
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gca tgt ggc gtg tcc gat gag tcc ctg cgt gct gca gat atc tac tgc		835

Ala Cys Gly Val Ser Asp Glu Ser Leu Arg Ala Ala Asp Ile Tyr Cys	
230 235 240 245	
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Ser His Glu Ala Leu Leu Val Asp Tyr Glu Arg Ser Met Leu Arg Leu	
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Ala Thr Asp Glu Glu Gly Asn Glu Glu Leu Tyr Asp Leu Ser Ala His	
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Gln Leu Trp Ile Gly Glu Arg Thr Arg Gly Met Asp Asp Phe His Val	
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Asn Phe Ala Ser Met Ile Ser Asn Pro Ile Gly Ile Lys Ile Gly Pro	
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ggt atc acc cct gaa gag gct gtt gca tac gct gac aag ctc gat ccg	1075
Gly Ile Thr Pro Glu Glu Ala Val Ala Tyr Ala Asp Lys Leu Asp Pro	
310 315 320 325	
aac ttc gag cct ggc cgt ttg acc atc gtt gct cgc atg ggc cac gac	1123
Asn Phe Glu Pro Gly Arg Leu Thr Ile Val Ala Arg Met Gly His Asp	
330 335 340	
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Lys Val Arg Ser Val Leu Pro Gly Val Ile Gln Ala Val Glu Ala Ser	
345 350 355	
gga cac aag gtt att tgg cag tcc gat ccg atg cac ggc aac act ttc	1219
Gly His Lys Val Ile Trp Gln Ser Asp Pro Met His Gly Asn Thr Phe	
360 365 370	
acc gca tcc aat ggc tac aag acc cgt cac ttc gac aag gtt atc gat	1267
Thr Ala Ser Asn Gly Tyr Lys Thr Arg His Phe Asp Lys Val Ile Asp	
375 380 385	
gag gtc cag ggc ttc ttc gag gtc cac cgc gca ttg ggc acc cac cca	1315
Glu Val Gln Gly Phe Phe Glu Val His Arg Ala Leu Gly Thr His Pro	
390 395 400 405	
ggc gga atc cac att gag ttc act ggt gaa gat gtc acc gag tgc ctc	1363
Gly Gly Ile His Ile Glu Phe Thr Gly Glu Asp Val Thr Glu Cys Leu	
410 415 420	
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Gly Gly Ala Glu Asp Ile Thr Asp Val Asp Leu Pro Gly Arg Tyr Glu	
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Ser Ala Cys Asp Pro Arg Leu Asn Thr Gln Gln Ser Leu Glu Leu Ala	
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<213> Corynebacterium glutamicum

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Asp Ala Lys Gln Gln Pro Thr Trp Asp Arg Ala Gln Ala Glu Asn Val
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Arg Lys Ile Leu Glu Ser Val Pro Pro Ile Val Val Ala Pro Glu Val
      50              55              60

Leu Glu Leu Lys Gln Lys Leu Ala Asp Val Ala Asn Gly Lys Ala Phe
 65              70              75              80

Leu Leu Gln Gly Gly Asp Cys Ala Glu Thr Phe Glu Ser Asn Thr Glu
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Pro His Ile Arg Ala Asn Val Lys Thr Leu Leu Gln Met Ala Val Val
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Leu Thr Tyr Gly Ala Ser Thr Pro Val Ile Lys Met Ala Arg Ile Ala
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Gly Gln Tyr Ala Lys Pro Arg Ser Ser Asp Leu Asp Gly Asn Gly Leu
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Pro Asn Tyr Arg Gly Asp Ile Val Asn Gly Val Glu Ala Thr Pro Glu
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Ala Arg Arg His Asp Pro Ala Arg Met Ile Arg Ala Tyr Ala Asn Ala
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Ser Ala Ala Met Asn Leu Val Arg Ala Leu Thr Ser Ser Gly Thr Ala
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Asp Leu Tyr Arg Leu Ser Glu Trp Asn Arg Glu Phe Val Ala Asn Ser
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Pro Ala Gly Ala Arg Tyr Glu Ala Leu Ala Arg Glu Ile Asp Ser Gly
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Leu Arg Phe Met Glu Ala Cys Gly Val Ser Asp Glu Ser Leu Arg Ala
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Ala Asp Ile Tyr Cys Ser His Glu Ala Leu Leu Val Asp Tyr Glu Arg
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Ser Met Leu Arg Leu Ala Thr Asp Glu Glu Gly Asn Glu Glu Leu Tyr
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Asp Leu Ser Ala His Gln Leu Trp Ile Gly Glu Arg Thr Arg Gly Met
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Asp Asp Phe His Val Asn Phe Ala Ser Met Ile Ser Asn Pro Ile Gly
 290 295 300
 Ile Lys Ile Gly Pro Gly Ile Thr Pro Glu Glu Ala Val Ala Tyr Ala
 305 310 315 320
 Asp Lys Leu Asp Pro Asn Phe Glu Pro Gly Arg Leu Thr Ile Val Ala
 325 330 335
 Arg Met Gly His Asp Lys Val Arg Ser Val Leu Pro Gly Val Ile Gln
 340 345 350
 Ala Val Glu Ala Ser Gly His Lys Val Ile Trp Gln Ser Asp Pro Met
 355 360 365
 His Gly Asn Thr Phe Thr Ala Ser Asn Gly Tyr Lys Thr Arg His Phe
 370 375 380
 Asp Lys Val Ile Asp Glu Val Gln Gly Phe Phe Glu Val His Arg Ala
 385 390 395 400
 Leu Gly Thr His Pro Gly Gly Ile His Ile Glu Phe Thr Gly Glu Asp
 405 410 415
 Val Thr Glu Cys Leu Gly Gly Ala Glu Asp Ile Thr Asp Val Asp Leu
 420 425 430
 Pro Gly Arg Tyr Glu Ser Ala Cys Asp Pro Arg Leu Asn Thr Gln Gln
 435 440 445
 Ser Leu Glu Leu Ala Phe Leu Val Ala Glu Met Leu Arg Asn
 450 455 460

<210> 479
 <211> 984
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
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 <222> (101)..(961)
 <223> RXN01376

<400> 479
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 cttcgtgagt actttgaaat ccccatcgc tgtgatcaca gtg acc tat tca cca 115
 Val Thr Tyr Ser Pro
 1 5
 ggt aaa tac ttg gcg tcg ttc ctg gat tct ttg cct ggt gcg act tca 163
 Gly Lys Tyr Leu Ala Ser Phe Leu Asp Ser Leu Pro Gly Ala Thr Ser
 10 15 20
 cga gac acc cac gtt gtg atg gca gac aat ggt tct gtg gac ggt gtt 211
 Arg Asp Thr His Val Val Met Ala Asp Asn Gly Ser Val Asp Gly Val
 25 30 35
 cct gag cag gca gca gcc tca cgc agc aac gtg gag ttc ctc tca act 259
 Pro Glu Gln Ala Ala Ala Ser Arg Ser Asn Val Glu Phe Leu Ser Thr

40	45	50	
ggc ggc aac tta ggc tac gga acg gct att aat att gcc gcc cga tcg Gly Gly Asn Leu Gly Tyr Gly Thr Ala Ile Asn Ile Ala Ala Arg Ser 55 60 65			307
ttg cgt gcg cgc cgg gag gca gga gag atc gat ggg gag ttc ttc ctc Leu Arg Ala Arg Arg Glu Ala Gly Glu Ile Asp Gly Glu Phe Phe Leu 70 75 80 85			355
gtc tca aac cct gat gtt gtt ttt gac gaa gac tct att gat caa ttg Val Ser Asn Pro Asp Val Val Phe Asp Glu Asp Ser Ile Asp Gln Leu 90 95 100			403
ctt gaa tgt gcg aaa cgt cac cct gaa gca gga gcg gtt ggc ccg ttg Leu Glu Cys Ala Lys Arg His Pro Glu Ala Gly Ala Val Gly Pro Leu 105 110 115			451
atc cgt gag gcg gac ggt tcg gcg tat ccg tcg gct cgg gcg gta ccc Ile Arg Glu Ala Asp Gly Ser Ala Tyr Pro Ser Ala Arg Ala Val Pro 120 125 130			499
act ttg gcg aat ggc att ggt cac gct ttg ttg ggt gct gtg tgg aaa Thr Leu Ala Asn Gly Ile Gly His Ala Leu Leu Gly Ala Val Trp Lys 135 140 145			547
tcc aat ccg tgg tcg gcg gct tac cgt gac gat gaa gat atg gac act Ser Asn Pro Trp Ser Ala Ala Tyr Arg Asp Asp Glu Asp Met Asp Thr 150 155 160 165			595
gag cgc act gct ggc tgg ctg tcg gga tcg tgc ctg tta tta agg tgg Glu Arg Thr Ala Gly Trp Leu Ser Gly Ser Cys Leu Leu Leu Arg Trp 170 175 180			643
gat gcg ttt gat cga gtt ggt ggt ttt gat gag cgc tac ttc atg tac Asp Ala Phe Asp Arg Val Gly Gly Phe Asp Glu Arg Tyr Phe Met Tyr 185 190 195			691
atg gaa gac gtt gac ctg gga gat cgg ctg gtt cgc gcc ggt ttc acc Met Glu Asp Val Asp Leu Gly Asp Arg Leu Val Arg Ala Gly Phe Thr 200 205 210			739
aac gtc ttt tgc cca agt gcg cag atc atc cac gcg aaa ggt cat gtt Asn Val Phe Cys Pro Ser Ala Gln Ile Ile His Ala Lys Gly His Val 215 220 225			787
gcg ggt aaa aac cca gag aac atg ttg ccc gca cac cac gag agc gcg Ala Gly Lys Asn Pro Glu Asn Met Leu Pro Ala His His Glu Ser Ala 230 235 240 245			835
tat cgc ttc cag gct gat cgc ctc gcg aag ccg tgg caa gcc cca att Tyr Arg Phe Gln Ala Asp Arg Leu Ala Lys Pro Trp Gln Ala Pro Ile 250 255 260			883
cgg ttg gct ctg cga att ggt ttg aaa tta cga gcc gga gtc gcg gtt Arg Leu Ala Leu Arg Ile Gly Leu Lys Leu Arg Ala Gly Val Ala Val 265 270 275			931
ggt gtc tct aag atg aga acg aaa gcc tct tagaccgtcg acgaccaccg Gly Val Ser Lys Met Arg Thr Lys Ala Ser 280 285			981

gac

984

<210> 480

<211> 287

<212> PRT

<213> Corynebacterium glutamicum

<400> 480

Val Thr Tyr Ser Pro Gly Lys Tyr Leu Ala Ser Phe Leu Asp Ser Leu
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 Pro Gly Ala Thr Ser Arg Asp Thr His Val Val Met Ala Asp Asn Gly
 20 25 30
 Ser Val Asp Gly Val Pro Glu Gln Ala Ala Ala Ser Arg Ser Asn Val
 35 40 45
 Glu Phe Leu Ser Thr Gly Gly Asn Leu Gly Tyr Gly Thr Ala Ile Asn
 50 55 60
 Ile Ala Ala Arg Ser Leu Arg Ala Arg Arg Glu Ala Gly Glu Ile Asp
 65 70 75 80
 Gly Glu Phe Phe Leu Val Ser Asn Pro Asp Val Val Phe Asp Glu Asp
 85 90 95
 Ser Ile Asp Gln Leu Leu Glu Cys Ala Lys Arg His Pro Glu Ala Gly
 100 105 110
 Ala Val Gly Pro Leu Ile Arg Glu Ala Asp Gly Ser Ala Tyr Pro Ser
 115 120 125
 Ala Arg Ala Val Pro Thr Leu Ala Asn Gly Ile Gly His Ala Leu Leu
 130 135 140
 Gly Ala Val Trp Lys Ser Asn Pro Trp Ser Ala Ala Tyr Arg Asp Asp
 145 150 155 160
 Glu Asp Met Asp Thr Glu Arg Thr Ala Gly Trp Leu Ser Gly Ser Cys
 165 170 175
 Leu Leu Leu Arg Trp Asp Ala Phe Asp Arg Val Gly Gly Phe Asp Glu
 180 185 190
 Arg Tyr Phe Met Tyr Met Glu Asp Val Asp Leu Gly Asp Arg Leu Val
 195 200 205
 Arg Ala Gly Phe Thr Asn Val Phe Cys Pro Ser Ala Gln Ile Ile His
 210 215 220
 Ala Lys Gly His Val Ala Gly Lys Asn Pro Glu Asn Met Leu Pro Ala
 225 230 235 240
 His His Glu Ser Ala Tyr Arg Phe Gln Ala Asp Arg Leu Ala Lys Pro
 245 250 255
 Trp Gln Ala Pro Ile Arg Leu Ala Leu Arg Ile Gly Leu Lys Leu Arg
 260 265 270

Ala Gly Val Ala Val Gly Val Ser Lys Met Arg Thr Lys Ala Ser
 275 280 285

<210> 481
 <211> 1002
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
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 <222> (101)..(979)
 <223> RXN01631

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 caaccagggc atttccgtaa acatctaaga ggagcactcc atg aaa cca caa ctt 115
 Met Lys Pro Gln Leu
 1 5
 att gca tct tgc tgg acc agc gcg gga gac gcc gca ccc gat cgt gac 163
 Ile Ala Ser Cys Trp Thr Ser Ala Gly Asp Ala Ala Pro Asp Arg Asp
 10 15 20
 gat ctc agc agc cca gta gca atc gat gag cgc atc gct cta gtc gct 211
 Asp Leu Ser Ser Pro Val Ala Ile Asp Glu Arg Ile Ala Leu Val Ala
 25 30 35
 gaa acc ggt tgg gca ggc att ggg ctt gtt cac gcc gat ctc atc aaa 259
 Glu Thr Gly Trp Ala Gly Ile Gly Leu Val His Ala Asp Leu Ile Lys
 40 45 50
 gca cgc gac acc att ggc tac gag gaa ttg cgc cga cgc atc cac gct 307
 Ala Arg Asp Thr Ile Gly Tyr Glu Glu Leu Arg Arg Arg Ile His Ala
 55 60 65
 gca gga att gaa atc att gag gtg gag ttc ctc aat ggt tgg tgg gcg 355
 Ala Gly Ile Glu Ile Ile Glu Val Glu Phe Leu Asn Gly Trp Trp Ala
 70 75 80 85
 act ggt gcg gaa cgc caa gag tcc gat gcc gtt cgt gcg gat ctg ttt 403
 Thr Gly Ala Glu Arg Gln Glu Ser Asp Ala Val Arg Ala Asp Leu Phe
 90 95 100
 gct gcg gcg caa gct ctt ggt tcc cca cac att aag gtc gga gca gga 451
 Ala Ala Ala Gln Ala Leu Gly Ser Pro His Ile Lys Val Gly Ala Gly
 105 110 115
 gag ggc acc aat ggt gtg gtt ccc att gct cac atg gcc agt gcg ttt 499
 Glu Gly Thr Asn Gly Val Val Pro Ile Ala His Met Ala Ser Ala Phe
 120 125 130
 act gat ctc gct gcg gaa gct gaa gct cat ggc gtc aag ctc gcg ttg 547
 Thr Asp Leu Ala Ala Glu Ala Glu Ala His Gly Val Lys Leu Ala Leu
 135 140 145
 gaa gca act ccg ttt tct cac ctg aag acc atc tac gac gcg ctg gaa 595
 Glu Ala Thr Pro Phe Ser His Leu Lys Thr Ile Tyr Asp Ala Leu Glu
 150 155 160 165

gtt gtc agc cat tcc gat agc cca tcg gct gga ctc atg gtt gat atc 643
 Val Val Ser His Ser Asp Ser Pro Ser Ala Gly Leu Met Val Asp Ile
 170 175 180

 tgg cac acc gcg aaa atc gga atc ccc aac gat gaa ctg tgg cgc aac 691
 Trp His Thr Ala Lys Ile Gly Ile Pro Asn Asp Glu Leu Trp Arg Asn
 185 190 195

 att cca ctg tcc aag gtc aac gca gtg gag gtt gat gat ggt ttc att 739
 Ile Pro Leu Ser Lys Val Asn Ala Val Glu Val Asp Asp Gly Phe Ile
 200 205 210

 gac acc cca att gat ctt ttc gat gac tcc acc aac cgt cgc gcg tac 787
 Asp Thr Pro Ile Asp Leu Phe Asp Asp Ser Thr Asn Arg Arg Ala Tyr
 215 220 225

 tgc ggt gaa ggc gaa ttt gat ccc gca agc ttc atc cgt ggc gcc atc 835
 Cys Gly Glu Gly Glu Phe Asp Pro Ala Ser Phe Ile Arg Gly Ala Ile
 230 235 240 245

 gac gcc ggt tgg acg ggc gca tat ggt gtg gaa att att tcc gca gag 883
 Asp Ala Gly Trp Thr Gly Ala Tyr Gly Val Glu Ile Ile Ser Ala Glu
 250 255 260

 cac cga agc ctc ccg gtg aaa gaa ggg ctg caa cgt gct ttc gac acc 931
 His Arg Ser Leu Pro Val Lys Glu Gly Leu Gln Arg Ala Phe Asp Thr
 265 270 275

 acc atc gca gcg ttt gaa caa gct gct cgt ctc gcc ccc tcc act aac 979
 Thr Ile Ala Ala Phe Glu Gln Ala Ala Arg Leu Ala Pro Ser Thr Asn
 280 285 290

 tgatctttga aaggctgaaa aaa 1002

<210> 482

<211> 293

<212> PRT

<213> Corynebacterium glutamicum

<400> 482

Met Lys Pro Gln Leu Ile Ala Ser Cys Trp Thr Ser Ala Gly Asp Ala
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 Ala Pro Asp Arg Asp Asp Leu Ser Ser Pro Val Ala Ile Asp Glu Arg
 20 25 30

 Ile Ala Leu Val Ala Glu Thr Gly Trp Ala Gly Ile Gly Leu Val His
 35 40 45

 Ala Asp Leu Ile Lys Ala Arg Asp Thr Ile Gly Tyr Glu Glu Leu Arg
 50 55 60

 Arg Arg Ile His Ala Ala Gly Ile Glu Ile Ile Glu Val Glu Phe Leu
 65 70 75 80

 Asn Gly Trp Trp Ala Thr Gly Ala Glu Arg Gln Glu Ser Asp Ala Val
 85 90 95

 Arg Ala Asp Leu Phe Ala Ala Ala Gln Ala Leu Gly Ser Pro His Ile
 100 105 110

Lys Val Gly Ala Gly Glu Gly Thr Asn Gly Val Val Pro Ile Ala His
 115 120 125
 Met Ala Ser Ala Phe Thr Asp Leu Ala Ala Glu Ala Glu Ala His Gly
 130 135 140
 Val Lys Leu Ala Leu Glu Ala Thr Pro Phe Ser His Leu Lys Thr Ile
 145 150 155 160
 Tyr Asp Ala Leu Glu Val Val Ser His Ser Asp Ser Pro Ser Ala Gly
 165 170 175
 Leu Met Val Asp Ile Trp His Thr Ala Lys Ile Gly Ile Pro Asn Asp
 180 185 190
 Glu Leu Trp Arg Asn Ile Pro Leu Ser Lys Val Asn Ala Val Glu Val
 195 200 205
 Asp Asp Gly Phe Ile Asp Thr Pro Ile Asp Leu Phe Asp Asp Ser Thr
 210 215 220
 Asn Arg Arg Ala Tyr Cys Gly Glu Gly Glu Phe Asp Pro Ala Ser Phe
 225 230 235 240
 Ile Arg Gly Ala Ile Asp Ala Gly Trp Thr Gly Ala Tyr Gly Val Glu
 245 250 255
 Ile Ile Ser Ala Glu His Arg Ser Leu Pro Val Lys Glu Gly Leu Gln
 260 265 270
 Arg Ala Phe Asp Thr Thr Ile Ala Ala Phe Glu Gln Ala Ala Arg Leu
 275 280 285
 Ala Pro Ser Thr Asn
 290

<210> 483
 <211> 990
 <212> DNA
 <213> *Corynebacterium glutamicum*

<220>
 <221> CDS
 <222> (101)..(967)
 <223> RXN01593

<400> 483
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 gcacgtagtt tctgcgctct ctggcgccgg cctaccgctc atg tat gtc acc aat 115
 Met Tyr Val Thr Asn
 1 5
 aat gcc tcc cgt gct ccg gag gtg gtg gct gcg caa ctc cgt gag att 163
 Asn Ala Ser Arg Ala Pro Glu Val Val Ala Ala Gln Leu Arg Glu Ile
 10 15 20
 ggc ctt gcc gac acc act gcg gac aat gtg atg aca tct gct caa gct 211
 Gly Leu Ala Asp Thr Thr Ala Asp Asn Val Met Thr Ser Ala Gln Ala

25										30										35										
gcc	tgc	aag	atg	gcg	gcg	gag	aag	att	ccc	gct	gga	tcc	aag	gtg	tat	259														
Ala	Cys	Lys	Met	Ala	Ala	Glu	Lys	Ile	Pro	Ala	Gly	Ser	Lys	Val	Tyr															
		40				45						50																		
gtt	ttg	ggt	tca	gaa	tcc	ttc	cgc	gag	cta	gct	act	gaa	gct	ggt	ttt	307														
Val	Leu	Gly	Ser	Glu	Ser	Phe	Arg	Glu	Leu	Ala	Thr	Glu	Ala	Gly	Phe															
		55				60						65																		
gtg	gtg	gtt	gat	tcg	gct	gat	gat	aaa	cct	gtg	gct	gtg	ctt	cac	ggc	355														
Val	Val	Val	Asp	Ser	Ala	Asp	Asp	Lys	Pro	Val	Ala	Val	Leu	His	Gly															
		70				75						80		85																
cac	aac	cct	gag	acc	ggt	tgg	gct	cag	ttg	agc	gag	gct	gcg	ctg	tca	403														
His	Asn	Pro	Glu	Thr	Gly	Trp	Ala	Gln	Leu	Ser	Glu	Ala	Ala	Leu	Ser															
				90				95						100																
att	aat	gct	ggc	gcg	cag	tat	ttt	gca	tca	aat	ttg	gat	tcc	acc	ctt	451														
Ile	Asn	Ala	Gly	Ala	Gln	Tyr	Phe	Ala	Ser	Asn	Leu	Asp	Ser	Thr	Leu															
		105						110						115																
ccc	atg	gaa	cgc	ggt	cgt	cac	att	ggc	aac	ggt	tcc	atg	gtg	gct	gcc	499														
Pro	Met	Glu	Arg	Gly	Arg	His	Ile	Gly	Asn	Gly	Ser	Met	Val	Ala	Ala															
		120				125						130																		
gtg	gtc	aac	gcg	act	ggc	gta	aag	cct	ctt	tcc	gca	ggt	aag	cca	ggc	547														
Val	Val	Asn	Ala	Thr	Gly	Val	Lys	Pro	Leu	Ser	Ala	Gly	Lys	Pro	Gly															
		135				140						145																		
ccc	gcg	atg	ttc	tat	gcg	ggg	gct	gaa	act	ctt	aat	tct	tca	aag	cct	595														
Pro	Ala	Met	Phe	Tyr	Ala	Gly	Ala	Glu	Thr	Leu	Asn	Ser	Ser	Lys	Pro															
		150				155						160		165																
ttg	gct	gtc	ggc	gat	cgt	ctc	gat	acc	gat	atc	gcc	ggc	gga	aac	gct	643														
Leu	Ala	Val	Gly	Asp	Arg	Leu	Asp	Thr	Asp	Ile	Ala	Gly	Gly	Asn	Ala															
				170				175						180																
gca	ggc	atg	gac	aca	ttc	cag	gtc	ctg	acc	ggc	gtc	agc	ggc	tac	tac	691														
Ala	Gly	Met	Asp	Thr	Phe	Gln	Val	Leu	Thr	Gly	Val	Ser	Gly	Tyr	Tyr															
		185						190						195																
gat	ttg	gtg	cgc	gcc	att	ccc	aga	gca	gcg	ccc	cac	cta	tat	cgc	cac	739														
Asp	Leu	Val	Arg	Ala	Ile	Pro	Arg	Ala	Ala	Pro	His	Leu	Tyr	Arg	His															
		200				205						210																		
ctc	gat	gca	gga	tct	cta	cag	cga	tcc	ggg	cga	gct	caa	gcc	agg	tgc	787														
Leu	Asp	Ala	Gly	Ser	Leu	Gln	Arg	Ser	Gly	Arg	Ala	Gln	Ala	Arg	Cys															
		215				220						225																		
cca	ggg	cgg	ttt	ttc	agc	gct	tat	cga	cgg	cga	cac	cct	ggt	cat	ttc	835														
Pro	Gly	Arg	Phe	Phe	Ser	Ala	Tyr	Arg	Arg	Arg	His	Pro	Gly	His	Phe															
		230				235				240				245																
cgg	cgg	cga	tgc	cgg	cgc	aac	tcc	ggt	tgc	agc	act	ccg	cac	tgc	gtt	883														
Arg	Arg	Arg	Cys	Arg	Arg	Asn	Ser	Gly	Cys	Ser	Thr	Pro	His	Cys	Val															
				250				255						260																
gga	tgt	ggc	ctg	ggc	ggc	cac	aga	gca	gtc	acc	gag	gta	cgc	gct	gat	931														
Gly	Cys	Gly	Leu	Gly	Gly	His	Arg	Ala	Val	Thr	Glu	Val	Arg	Ala	Asp															
		265						270						275																

tca gag gta gct gct act gca ttg cag agc tgg tgg taaacggtga 977
 Ser Glu Val Ala Ala Thr Ala Leu Gln Ser Trp Trp
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attcaccaaaa gcc 990

<210> 484
 <211> 289
 <212> PRT
 <213> Corynebacterium glutamicum

<400> 484
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Gln Leu Arg Glu Ile Gly Leu Ala Asp Thr Thr Ala Asp Asn Val Met
 20 25 30

Thr Ser Ala Gln Ala Ala Cys Lys Met Ala Ala Glu Lys Ile Pro Ala
 35 40 45

Gly Ser Lys Val Tyr Val Leu Gly Ser Glu Ser Phe Arg Glu Leu Ala
 50 55 60

Thr Glu Ala Gly Phe Val Val Val Asp Ser Ala Asp Asp Lys Pro Val
 65 70 75 80

Ala Val Leu His Gly His Asn Pro Glu Thr Gly Trp Ala Gln Leu Ser
 85 90 95

Glu Ala Ala Leu Ser Ile Asn Ala Gly Ala Gln Tyr Phe Ala Ser Asn
 100 105 110

Leu Asp Ser Thr Leu Pro Met Glu Arg Gly Arg His Ile Gly Asn Gly
 115 120 125

Ser Met Val Ala Ala Val Val Asn Ala Thr Gly Val Lys Pro Leu Ser
 130 135 140

Ala Gly Lys Pro Gly Pro Ala Met Phe Tyr Ala Gly Ala Glu Thr Leu
 145 150 155 160

Asn Ser Ser Lys Pro Leu Ala Val Gly Asp Arg Leu Asp Thr Asp Ile
 165 170 175

Ala Gly Gly Asn Ala Ala Gly Met Asp Thr Phe Gln Val Leu Thr Gly
 180 185 190

Val Ser Gly Tyr Tyr Asp Leu Val Arg Ala Ile Pro Arg Ala Ala Pro
 195 200 205

His Leu Tyr Arg His Leu Asp Ala Gly Ser Leu Gln Arg Ser Gly Arg
 210 215 220

Ala Gln Ala Arg Cys Pro Gly Arg Phe Phe Ser Ala Tyr Arg Arg Arg
 225 230 235 240

His Pro Gly His Phe Arg Arg Arg Cys Arg Arg Asn Ser Gly Cys Ser
 245 250 255

Thr Pro His Cys Val Gly Cys Gly Leu Gly Gly His Arg Ala Val Thr
 260 265 270

Glu Val Arg Ala Asp Ser Glu Val Ala Ala Thr Ala Leu Gln Ser Trp
 275 280 285

Trp

<210> 485

<211> 1173

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(1150)

<223> RXN00337

<400> 485

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attgccggac tgcggctgcc gtcaataaag aaccgcgacg atg ttg tta acg tat 115
 Met Leu Leu Thr Tyr
 1 5

gcg ttt gtg gat gtg gag gga ggc gtc gaa aag cat tct tta agc act 163
 Ala Phe Val Asp Val Glu Gly Gly Val Glu Lys His Ser Leu Ser Thr
 10 15 20

gcg gac att gca gct cgc gca cac gcc cat atg aaa tcc cat gat gtt 211
 Ala Asp Ile Ala Ala Arg Ala His Ala His Met Lys Ser His Asp Val
 25 30 35

ttg ggg cgg cag act acg ccg cct cag ccg gag ggc ggc gtt gct gcc 259
 Leu Gly Arg Gln Thr Thr Pro Pro Gln Pro Glu Gly Gly Val Ala Ala
 40 45 50

cgg ttg ggc ggg att gcg tgg aca atg atc cat aag caa atg ctt tcg 307
 Arg Leu Gly Gly Ile Ala Trp Thr Met Ile His Lys Gln Met Leu Ser
 55 60 65

cgt gac aca aaa ggc ctg gat atc acc gtg ttg agc acc att cct gag 355
 Arg Asp Thr Lys Gly Leu Asp Ile Thr Val Leu Ser Thr Ile Pro Glu
 70 75 80 85

ggg gtg ggc ctg ggt gaa aat tcc gcc atg gat gtg gcg ctc gca ttg 403
 Gly Val Gly Leu Gly Glu Asn Ser Ala Met Asp Val Ala Leu Ala Leu
 90 95 100

gcg ctg tat cgg gaa aat att gag gaa gcc ccc acg aag gcg cgc att 451
 Ala Leu Tyr Arg Glu Asn Ile Glu Glu Ala Pro Thr Lys Ala Arg Ile
 105 110 115

gcg gag att tgt tcg cag tcc gca ttc atg ttc agt gag act tca gtg 499
 Ala Glu Ile Cys Ser Gln Ser Ala Phe Met Phe Ser Glu Thr Ser Val
 120 125 130

ttg cgt gcg cgg cac acc gtg gcg ttg cgg ggt gaa act gga cag att 547

Leu Arg Ala Arg His Thr Val Ala Leu Arg Gly Glu Thr Gly Gln Ile
 135 140 145
 tcg gtg gtt gat tac gcc gat ggt tcg gtc act cag gcg cca cat ccg 595
 Ser Val Val Asp Tyr Ala Asp Gly Ser Val Thr Gln Ala Pro His Pro
 150 155 160 165
 gtg agt cgt tcc gct ggt ttg tcg gca ttt gtt gtt gct gcg caa act 643
 Val Ser Arg Ser Ala Gly Leu Ser Ala Phe Val Val Ala Ala Gln Thr
 170 175 180
 gaa act gat ccg agc att tac cgc gag atc tat gct cga cat gcg ttt 691
 Glu Thr Asp Pro Ser Ile Tyr Arg Glu Ile Tyr Ala Arg His Ala Phe
 185 190 195
 atc gat gaa gct gcg cgc gct ttc agt gtg gaa tct ttg cgg ttg ctt 739
 Ile Asp Glu Ala Ala Arg Ala Phe Ser Val Glu Ser Leu Arg Leu Leu
 200 205 210
 ccc gac gct tcc act cgt gtt gtg gat tgg ttg cag gcc gtg att gag 787
 Pro Asp Ala Ser Thr Arg Val Val Asp Trp Leu Gln Ala Val Ile Glu
 215 220 225
 gtg act ggt cga gag gat ctg ccc tcg att gaa caa gcc cag cgc tgg 835
 Val Thr Gly Arg Glu Asp Leu Pro Ser Ile Glu Gln Ala Gln Arg Trp
 230 235 240 245
 ttg aat ctg tgg gaa aac gaa acc cgg cgc gct cag agg aca gcc aat 883
 Leu Asn Leu Trp Glu Asn Glu Thr Arg Arg Ala Gln Arg Thr Ala Asn
 250 255 260
 gcc ctg cgt tcg aga agg ctg agt gag ttt tct gag ctg ctg atg gaa 931
 Ala Leu Arg Ser Arg Arg Leu Ser Glu Phe Ser Glu Leu Leu Met Glu
 265 270 275
 tcc caa gat gat ttg agc gac acc ttc gat ttc ccc cct gct gat ttg 979
 Ser Gln Asp Asp Leu Ser Asp Thr Phe Asp Phe Pro Pro Ala Asp Leu
 280 285 290
 gcg ctt gct cgt ttg tgc gtc gag cgg ggt gcc aca gct gct cgg tcc 1027
 Ala Leu Ala Arg Leu Cys Val Glu Arg Gly Ala Thr Ala Ala Arg Ser
 295 300 305
 acg tca gcg cgc ggt gtg att gcg ttg gtt gat gcc cat cat gcg cac 1075
 Thr Ser Ala Arg Gly Val Ile Ala Leu Val Asp Ala His His Ala His
 310 315 320 325
 aat ttt gct gcg gat ctc agc gag gat ggc ttg ttg gtg gtt cct ctc 1123
 Asn Phe Ala Ala Asp Leu Ser Glu Asp Gly Leu Leu Val Val Pro Leu
 330 335 340
 ggg cac ggg gac gtc gcg gaa cag ggc tagcacgcct acttaaccag 1170
 Gly His Gly Asp Val Ala Glu Gln Gly
 345 350
 cct 1173
 <210> 486
 <211> 350
 <212> PRT

<213> Corynebacterium glutamicum

<400> 486

Met Leu Leu Thr Tyr Ala Phe Val Asp Val Glu Gly Gly Val Glu Lys
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 His Ser Leu Ser Thr Ala Asp Ile Ala Ala Arg Ala His Ala His Met
 20 25 30
 Lys Ser His Asp Val Leu Gly Arg Gln Thr Thr Pro Pro Gln Pro Glu
 35 40 45
 Gly Gly Val Ala Ala Arg Leu Gly Gly Ile Ala Trp Thr Met Ile His
 50 55 60
 Lys Gln Met Leu Ser Arg Asp Thr Lys Gly Leu Asp Ile Thr Val Leu
 65 70 75 80
 Ser Thr Ile Pro Glu Gly Val Gly Leu Gly Glu Asn Ser Ala Met Asp
 85 90 95
 Val Ala Leu Ala Leu Ala Leu Tyr Arg Glu Asn Ile Glu Glu Ala Pro
 100 105 110
 Thr Lys Ala Arg Ile Ala Glu Ile Cys Ser Gln Ser Ala Phe Met Phe
 115 120 125
 Ser Glu Thr Ser Val Leu Arg Ala Arg His Thr Val Ala Leu Arg Gly
 130 135 140
 Glu Thr Gly Gln Ile Ser Val Val Asp Tyr Ala Asp Gly Ser Val Thr
 145 150 155 160
 Gln Ala Pro His Pro Val Ser Arg Ser Ala Gly Leu Ser Ala Phe Val
 165 170 175
 Val Ala Ala Gln Thr Glu Thr Asp Pro Ser Ile Tyr Arg Glu Ile Tyr
 180 185 190
 Ala Arg His Ala Phe Ile Asp Glu Ala Ala Arg Ala Phe Ser Val Glu
 195 200 205
 Ser Leu Arg Leu Leu Pro Asp Ala Ser Thr Arg Val Val Asp Trp Leu
 210 215 220
 Gln Ala Val Ile Glu Val Thr Gly Arg Glu Asp Leu Pro Ser Ile Glu
 225 230 235 240
 Gln Ala Gln Arg Trp Leu Asn Leu Trp Glu Asn Glu Thr Arg Arg Ala
 245 250 255
 Gln Arg Thr Ala Asn Ala Leu Arg Ser Arg Arg Leu Ser Glu Phe Ser
 260 265 270
 Glu Leu Leu Met Glu Ser Gln Asp Asp Leu Ser Asp Thr Phe Asp Phe
 275 280 285
 Pro Pro Ala Asp Leu Ala Leu Ala Arg Leu Cys Val Glu Arg Gly Ala
 290 295 300
 Thr Ala Ala Arg Ser Thr Ser Ala Arg Gly Val Ile Ala Leu Val Asp

305					310					315					320
Ala	His	His	Ala	His	Asn	Phe	Ala	Ala	Asp	Leu	Ser	Glu	Asp	Gly	Leu
				325					330					335	
Leu	Val	Val	Pro	Leu	Gly	His	Gly	Asp	Val	Ala	Glu	Gln	Gly		
			340					345					350		
<p><210> 487</p> <p><211> 1248</p> <p><212> DNA</p> <p><213> <i>Corynebacterium glutamicum</i></p> <p><220></p> <p><221> CDS</p> <p><222> (101)..(1225)</p> <p><223> RXS00584</p> <p><400> 487</p>															
tagttgtgcc acctaaaacg cgaacagAAC cggagtcgag cagcacctcc ccgcaagggt															60
agaggggctg cttttttgtt tcctaaattc accccatccc atg cat agc cct gaa															115
Met His Ser Pro Glu															
1 5															
agg caa gaa aaa atg agt tct cca gtc tca ctc gaa aac gcg gcg tca															163
Arg Gln Glu Lys Met Ser Ser Pro Val Ser Leu Glu Asn Ala Ala Ser															
10 15 20															
acc agc aac aag cgc gtc gtg gct ttc cac gag ctg cct agc cct aca															211
Thr Ser Asn Lys Arg Val Val Ala Phe His Glu Leu Pro Ser Pro Thr															
25 30 35															
gat ctc atc gcc gca aac cca ctg aca cca aag cag gct tcc aag gtg															259
Asp Leu Ile Ala Ala Asn Pro Leu Thr Pro Lys Gln Ala Ser Lys Val															
40 45 50															
gag cag gat cgc cag gac atc gct gat atc ttc gct ggc gac gat gac															307
Glu Gln Asp Arg Gln Asp Ile Ala Asp Ile Phe Ala Gly Asp Asp Asp															
55 60 65															
cgc ctc gtt gtc gtt gtg gga cct tgc tca gtt cac gat cct gaa gca															355
Arg Leu Val Val Val Val Gly Pro Cys Ser Val His Asp Pro Glu Ala															
70 75 80 85															
gcc atc gat tac gca aac cgc ctg gct ccg ctg gca aag cgc ctt gat															403
Ala Ile Asp Tyr Ala Asn Arg Leu Ala Pro Leu Ala Lys Arg Leu Asp															
90 95 100															
cag gac ctc aag att gtc atg cgc gtg tac ttc gag aag cct cgc acc															451
Gln Asp Leu Lys Ile Val Met Arg Val Tyr Phe Glu Lys Pro Arg Thr															
105 110 115															
atc gtc gga tgg aag gga ttg atc aat gat cct cac ctc aac gaa acc															499
Ile Val Gly Trp Lys Gly Leu Ile Asn Asp Pro His Leu Asn Glu Thr															
120 125 130															
tac gac atc cca gag ggc ttg cgc att gcg cgc aaa gtg ctt atc gac															547
Tyr Asp Ile Pro Glu Gly Leu Arg Ile Ala Arg Lys Val Leu Ile Asp															
135 140 145															

gtt gtg aac ctt gat ctc cca gtc ggc tgc gaa ttc ctc gaa cca aac	595
Val Val Asn Leu Asp Leu Pro Val Gly Cys Glu Phe Leu Glu Pro Asn	
150 155 160 165	
agc cct cag tac tac gcc gac act gtc gca tgg gga gca atc ggc gct	643
Ser Pro Gln Tyr Tyr Ala Asp Thr Val Ala Trp Gly Ala Ile Gly Ala	
170 175 180	
cgt acc acc gaa tct cag gtg cac cgc cag ctg gct tct ggg atg tct	691
Arg Thr Thr Glu Ser Gln Val His Arg Gln Leu Ala Ser Gly Met Ser	
185 190 195	
atg cca att ggt ttc aag aac gga act gac gga aac atc cag gtt gca	739
Met Pro Ile Gly Phe Lys Asn Gly Thr Asp Gly Asn Ile Gln Val Ala	
200 205 210	
gtc gac gcg gta cag gct gcc cag aac cca cac ttc ttc ttc gga acc	787
Val Asp Ala Val Gln Ala Ala Gln Asn Pro His Phe Phe Phe Gly Thr	
215 220 225	
tcc gac gac ggc gcg ctg agc gtc gtg gag acc gca ggc aac agc aac	835
Ser Asp Asp Gly Ala Leu Ser Val Val Glu Thr Ala Gly Asn Ser Asn	
230 235 240 245	
tcc cac atc att ttg cgc ggc ggt acc tcc ggc ccg aat cat gat gca	883
Ser His Ile Ile Leu Arg Gly Gly Thr Ser Gly Pro Asn His Asp Ala	
250 255 260	
gct tcg gtg gag gcc gtc gtc gag aag ctt ggt gaa aac gct cgt ctc	931
Ala Ser Val Glu Ala Val Val Glu Lys Leu Gly Glu Asn Ala Arg Leu	
265 270 275	
atg atc gat gct tcc cat gct aac tcc ggc aag gat cat atc cga cag	979
Met Ile Asp Ala Ser His Ala Asn Ser Gly Lys Asp His Ile Arg Gln	
280 285 290	
gtt gag gtt gtt cgt gaa atc gca gag cag att tct ggc ggt tct gaa	1027
Val Glu Val Val Arg Glu Ile Ala Glu Gln Ile Ser Gly Gly Ser Glu	
295 300 305	
gct gtg gct gga atc atg att gag tcc ttc ctc gtt ggt ggc gca cag	1075
Ala Val Ala Gly Ile Met Ile Glu Ser Phe Leu Val Gly Gly Ala Gln	
310 315 320 325	
aac ctt gat cct gcg aaa ttg cgc atc aat ggc ggt gaa ggc ctg gtg	1123
Asn Leu Asp Pro Ala Lys Leu Arg Ile Asn Gly Gly Glu Gly Leu Val	
330 335 340	
tac gga cag tct gtg acc gat aag tgc atc gat att gac acc acc atc	1171
Tyr Gly Gln Ser Val Thr Asp Lys Cys Ile Asp Ile Asp Thr Thr Ile	
345 350 355	
gat ttg ctc gct gag ctg gcc gca gca gta agg gaa cgc cga gca gca	1219
Asp Leu Leu Ala Glu Leu Ala Ala Ala Val Arg Glu Arg Arg Ala Ala	
360 365 370	
gcc aag taattaaggg cgctagactg tta	1248
Ala Lys	
375	

<210> 488

<211> 375

<212> PRT

<213> Corynebacterium glutamicum

<400> 488

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Met His Ser Pro Glu Arg Gln Glu Lys Met Ser Ser Pro Val Ser Leu
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          20          25          30

Leu Pro Ser Pro Thr Asp Leu Ile Ala Ala Asn Pro Leu Thr Pro Lys
          35          40          45

Gln Ala Ser Lys Val Glu Gln Asp Arg Gln Asp Ile Ala Asp Ile Phe
          50          55          60

Ala Gly Asp Asp Asp Arg Leu Val Val Val Val Gly Pro Cys Ser Val
          65          70          75          80

His Asp Pro Glu Ala Ala Ile Asp Tyr Ala Asn Arg Leu Ala Pro Leu
          85          90          95

Ala Lys Arg Leu Asp Gln Asp Leu Lys Ile Val Met Arg Val Tyr Phe
          100          105          110

Glu Lys Pro Arg Thr Ile Val Gly Trp Lys Gly Leu Ile Asn Asp Pro
          115          120          125

His Leu Asn Glu Thr Tyr Asp Ile Pro Glu Gly Leu Arg Ile Ala Arg
          130          135          140

Lys Val Leu Ile Asp Val Val Asn Leu Asp Leu Pro Val Gly Cys Glu
          145          150          155          160

Phe Leu Glu Pro Asn Ser Pro Gln Tyr Tyr Ala Asp Thr Val Ala Trp
          165          170          175

Gly Ala Ile Gly Ala Arg Thr Thr Glu Ser Gln Val His Arg Gln Leu
          180          185          190

Ala Ser Gly Met Ser Met Pro Ile Gly Phe Lys Asn Gly Thr Asp Gly
          195          200          205

Asn Ile Gln Val Ala Val Asp Ala Val Gln Ala Ala Gln Asn Pro His
          210          215          220

Phe Phe Phe Gly Thr Ser Asp Asp Gly Ala Leu Ser Val Val Glu Thr
          225          230          235          240

Ala Gly Asn Ser Asn Ser His Ile Ile Leu Arg Gly Gly Thr Ser Gly
          245          250          255

Pro Asn His Asp Ala Ala Ser Val Glu Ala Val Val Glu Lys Leu Gly
          260          265          270

Glu Asn Ala Arg Leu Met Ile Asp Ala Ser His Ala Asn Ser Gly Lys
          275          280          285

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Asp His Ile Arg Gln Val Glu Val Val Arg Glu Ile Ala Glu Gln Ile
 290 295 300

Ser Gly Gly Ser Glu Ala Val Ala Gly Ile Met Ile Glu Ser Phe Leu
 305 310 315 320

Val Gly Gly Ala Gln Asn Leu Asp Pro Ala Lys Leu Arg Ile Asn Gly
 325 330 335

Gly Glu Gly Leu Val Tyr Gly Gln Ser Val Thr Asp Lys Cys Ile Asp
 340 345 350

Ile Asp Thr Thr Ile Asp Leu Leu Ala Glu Leu Ala Ala Ala Val Arg
 355 360 365

Glu Arg Arg Ala Ala Ala Lys
 370 375

<210> 489
 <211> 1131
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(1108)
 <223> RXS02574

<400> 489
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gacgtccccc tccaccctc ccgcaccgac cgcgaggat ttg gcg cgc gcg caa 115
 Leu Ala Arg Ala Gln
 1 5

atc cct gaa cag caa cgc gac caa gtc gcg tcg ctg atg atg gtt gga 163
 Ile Pro Glu Gln Gln Arg Asp Gln Val Ala Ser Leu Met Met Val Gly
 10 15 20

gtt gcg aat tat gat cag gca ttg gat gcg ctc aat cag ggg gtg ggt 211
 Val Ala Asn Tyr Asp Gln Ala Leu Asp Ala Leu Asn Gln Gly Val Gly
 25 30 35

ggc atc ttt att ggt tcc tgg aca gat gaa aat ctg ctc acg gaa cct 259
 Gly Ile Phe Ile Gly Ser Trp Thr Asp Glu Asn Leu Leu Thr Glu Pro
 40 45 50

ggc cgt aat att gag gcg ctc cgc gaa gcc gtc ggc agg gat ttc tcc 307
 Gly Arg Asn Ile Glu Ala Leu Arg Glu Ala Val Gly Arg Asp Phe Ser
 55 60 65

gtc agc atc gac ttc gaa ggc ggc cgc gtc cag cgt gcc acc aat att 355
 Val Ser Ile Asp Phe Glu Gly Gly Arg Val Gln Arg Ala Thr Asn Ile
 70 75 80 85

ctt ggt gat ttc ccc tca ccg cgc gtg atg gcg caa acc atg acg ccg 403
 Leu Gly Asp Phe Pro Ser Pro Arg Val Met Ala Gln Thr Met Thr Pro
 90 95 100

gaa caa gta gaa gat ctc gca gaa atc cta ggc act ggt tta gct gca 451

Glu Gln Val Glu Asp Leu Ala Glu Ile Leu Gly Thr Gly Leu Ala Ala	
105 110 115	
cat ggt gtg aca gtt aac ttt gca cct gtt gta gat gta gat gct tgg	499
His Gly Val Thr Val Asn Phe Ala Pro Val Val Asp Val Asp Ala Trp	
120 125 130	
ggt ctc ccc gtc gtt ggc gat cgt tcc ttt tcc aac gac cca gcc gta	547
Gly Leu Pro Val Val Gly Asp Arg Ser Phe Ser Asn Asp Pro Ala Val	
135 140 145	
gca gct act tat gcc aca gct ttt gca aag ggc tta agc aaa gta gga	595
Ala Ala Thr Tyr Ala Thr Ala Phe Ala Lys Gly Leu Ser Lys Val Gly	
150 155 160 165	
att acc cca gta ttc aaa cat ttc cca ggt cac ggt cgt gca agt ggc	643
Ile Thr Pro Val Phe Lys His Phe Pro Gly His Gly Arg Ala Ser Gly	
170 175 180	
gat tcg cac acc caa gat gtg gtg acc ccc gca ctt gat gag ctt aaa	691
Asp Ser His Thr Gln Asp Val Val Thr Pro Ala Leu Asp Glu Leu Lys	
185 190 195	
act tac gac ctc atc cct tat ggt caa gca ctt tct gaa act gac gga	739
Thr Tyr Asp Leu Ile Pro Tyr Gly Gln Ala Leu Ser Glu Thr Asp Gly	
200 205 210	
gcc gtc atg gtg ggc cac atg att gtt cca ggt ctt ggc acc gac gga	787
Ala Val Met Val Gly His Met Ile Val Pro Gly Leu Gly Thr Asp Gly	
215 220 225	
gtt cca tcc tct atc gac ccc gcc acc tat caa ctg ctc cgc agt ggc	835
Val Pro Ser Ser Ile Asp Pro Ala Thr Tyr Gln Leu Leu Arg Ser Gly	
230 235 240 245	
gat tac cca ggt ggc gtg cct ttc gat ggc gtg atc tac acc gac gat	883
Asp Tyr Pro Gly Gly Val Pro Phe Asp Gly Val Ile Tyr Thr Asp Asp	
250 255 260	
ctc tct gga atg agt gcc att tcc gcc acc cat tca ccc gca gaa gca	931
Leu Ser Gly Met Ser Ala Ile Ser Ala Thr His Ser Pro Ala Glu Ala	
265 270 275	
gtg ctt gcc tcc ctc aaa gca ggc gca gac caa gca cta tgg atc gac	979
Val Leu Ala Ser Leu Lys Ala Gly Ala Asp Gln Ala Leu Trp Ile Asp	
280 285 290	
tat ggg tcg ttg ggc tcc gcg att gat cgc gtt gat gct gcc gtt agc	1027
Tyr Gly Ser Leu Gly Ser Ala Ile Asp Arg Val Asp Ala Ala Val Ser	
295 300 305	
agc ggt gaa tac cct caa gaa caa atg ctg gca tct gcg tta aga gtc	1075
Ser Gly Glu Tyr Pro Gln Glu Gln Met Leu Ala Ser Ala Leu Arg Val	
310 315 320 325	
caa ttg ctc tac atc aca cgt ctc gaa caa aag tgaagttacc agtccgtaac	1128
Gln Leu Leu Tyr Ile Thr Arg Leu Glu Gln Lys	
330 335	
ccc	1131

<210> 490

<211> 336

<212> PRT

<213> Corynebacterium glutamicum

<400> 490

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Leu Ala Arg Ala Gln Ile Pro Glu Gln Gln Arg Asp Gln Val Ala Ser
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Leu Met Met Val Gly Val Ala Asn Tyr Asp Gln Ala Leu Asp Ala Leu
          20              25              30

Asn Gln Gly Val Gly Gly Ile Phe Ile Gly Ser Trp Thr Asp Glu Asn
 35              40              45

Leu Leu Thr Glu Pro Gly Arg Asn Ile Glu Ala Leu Arg Glu Ala Val
 50              55              60

Gly Arg Asp Phe Ser Val Ser Ile Asp Phe Glu Gly Gly Arg Val Gln
 65              70              75              80

Arg Ala Thr Asn Ile Leu Gly Asp Phe Pro Ser Pro Arg Val Met Ala
          85              90              95

Gln Thr Met Thr Pro Glu Gln Val Glu Asp Leu Ala Glu Ile Leu Gly
          100              105              110

Thr Gly Leu Ala Ala His Gly Val Thr Val Asn Phe Ala Pro Val Val
          115              120              125

Asp Val Asp Ala Trp Gly Leu Pro Val Val Gly Asp Arg Ser Phe Ser
          130              135              140

Asn Asp Pro Ala Val Ala Ala Thr Tyr Ala Thr Ala Phe Ala Lys Gly
          145              150              155              160

Leu Ser Lys Val Gly Ile Thr Pro Val Phe Lys His Phe Pro Gly His
          165              170              175

Gly Arg Ala Ser Gly Asp Ser His Thr Gln Asp Val Val Thr Pro Ala
          180              185              190

Leu Asp Glu Leu Lys Thr Tyr Asp Leu Ile Pro Tyr Gly Gln Ala Leu
          195              200              205

Ser Glu Thr Asp Gly Ala Val Met Val Gly His Met Ile Val Pro Gly
          210              215              220

Leu Gly Thr Asp Gly Val Pro Ser Ser Ile Asp Pro Ala Thr Tyr Gln
          225              230              235              240

Leu Leu Arg Ser Gly Asp Tyr Pro Gly Gly Val Pro Phe Asp Gly Val
          245              250              255

Ile Tyr Thr Asp Asp Leu Ser Gly Met Ser Ala Ile Ser Ala Thr His
          260              265              270

Ser Pro Ala Glu Ala Val Leu Ala Ser Leu Lys Ala Gly Ala Asp Gln
          275              280              285

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Ala Leu Trp Ile Asp Tyr Gly Ser Leu Gly Ser Ala Ile Asp Arg Val
 290 295 300

Asp Ala Ala Val Ser Ser Gly Glu Tyr Pro Gln Glu Gln Met Leu Ala
 305 310 315 320

Ser Ala Leu Arg Val Gln Leu Leu Tyr Ile Thr Arg Leu Glu Gln Lys
 325 330 335

<210> 491

<211> 1038

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (1)..(1008)

<223> RXS03215

<400> 491

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1 5 10 15	
gtg gaa gca ctt ctg gca tcc ggc aag cat gtg ctg tgc gag aag cca	96
Val Glu Ala Leu Leu Ala Ser Gly Lys His Val Leu Cys Glu Lys Pro	
20 25 30	
ctg tca gac acc atc gaa gat gca gaa gcc atg att gag gca gcc ggc	144
Leu Ser Asp Thr Ile Glu Asp Ala Glu Ala Met Ile Glu Ala Ala Gly	
35 40 45	
cgt gca gca aca aat ggc acc atc gcc cgc atc gga ctg acc tac cgc	192
Arg Ala Ala Thr Asn Gly Thr Ile Ala Arg Ile Gly Leu Thr Tyr Arg	
50 55 60	
cgt tcc cca ggc gtg gca cac atc cgt gat ctc gtg cag tcc ggc gag	240
Arg Ser Pro Gly Val Ala His Ile Arg Asp Leu Val Gln Ser Gly Glu	
65 70 75 80	
ctt ggc aag gtt cta cac gtc acc ggc cac tac tgg acc gac tac gga	288
Leu Gly Lys Val Leu His Val Thr Gly His Tyr Trp Thr Asp Tyr Gly	
85 90 95	
tcc aat gca cag gca cca atc agc tgg cgt tac aag ggg cca aac ggc	336
Ser Asn Ala Gln Ala Pro Ile Ser Trp Arg Tyr Lys Gly Pro Asn Gly	
100 105 110	
tcc ggc gca ctg gca gat gtg gga agc cac ctc acc tac ctg gca gaa	384
Ser Gly Ala Leu Ala Asp Val Gly Ser His Leu Thr Tyr Leu Ala Glu	
115 120 125	
ttc gtt gca gga tct gac ttc gcc gcc gtc cgt ggt ggc cag ttg tcc	432
Phe Val Ala Gly Ser Asp Phe Ala Ala Val Arg Gly Gly Gln Leu Ser	
130 135 140	
acc gtg atc acc gag cgc ccc aag cca ctc ggc gcg att gtc ggc cac	480

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Thr Val Ile Thr Glu Arg Pro Lys Pro Leu Gly Ala Ile Val Gly His
145                      150                      155                      160

gaa ggc ggc gca gtt tcc gat gaa tac gaa gca gtg gaa aat gat gac 528
Glu Gly Gly Ala Val Ser Asp Glu Tyr Glu Ala Val Glu Asn Asp Asp
                      165                      170                      175

att gca tca ttc tcc gga tcc ttc atc ggt ggc gga acc gca acc ctc 576
Ile Ala Ser Phe Ser Gly Ser Phe Ile Gly Gly Gly Thr Ala Thr Leu
                      180                      185                      190

cag gtc agc cgc att tcc cag gga cac cca aac acc cta ggt ttt gaa 624
Gln Val Ser Arg Ile Ser Gln Gly His Pro Asn Thr Leu Gly Phe Glu
                      195                      200                      205

gtg ttc tgt gaa aag ggc tcc gtg ctc ttt gat ttc cgc aac tca ggc 672
Val Phe Cys Glu Lys Gly Ser Val Leu Phe Asp Phe Arg Asn Ser Gly
                      210                      215                      220

gaa ttc aaa atc ttc acc cca gca acc tcc ggt gac atc agc caa gaa 720
Glu Phe Lys Ile Phe Thr Pro Ala Thr Ser Gly Asp Ile Ser Gln Glu
225                      230                      235                      240

gcc ggc tac cgc acc atc acc atc gga cca aag cac cca tac tgg cgc 768
Ala Gly Tyr Arg Thr Ile Thr Ile Gly Pro Lys His Pro Tyr Trp Arg
                      245                      250                      255

ggc ggc ctt gca atg gat gca cca ggc gtg gga att ggc caa aac gaa 816
Gly Gly Leu Ala Met Asp Ala Pro Gly Val Gly Ile Gly Gln Asn Glu
                      260                      265                      270

ggc ttc gtt ttc cag gcg cgc gca ttc ctc gaa gaa atc gca gga atc 864
Gly Phe Val Phe Gln Ala Arg Ala Phe Leu Glu Glu Ile Ala Gly Ile
                      275                      280                      285

tcc gaa gct gaa agc ctg cca cgc tgc gca act ttg gaa gaa ggg cta 912
Ser Glu Ala Glu Ser Leu Pro Arg Cys Ala Thr Leu Glu Glu Gly Leu
                      290                      295                      300

cac aat atg cag ctc att gat gct gta tca cag tca gct gca gca ggt 960
His Asn Met Gln Leu Ile Asp Ala Val Ser Gln Ser Ala Ala Ala Gly
305                      310                      315                      320

ggc gaa acc gtt gcg gtc cca gcg gct gct ctg atc cct gca aac aac 1008
Gly Glu Thr Val Ala Val Pro Ala Ala Leu Ile Pro Ala Asn Asn
                      325                      330                      335

tagaaactat tcagaaagca tcaccatgaa 1038

<210> 492
<211> 336
<212> PRT
<213> Corynebacterium glutamicum

<400> 492
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Val Glu Ala Leu Leu Ala Ser Gly Lys His Val Leu Cys Glu Lys Pro
20                      25                      30

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Leu Ser Asp Thr Ile Glu Asp Ala Glu Ala Met Ile Glu Ala Ala Gly
 35 40 45
 Arg Ala Ala Thr Asn Gly Thr Ile Ala Arg Ile Gly Leu Thr Tyr Arg
 50 55 60
 Arg Ser Pro Gly Val Ala His Ile Arg Asp Leu Val Gln Ser Gly Glu
 65 70 75 80
 Leu Gly Lys Val Leu His Val Thr Gly His Tyr Trp Thr Asp Tyr Gly
 85 90 95
 Ser Asn Ala Gln Ala Pro Ile Ser Trp Arg Tyr Lys Gly Pro Asn Gly
 100 105 110
 Ser Gly Ala Leu Ala Asp Val Gly Ser His Leu Thr Tyr Leu Ala Glu
 115 120 125
 Phe Val Ala Gly Ser Asp Phe Ala Ala Val Arg Gly Gly Gln Leu Ser
 130 135 140
 Thr Val Ile Thr Glu Arg Pro Lys Pro Leu Gly Ala Ile Val Gly His
 145 150 155 160
 Glu Gly Gly Ala Val Ser Asp Glu Tyr Glu Ala Val Glu Asn Asp Asp
 165 170 175
 Ile Ala Ser Phe Ser Gly Ser Phe Ile Gly Gly Gly Thr Ala Thr Leu
 180 185 190
 Gln Val Ser Arg Ile Ser Gln Gly His Pro Asn Thr Leu Gly Phe Glu
 195 200 205
 Val Phe Cys Glu Lys Gly Ser Val Leu Phe Asp Phe Arg Asn Ser Gly
 210 215 220
 Glu Phe Lys Ile Phe Thr Pro Ala Thr Ser Gly Asp Ile Ser Gln Glu
 225 230 235 240
 Ala Gly Tyr Arg Thr Ile Thr Ile Gly Pro Lys His Pro Tyr Trp Arg
 245 250 255
 Gly Gly Leu Ala Met Asp Ala Pro Gly Val Gly Ile Gly Gln Asn Glu
 260 265 270
 Gly Phe Val Phe Gln Ala Arg Ala Phe Leu Glu Glu Ile Ala Gly Ile
 275 280 285
 Ser Glu Ala Glu Ser Leu Pro Arg Cys Ala Thr Leu Glu Glu Gly Leu
 290 295 300
 His Asn Met Gln Leu Ile Asp Ala Val Ser Gln Ser Ala Ala Ala Gly
 305 310 315 320
 Gly Glu Thr Val Ala Val Pro Ala Ala Ala Leu Ile Pro Ala Asn Asn
 325 330 335

<210> 493
 <211> 1031
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (1)..(1008)
 <223> FRXA01915

<400> 493
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 gtg gaa gca ctt ctg gca tcc ggc aag cat gtg ctg tgc gag aag cca 96
 Val Glu Ala Leu Leu Ala Ser Gly Lys His Val Leu Cys Glu Lys Pro
 20 25 30
 ctg tca gac acc atc gaa gat gca gaa gcc atg att gag gca gcc ggc 144
 Leu Ser Asp Thr Ile Glu Asp Ala Glu Ala Met Ile Glu Ala Ala Gly
 35 40 45
 cgt gca gca aca aat ggc acc atc gcc cgc atc gga ctg acc tac cgc 192
 Arg Ala Ala Thr Asn Gly Thr Ile Ala Arg Ile Gly Leu Thr Tyr Arg
 50 55 60
 cgt tcc cca ggc gtg gca cac atc cgt gat ctc gtg cag tcc ggc gag 240
 Arg Ser Pro Gly Val Ala His Ile Arg Asp Leu Val Gln Ser Gly Glu
 65 70 75 80
 ctt ggc aag gtt cta cac gtc acc ggc cac tac tgg acc gac tac gga 288
 Leu Gly Lys Val Leu His Val Thr Gly His Tyr Trp Thr Asp Tyr Gly
 85 90 95
 tcc aat gca cag gca cca atc agc tgg cgt tac aag ggc cca aac ggc 336
 Ser Asn Ala Gln Ala Pro Ile Ser Trp Arg Tyr Lys Gly Pro Asn Gly
 100 105 110
 tcc ggc gca ctg gca gat gtg gga agc cac ctc acc tac ctg gca gaa 384
 Ser Gly Ala Leu Ala Asp Val Gly Ser His Leu Thr Tyr Leu Ala Glu
 115 120 125
 ttc gtt gca gga tct gac ttc gcc gcc gtc cgt ggt ggc cag ttg tcc 432
 Phe Val Ala Gly Ser Asp Phe Ala Ala Val Arg Gly Gly Gln Leu Ser
 130 135 140
 acc gtg atc acc gag cgc ccc aag cca ctc ggc gcg att gtc ggc cac 480
 Thr Val Ile Thr Glu Arg Pro Lys Pro Leu Gly Ala Ile Val Gly His
 145 150 155 160
 gaa ggc ggc gca gtt tcc gat gaa tac gaa gca gtg gaa aat gat gac 528
 Glu Gly Gly Ala Val Ser Asp Glu Tyr Glu Ala Val Glu Asn Asp Asp
 165 170 175
 att gca tca ttc tcc gga tcc ttc atc ggt ggc gga acc gca acc ctc 576
 Ile Ala Ser Phe Ser Gly Ser Phe Ile Gly Gly Gly Thr Ala Thr Leu
 180 185 190
 cag gtc agc cgc att tcc cag gga cac cca aac acc cta ggt ttt gaa 624

Gln Val Ser Arg Ile Ser Gln Gly His Pro Asn Thr Leu Gly Phe Glu
 195 200 205
 gtg ttc tgt gaa aag ggc tcc gtg ctc ttt gat ttc cgc aac tca ggc 672
 Val Phe Cys Glu Lys Gly Ser Val Leu Phe Asp Phe Arg Asn Ser Gly
 210 215 220
 gaa ttc aaa atc ttc acc cca gca acc tcc ggt gac atc agc caa gaa 720
 Glu Phe Lys Ile Phe Thr Pro Ala Thr Ser Gly Asp Ile Ser Gln Glu
 225 230 235 240
 gcc ggc tac cgc acc atc acc atc gga cca aag cac cca tac tgg cgc 768
 Ala Gly Tyr Arg Thr Ile Thr Ile Gly Pro Lys His Pro Tyr Trp Arg
 245 250 255
 ggc ggc ctt gca atg gat gca cca ggc gtg gga att ggc caa aac gaa 816
 Gly Gly Leu Ala Met Asp Ala Pro Gly Val Gly Ile Gly Gln Asn Glu
 260 265 270
 ggc ttc gtt ttc cag gcg cgc gca ttc ctc gaa gaa atc gca gga atc 864
 Gly Phe Val Phe Gln Ala Arg Ala Phe Leu Glu Glu Ile Ala Gly Ile
 275 280 285
 tcc gaa gct gaa agc ctg cca cgc tgc gca act ttg gaa gaa ggg cta 912
 Ser Glu Ala Glu Ser Leu Pro Arg Cys Ala Thr Leu Glu Glu Gly Leu
 290 295 300
 cac aat atg cag ctc att gat gct gta tca cag tca gct gca gca ggt 960
 His Asn Met Gln Leu Ile Asp Ala Val Ser Gln Ser Ala Ala Ala Gly
 305 310 315 320
 ggc gaa acc gtt gcg gtc cca gcg gct gct ctg atc cct gca aac aac 1008
 Gly Glu Thr Val Ala Val Pro Ala Ala Ala Leu Ile Pro Ala Asn Asn
 325 330 335
 tagaaactat tcagaaagca tca 1031

<210> 494

<211> 336

<212> PRT

<213> Corynebacterium glutamicum

<400> 494

Ile Asp Val Val Ser Val Val Val Ala Asn Phe Leu His Arg Glu Ile
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 20 25 30
 Leu Ser Asp Thr Ile Glu Asp Ala Glu Ala Met Ile Glu Ala Ala Gly
 35 40 45
 Arg Ala Ala Thr Asn Gly Thr Ile Ala Arg Ile Gly Leu Thr Tyr Arg
 50 55 60
 Arg Ser Pro Gly Val Ala His Ile Arg Asp Leu Val Gln Ser Gly Glu
 65 70 75 80
 Leu Gly Lys Val Leu His Val Thr Gly His Tyr Trp Thr Asp Tyr Gly
 85 90 95

Ser Asn Ala Gln Ala Pro Ile Ser Trp Arg Tyr Lys Gly Pro Asn Gly
 100 105 110
 Ser Gly Ala Leu Ala Asp Val Gly Ser His Leu Thr Tyr Leu Ala Glu
 115 120 125
 Phe Val Ala Gly Ser Asp Phe Ala Ala Val Arg Gly Gly Gln Leu Ser
 130 135 140
 Thr Val Ile Thr Glu Arg Pro Lys Pro Leu Gly Ala Ile Val Gly His
 145 150 155 160
 Glu Gly Gly Ala Val Ser Asp Glu Tyr Glu Ala Val Glu Asn Asp Asp
 165 170 175
 Ile Ala Ser Phe Ser Gly Ser Phe Ile Gly Gly Gly Thr Ala Thr Leu
 180 185 190
 Gln Val Ser Arg Ile Ser Gln Gly His Pro Asn Thr Leu Gly Phe Glu
 195 200 205
 Val Phe Cys Glu Lys Gly Ser Val Leu Phe Asp Phe Arg Asn Ser Gly
 210 215 220
 Glu Phe Lys Ile Phe Thr Pro Ala Thr Ser Gly Asp Ile Ser Gln Glu
 225 230 235 240
 Ala Gly Tyr Arg Thr Ile Thr Ile Gly Pro Lys His Pro Tyr Trp Arg
 245 250 255
 Gly Gly Leu Ala Met Asp Ala Pro Gly Val Gly Ile Gly Gln Asn Glu
 260 265 270
 Gly Phe Val Phe Gln Ala Arg Ala Phe Leu Glu Glu Ile Ala Gly Ile
 275 280 285
 Ser Glu Ala Glu Ser Leu Pro Arg Cys Ala Thr Leu Glu Glu Gly Leu
 290 295 300
 His Asn Met Gln Leu Ile Asp Ala Val Ser Gln Ser Ala Ala Ala Gly
 305 310 315 320
 Gly Glu Thr Val Ala Val Pro Ala Ala Ala Leu Ile Pro Ala Asn Asn
 325 330 335

<210> 495
 <211> 1288
 <212> DNA
 <213> Corynebacterium glutamicum

 <220>
 <221> CDS
 <222> (101)..(1258)
 <223> RXS03224

 <400> 495

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tggaactcat tgaacgcgcg gcccggtctaa ggtgggaggc atg agt ttt gct gaa 115
Met Ser Phe Ala Glu
1 5

cat gcg atc atc tgg cac gtc tac ccc ctg ggc gct ttg ggt gct ccc 163
His Ala Ile Ile Trp His Val Tyr Pro Leu Gly Ala Leu Gly Ala Pro
10 15 20

atc cgg cct gaa gcc ccc gca cct gtc aca cat cgg ctc ccc aat cta 211
Ile Arg Pro Glu Ala Pro Ala Pro Val Thr His Arg Leu Pro Asn Leu
25 30 35

att ggg tgg ctg gat tat gtt gtc gaa cta ggc tgc aac gcc ctc atg 259
Ile Gly Trp Leu Asp Tyr Val Val Glu Leu Gly Cys Asn Ala Leu Met
40 45 50

ctg gga ccg gta ttc gag tcc gtc agc cac ggc tac gac acc ctc gat 307
Leu Gly Pro Val Phe Glu Ser Val Ser His Gly Tyr Asp Thr Leu Asp
55 60 65

ttc tac cgc atc gac ccg cgc ctc ggc acc gag gaa gac atg gac gcg 355
Phe Tyr Arg Ile Asp Pro Arg Leu Gly Thr Glu Glu Asp Met Asp Ala
70 75 80 85

ctg ctg gag gct gcg aat cag cgg ggc att gga gtg ctt ttc gac ggc 403
Leu Leu Glu Ala Ala Asn Gln Arg Gly Ile Gly Val Leu Phe Asp Gly
90 95 100

gtc ttc aat cat gtt tcc agt tcc tct aaa tat ctc gac ctg acc acc 451
Val Phe Asn His Val Ser Ser Ser Ser Lys Tyr Leu Asp Leu Thr Thr
105 110 115

ggg gcg tca ttt gaa ggc cac gac atc ctg gcg gaa ctc gac cac acg 499
Gly Ala Ser Phe Glu Gly His Asp Ile Leu Ala Glu Leu Asp His Thr
120 125 130

aat ccc gcc gta gtg gat ctg gtt gtc gat gtc atg aac cac tgg ctc 547
Asn Pro Ala Val Val Asp Leu Val Val Asp Val Met Asn His Trp Leu
135 140 145

gac cgc gga atc gca ggc tgg cga ctc gac gct gtc tac gcc atc gcc 595
Asp Arg Gly Ile Ala Gly Trp Arg Leu Asp Ala Val Tyr Ala Ile Ala
150 155 160 165

cct gaa ttt tgg gaa aaa gtc ctg cca gaa gtg cga cga aaa cac cca 643
Pro Glu Phe Trp Glu Lys Val Leu Pro Glu Val Arg Arg Lys His Pro
170 175 180

cac gca tgg atc gtg ggg gag atg atc cat gga gat tac tcc gac tac 691
His Ala Trp Ile Val Gly Glu Met Ile His Gly Asp Tyr Ser Asp Tyr
185 190 195

gtg aaa agc tcc ggc att gat tcc gtt acc gaa tac gaa ctg tgg aaa 739
Val Lys Ser Ser Gly Ile Asp Ser Val Thr Glu Tyr Glu Leu Trp Lys
200 205 210

gcc att tgg agc agc atc aaa gag cgc aat ttc ttt gaa ctc gaa tgg 787
Ala Ile Trp Ser Ser Ile Lys Glu Arg Asn Phe Phe Glu Leu Glu Trp
215 220 225

act ttg agt cgc cac aat gaa ttc ctc gat act ttc gta ccg cag aca 835
 Thr Leu Ser Arg His Asn Glu Phe Leu Asp Thr Phe Val Pro Gln Thr
 230 235 240 245

 ttc att ggt aac cat gac gtc acc cgc att gcc acc cga atc ggt caa 883
 Phe Ile Gly Asn His Asp Val Thr Arg Ile Ala Thr Arg Ile Gly Gln
 250 255 260

 tca aat gcg atc ctg gcc gca gcg atc ctc ttc acg gtc gga gga acc 931
 Ser Asn Ala Ile Leu Ala Ala Ala Ile Leu Phe Thr Val Gly Gly Thr
 265 270 275

 cca agc att tac tac ggc gat gag cag ggc ttt acg gga ttg aaa gag 979
 Pro Ser Ile Tyr Tyr Gly Asp Glu Gln Gly Phe Thr Gly Leu Lys Glu
 280 285 290

 gat aac gtt ttc ggt gac gat gcc att agg cca cct ctt cct gcc gag 1027
 Asp Asn Val Phe Gly Asp Asp Ala Ile Arg Pro Pro Leu Pro Ala Glu
 295 300 305

 ttt tct cca ctg ggc acc tgg att gaa aac att tat aag gct ctg atc 1075
 Phe Ser Pro Leu Gly Thr Trp Ile Glu Asn Ile Tyr Lys Ala Leu Ile
 310 315 320 325

 gcg ctg cgc agg caa cac ccg tgg ttg tat cag gcg cac acc gaa gtc 1123
 Ala Leu Arg Arg Gln His Pro Trp Leu Tyr Gln Ala His Thr Glu Val
 330 335 340

 ctt gag att gct aat gaa gcg atg acc tat aag tcc gtc ggt ctt gga 1171
 Leu Glu Ile Ala Asn Glu Ala Met Thr Tyr Lys Ser Val Gly Leu Gly
 345 350 355

 ggt gaa gag ctg aca gtg cat ctt gat ttg gaa gag gtg tct gtt cgg 1219
 Gly Glu Glu Leu Thr Val His Leu Asp Leu Glu Glu Val Ser Val Arg
 360 365 370

 atc ctt gat ggc gag aag gtg ctg ttt cag tac agc gct tagttgtcgg 1268
 Ile Leu Asp Gly Glu Lys Val Leu Phe Gln Tyr Ser Ala
 375 380 385

 ttcaagggta gggaacaaa 1288

<210> 496

<211> 386

<212> PRT

<213> Corynebacterium glutamicum

<400> 496

Met Ser Phe Ala Glu His Ala Ile Ile Trp His Val Tyr Pro Leu Gly
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Ala Leu Gly Ala Pro Ile Arg Pro Glu Ala Pro Ala Pro Val Thr His
 20 25 30

Arg Leu Pro Asn Leu Ile Gly Trp Leu Asp Tyr Val Val Glu Leu Gly
 35 40 45

Cys Asn Ala Leu Met Leu Gly Pro Val Phe Glu Ser Val Ser His Gly
 50 55 60

Tyr Asp Thr Leu Asp Phe Tyr Arg Ile Asp Pro Arg Leu Gly Thr Glu
 65 70 75 80
 Glu Asp Met Asp Ala Leu Leu Glu Ala Ala Asn Gln Arg Gly Ile Gly
 85 90 95
 Val Leu Phe Asp Gly Val Phe Asn His Val Ser Ser Ser Ser Lys Tyr
 100 105 110
 Leu Asp Leu Thr Thr Gly Ala Ser Phe Glu Gly His Asp Ile Leu Ala
 115 120 125
 Glu Leu Asp His Thr Asn Pro Ala Val Val Asp Leu Val Val Asp Val
 130 135 140
 Met Asn His Trp Leu Asp Arg Gly Ile Ala Gly Trp Arg Leu Asp Ala
 145 150 155 160
 Val Tyr Ala Ile Ala Pro Glu Phe Trp Glu Lys Val Leu Pro Glu Val
 165 170 175
 Arg Arg Lys His Pro His Ala Trp Ile Val Gly Glu Met Ile His Gly
 180 185 190
 Asp Tyr Ser Asp Tyr Val Lys Ser Ser Gly Ile Asp Ser Val Thr Glu
 195 200 205
 Tyr Glu Leu Trp Lys Ala Ile Trp Ser Ser Ile Lys Glu Arg Asn Phe
 210 215 220
 Phe Glu Leu Glu Trp Thr Leu Ser Arg His Asn Glu Phe Leu Asp Thr
 225 230 235 240
 Phe Val Pro Gln Thr Phe Ile Gly Asn His Asp Val Thr Arg Ile Ala
 245 250 255
 Thr Arg Ile Gly Gln Ser Asn Ala Ile Leu Ala Ala Ala Ile Leu Phe
 260 265 270
 Thr Val Gly Gly Thr Pro Ser Ile Tyr Tyr Gly Asp Glu Gln Gly Phe
 275 280 285
 Thr Gly Leu Lys Glu Asp Asn Val Phe Gly Asp Asp Ala Ile Arg Pro
 290 295 300
 Pro Leu Pro Ala Glu Phe Ser Pro Leu Gly Thr Trp Ile Glu Asn Ile
 305 310 315 320
 Tyr Lys Ala Leu Ile Ala Leu Arg Arg Gln His Pro Trp Leu Tyr Gln
 325 330 335
 Ala His Thr Glu Val Leu Glu Ile Ala Asn Glu Ala Met Thr Tyr Lys
 340 345 350
 Ser Val Gly Leu Gly Gly Glu Glu Leu Thr Val His Leu Asp Leu Glu
 355 360 365
 Glu Val Ser Val Arg Ile Leu Asp Gly Glu Lys Val Leu Phe Gln Tyr
 370 375 380

Ser Ala
385

<210> 497
<211> 1281
<212> DNA
<213> Corynebacterium glutamicum

<220>
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<222> (101)..(1258)
<223> FRXA00038

<400> 497
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Met Ser Phe Ala Glu
1 5

cat gcg atc atc tgg cac gtc tac ccc ctg ggc gct ttg ggt gct ccc 163
His Ala Ile Ile Trp His Val Tyr Pro Leu Gly Ala Leu Gly Ala Pro
10 15 20

atc cgg cct gaa gcc ccc gca cct gtc aca cat cgg ctg ccc aat cta 211
Ile Arg Pro Glu Ala Pro Ala Pro Val Thr His Arg Leu Pro Asn Leu
25 30 35

att ggg tgg ctg gat tat gtt gtc gaa cta ggc tgc aac gcc ctg atg 259
Ile Gly Trp Leu Asp Tyr Val Val Glu Leu Gly Cys Asn Ala Leu Met
40 45 50

ctg gga ccg gta ttc gag tcc gtc agc cac ggc tac gac acc ctg gat 307
Leu Gly Pro Val Phe Glu Ser Val Ser His Gly Tyr Asp Thr Leu Asp
55 60 65

ttc tac cgc atc gac ccg cgc ctg ggc acc gag gaa gac atg gac gcg 355
Phe Tyr Arg Ile Asp Pro Arg Leu Gly Thr Glu Glu Asp Met Asp Ala
70 75 80 85

ctg ctg gag gct gcg aat cag cgg ggc att gga gtg ctt ttc gac ggc 403
Leu Leu Glu Ala Ala Asn Gln Arg Gly Ile Gly Val Leu Phe Asp Gly
90 95 100

gtc ttc aat cat gtt tcc agt tcc tct aaa tat ctg gac ctg acc acc 451
Val Phe Asn His Val Ser Ser Ser Ser Lys Tyr Leu Asp Leu Thr Thr
105 110 115

ggg gcg tca ttt gaa ggc cac gac atc ctg gcg gaa ctg gac cac acg 499
Gly Ala Ser Phe Glu Gly His Asp Ile Leu Ala Glu Leu Asp His Thr
120 125 130

aat ccc gcc gta gtg gat ctg gtt gtc gat gtc atg aac cac tgg ctg 547
Asn Pro Ala Val Val Asp Leu Val Val Asp Val Met Asn His Trp Leu
135 140 145

gac cgc gga atc gca ggc tgg cga ctg gac gct gtc tac gcc atc gcc 595
Asp Arg Gly Ile Ala Gly Trp Arg Leu Asp Ala Val Tyr Ala Ile Ala
150 155 160 165

cct gaa ttt tgg gaa aaa gtc ctg cca gaa gtg cga cga aaa cac cca 643
 Pro Glu Phe Trp Glu Lys Val Leu Pro Glu Val Arg Arg Lys His Pro
 170 175 180

cac gca tgg atc gtg ggg gag atg atc cat gga gat tac tcc gac tac 691
 His Ala Trp Ile Val Gly Glu Met Ile His Gly Asp Tyr Ser Asp Tyr
 185 190 195

gtg aaa agc tcc ggc att gat tcc gtt acc gaa tac gaa ctg tgg aaa 739
 Val Lys Ser Ser Gly Ile Asp Ser Val Thr Glu Tyr Glu Leu Trp Lys
 200 205 210

gcc att tgg agc agc atc aaa gag cgc aat ttc ttt gaa ctc gaa tgg 787
 Ala Ile Trp Ser Ser Ile Lys Glu Arg Asn Phe Phe Glu Leu Glu Trp
 215 220 225

act ttg agt cgc cac aat gaa ttc ctc gat act ttc gta ccg cag aca 835
 Thr Leu Ser Arg His Asn Glu Phe Leu Asp Thr Phe Val Pro Gln Thr
 230 235 240 245

ttc att ggt aac cat gac gtc acc cgc att gcc acc cga atc ggt caa 883
 Phe Ile Gly Asn His Asp Val Thr Arg Ile Ala Thr Arg Ile Gly Gln
 250 255 260

tca aat gcg atc ctg gcc gca gcg atc ctc ttc acg gtc gga gga acc 931
 Ser Asn Ala Ile Leu Ala Ala Ala Ile Leu Phe Thr Val Gly Gly Thr
 265 270 275

cca agc att tac tac ggc gat gag cag ggc ttt acg gga ttg aaa gag 979
 Pro Ser Ile Tyr Tyr Gly Asp Glu Gln Gly Phe Thr Gly Leu Lys Glu
 280 285 290

gat aac gtt ttc ggt gac gat gcc att agg cca cct ctt cct gcc gag 1027
 Asp Asn Val Phe Gly Asp Asp Ala Ile Arg Pro Pro Leu Pro Ala Glu
 295 300 305

ttt tct cca ctg ggc acc tgg att gaa aac att tat aag gct ctg atc 1075
 Phe Ser Pro Leu Gly Thr Trp Ile Glu Asn Ile Tyr Lys Ala Leu Ile
 310 315 320 325

gcg ctg cgc agg caa cac ccg tgg ttg tat cag gcg cac acc gaa gtc 1123
 Ala Leu Arg Arg Gln His Pro Trp Leu Tyr Gln Ala His Thr Glu Val
 330 335 340

ctt gag att gct aat gaa gcg atg acc tat aag tcc gtc ggt ctt gga 1171
 Leu Glu Ile Ala Asn Glu Ala Met Thr Tyr Lys Ser Val Gly Leu Gly
 345 350 355

ggt gaa gag ctg aca gtg cat ctt gat ttg gaa gag gtg tct gtt cgg 1219
 Gly Glu Glu Leu Thr Val His Leu Asp Leu Glu Glu Val Ser Val Arg
 360 365 370

atc ctt gat ggc gag aag gtg ctg ttt cag tac agc gct tagttgtcgg 1268
 Ile Leu Asp Gly Glu Lys Val Leu Phe Gln Tyr Ser Ala
 375 380 385

ttcaagggtgta ggg 1281

<210> 498

<211> 386

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 498

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Arg Leu Pro Asn Leu Ile Gly Trp Leu Asp Tyr Val Val Glu Leu Gly
      35           40           45

Cys Asn Ala Leu Met Leu Gly Pro Val Phe Glu Ser Val Ser His Gly
      50           55           60

Tyr Asp Thr Leu Asp Phe Tyr Arg Ile Asp Pro Arg Leu Gly Thr Glu
      65           70           75           80

Glu Asp Met Asp Ala Leu Leu Glu Ala Ala Asn Gln Arg Gly Ile Gly
      85           90           95

Val Leu Phe Asp Gly Val Phe Asn His Val Ser Ser Ser Ser Lys Tyr
      100          105          110

Leu Asp Leu Thr Thr Gly Ala Ser Phe Glu Gly His Asp Ile Leu Ala
      115          120          125

Glu Leu Asp His Thr Asn Pro Ala Val Val Asp Leu Val Val Asp Val
      130          135          140

Met Asn His Trp Leu Asp Arg Gly Ile Ala Gly Trp Arg Leu Asp Ala
      145          150          155          160

Val Tyr Ala Ile Ala Pro Glu Phe Trp Glu Lys Val Leu Pro Glu Val
      165          170          175

Arg Arg Lys His Pro His Ala Trp Ile Val Gly Glu Met Ile His Gly
      180          185          190

Asp Tyr Ser Asp Tyr Val Lys Ser Ser Gly Ile Asp Ser Val Thr Glu
      195          200          205

Tyr Glu Leu Trp Lys Ala Ile Trp Ser Ser Ile Lys Glu Arg Asn Phe
      210          215          220

Phe Glu Leu Glu Trp Thr Leu Ser Arg His Asn Glu Phe Leu Asp Thr
      225          230          235          240

Phe Val Pro Gln Thr Phe Ile Gly Asn His Asp Val Thr Arg Ile Ala
      245          250          255

Thr Arg Ile Gly Gln Ser Asn Ala Ile Leu Ala Ala Ala Ile Leu Phe
      260          265          270

Thr Val Gly Gly Thr Pro Ser Ile Tyr Tyr Gly Asp Glu Gln Gly Phe
      275          280          285

Thr Gly Leu Lys Glu Asp Asn Val Phe Gly Asp Asp Ala Ile Arg Pro
      290          295          300

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Pro Leu Pro Ala Glu Phe Ser Pro Leu Gly Thr Trp Ile Glu Asn Ile
 305 310 315 320

Tyr Lys Ala Leu Ile Ala Leu Arg Arg Gln His Pro Trp Leu Tyr Gln
 325 330 335

Ala His Thr Glu Val Leu Glu Ile Ala Asn Glu Ala Met Thr Tyr Lys
 340 345 350

Ser Val Gly Leu Gly Gly Glu Glu Leu Thr Val His Leu Asp Leu Glu
 355 360 365

Glu Val Ser Val Arg Ile Leu Asp Gly Glu Lys Val Leu Phe Gln Tyr
 370 375 380

Ser Ala
 385

<210> 499
 <211> 517
 <212> DNA
 <213> Corynebacterium glutamicum

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 <222> (101)..(517)
 <223> RXC00233

<400> 499
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aatagcgctt tagacacaga ctcattgacag aatagaagac atg agt gtg aat gaa 115
 Met Ser Val Asn Glu
 1 5

gca gat ctg aac gct gtc gaa gag caa ttg gga agg gcc cca cga ggt 163
 Ala Asp Leu Asn Ala Val Glu Glu Gln Leu Gly Arg Ala Pro Arg Gly
 10 15 20

gtc ctc gat att tct tac cgc agc cct gat gga gta ccc ggt gtg gtg 211
 Val Leu Asp Ile Ser Tyr Arg Ser Pro Asp Gly Val Pro Gly Val Val
 25 30 35

atg acc gca cca aaa ctg gat gac gga acc cca ttc cca acc ctg tac 259
 Met Thr Ala Pro Lys Leu Asp Asp Gly Thr Pro Phe Pro Thr Leu Tyr
 40 45 50

tac ttg aca gat cca cgc ctg acc acc gag gca tcc cgc ctc gag gtc 307
 Tyr Leu Thr Asp Pro Arg Leu Thr Thr Glu Ala Ser Arg Leu Glu Val
 55 60 65

gca ttg gta atg aag tgg atg act gat cgc ctt tcc acc gac gaa gag 355
 Ala Leu Val Met Lys Trp Met Thr Asp Arg Leu Ser Thr Asp Glu Glu
 70 75 80 85

ctt cgt gcc gac tac cag cgc gcc cac gag cac ttc ctg gca aag cgc 403
 Leu Arg Ala Asp Tyr Gln Arg Ala His Glu His Phe Leu Ala Lys Arg
 90 95 100

aac gca att gaa gat ctc ggc acg gat ttt tcc ggc ggt ggc atg cct 451

Asn Ala Ile Glu Asp Leu Gly Thr Asp Phe Ser Gly Gly Gly Met Pro
 105 110 115
 gac cga gtg aag tgc ctt cac gtc ctc att gac tat gca ctg gca gaa 499
 Asp Arg Val Lys Cys Leu His Val Leu Ile Asp Tyr Ala Leu Ala Glu
 120 125 130
 ggc cca cac cat ttc ctt 517
 Gly Pro His His Phe Leu
 135

<210> 500
 <211> 139
 <212> PRT
 <213> Corynebacterium glutamicum

<400> 500
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 20 25 30
 Val Pro Gly Val Val Met Thr Ala Pro Lys Leu Asp Asp Gly Thr Pro
 35 40 45
 Phe Pro Thr Leu Tyr Tyr Leu Thr Asp Pro Arg Leu Thr Thr Glu Ala
 50 55 60
 Ser Arg Leu Glu Val Ala Leu Val Met Lys Trp Met Thr Asp Arg Leu
 65 70 75 80
 Ser Thr Asp Glu Glu Leu Arg Ala Asp Tyr Gln Arg Ala His Glu His
 85 90 95
 Phe Leu Ala Lys Arg Asn Ala Ile Glu Asp Leu Gly Thr Asp Phe Ser
 100 105 110
 Gly Gly Gly Met Pro Asp Arg Val Lys Cys Leu His Val Leu Ile Asp
 115 120 125
 Tyr Ala Leu Ala Glu Gly Pro His His Phe Leu
 130 135

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 <211> 849
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(826)
 <223> RXC00236

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 Met Val Ile Ser Phe

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gtt gga tgg gcg ctc agc ttc atg gat gga acg gca cct att cgc caa	163															
Val Gly Trp Ala Leu Ser Phe Met Asp Gly Thr Ala Pro Ile Arg Gln																
	10 15 20															
ctc cag caa atc cct gaa gat gtt ccg ccg gcg cgt ggt gta gaa gtt	211															
Leu Gln Gln Ile Pro Glu Asp Val Pro Pro Ala Arg Gly Val Glu Val																
	25 30 35															
ccg caa att gat aca gag gca gat gga cgc aca tcc aac cat ttg cgt	259															
Pro Gln Ile Asp Thr Glu Ala Asp Gly Arg Thr Ser Asn His Leu Arg																
	40 45 50															
ttt tgg gcg gaa cca att gct caa gat act ggt gtg tcc gct caa gcg	307															
Phe Trp Ala Glu Pro Ile Ala Gln Asp Thr Gly Val Ser Ala Gln Ala																
	55 60 65															
att gcg gct tat gga aac gca gag ctc atc gcg agt act gcg tgg cct	355															
Ile Ala Ala Tyr Gly Asn Ala Glu Leu Ile Ala Ser Thr Ala Trp Pro																
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Gly Cys Asn Leu Gly Trp Asn Thr Leu Ala Gly Ile Gly Gln Val Glu																
	90 95 100															
acc cgt cac ggt acc tac aac ggc aaa atg ttc ggg ggc agt tcc ctg	451															
Thr Arg His Gly Thr Tyr Asn Gly Lys Met Phe Gly Gly Ser Ser Leu																
	105 110 115															
gat gaa aat gga gtt gca acc cct cca atc atc ggc gtt cca ctt gat	499															
Asp Glu Asn Gly Val Ala Thr Pro Pro Ile Ile Gly Val Pro Leu Asp																
	120 125 130															
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Gly Ser Pro Gly Phe Ala Ile Pro Asp Thr Asp Gly Gly Glu Leu																
	135 140 145															
gat ggc gat act gaa tat gat cgc gcg gta ggt ccc atg cag ttc att	595															
Asp Gly Asp Thr Glu Tyr Asp Arg Ala Val Gly Pro Met Gln Phe Ile																
	150 155 160 165															
ccg gaa acg tgg cga ctt atg gga ttg gat gca aac ggt gat ggg gta	643															
Pro Glu Thr Trp Arg Leu Met Gly Leu Asp Ala Asn Gly Asp Gly Val																
	170 175 180															
gcg gac ccc aac caa att gat gac gca gca ttg agt gcc gca aac ctg	691															
Ala Asp Pro Asn Gln Ile Asp Asp Ala Ala Leu Ser Ala Ala Asn Leu																
	185 190 195															
ttg tgt tcc aac gat cgt gac ttg tcc act cct gaa gga tgg acc gca	739															
Leu Cys Ser Asn Asp Arg Asp Leu Ser Thr Pro Glu Gly Trp Thr Ala																
	200 205 210															
gct gtt cat tct tac aac atg tct aat cag tat ttg atg gac gtt cga	787															
Ala Val His Ser Tyr Asn Met Ser Asn Gln Tyr Leu Met Asp Val Arg																
	215 220 225															
gat gct gcc gcg tcc tac gct tta cga cag ccg gcg atc taaaacttaa	836															
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849

<210> 502

<211> 242

<212> PRT

<213> Corynebacterium glutamicum

<400> 502

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 20 25 30

Arg Gly Val Glu Val Pro Gln Ile Asp Thr Glu Ala Asp Gly Arg Thr
 35 40 45

Ser Asn His Leu Arg Phe Trp Ala Glu Pro Ile Ala Gln Asp Thr Gly
 50 55 60

Val Ser Ala Gln Ala Ile Ala Ala Tyr Gly Asn Ala Glu Leu Ile Ala
 65 70 75 80

Ser Thr Ala Trp Pro Gly Cys Asn Leu Gly Trp Asn Thr Leu Ala Gly
 85 90 95

Ile Gly Gln Val Glu Thr Arg His Gly Thr Tyr Asn Gly Lys Met Phe
 100 105 110

Gly Gly Ser Ser Leu Asp Glu Asn Gly Val Ala Thr Pro Pro Ile Ile
 115 120 125

Gly Val Pro Leu Asp Gly Ser Pro Gly Phe Ala Glu Ile Pro Asp Thr
 130 135 140

Asp Gly Gly Glu Leu Asp Gly Asp Thr Glu Tyr Asp Arg Ala Val Gly
 145 150 155 160

Pro Met Gln Phe Ile Pro Glu Thr Trp Arg Leu Met Gly Leu Asp Ala
 165 170 175

Asn Gly Asp Gly Val Ala Asp Pro Asn Gln Ile Asp Asp Ala Ala Leu
 180 185 190

Ser Ala Ala Asn Leu Leu Cys Ser Asn Asp Arg Asp Leu Ser Thr Pro
 195 200 205

Glu Gly Trp Thr Ala Ala Val His Ser Tyr Asn Met Ser Asn Gln Tyr
 210 215 220

Leu Met Asp Val Arg Asp Ala Ala Ala Ser Tyr Ala Leu Arg Gln Pro
 225 230 235 240

Ala Ile

<210> 503

<211> 1113

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(1090)

<223> RXC00271

<400> 503

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                                   Met Phe Ser Ser Arg
                                   1 5

tcg aag gta ctc gca agc atc ttt act gtt ggc gcc ttg gcg ttg gct 163
Ser Lys Val Leu Ala Ser Ile Phe Thr Val Gly Ala Leu Ala Leu Ala
          10                      15                      20

tcg tgc tca agc gat tcc agt gac agc tcc acc tcc act gat gct gca 211
Ser Cys Ser Ser Ser Asp Ser Ser Asp Ser Ser Thr Ser Thr Asp Ala Ala
          25                      30                      35

ggg ggc gac tct tac cga gtt ggc atc aac cag ctt gtt cag cac cct 259
Gly Gly Asp Ser Tyr Arg Val Gly Ile Asn Gln Leu Val Gln His Pro
          40                      45                      50

gca ctt gat gca gcg acc act ggt ttc aag gaa gct ttt gaa gag gca 307
Ala Leu Asp Ala Ala Thr Thr Gly Phe Lys Glu Ala Phe Glu Glu Ala
          55                      60                      65

ggc gtt gac gtc acc ttt gat gag caa aac gct aac ggc gag cag ggc 355
Gly Val Asp Val Thr Phe Asp Glu Gln Asn Ala Asn Gly Glu Gln Gly
          70                      75                      80                      85

act gca ctg act att tct cag cag ttc gct tct gac aat ttg gat ctc 403
Thr Ala Leu Thr Ile Ser Gln Gln Phe Ala Ser Asp Asn Leu Asp Leu
          90                      95                      100

gtg ttg gct gtt gca act cca gca gca cag gca act gcg cag aat atc 451
Val Leu Ala Val Ala Thr Pro Ala Ala Gln Ala Thr Ala Gln Asn Ile
          105                      110                      115

act gat atc cca gtc ctg ttc acc gca gtt acc gat gca gtg tcg gca 499
Thr Asp Ile Pro Val Leu Phe Thr Ala Val Thr Asp Ala Val Ser Ala
          120                      125                      130

gag ctg gtg gat tct aat gaa gca cct ggc gga aac gtc acc ggt act 547
Glu Leu Val Asp Ser Asn Glu Ala Pro Gly Gly Asn Val Thr Gly Thr
          135                      140                      145

tct gat atc gca ccg att gag cag cag ttg gag ctt ttg cag cag ctg 595
Ser Asp Ile Ala Pro Ile Glu Gln Gln Leu Glu Leu Leu Gln Gln Leu
          150                      155                      160                      165

gtt cct gac gca aag tcc atc ggc atc gtc tac gcg tct ggt gag gtc 643
Val Pro Asp Ala Lys Ser Ile Gly Ile Val Tyr Ala Ser Gly Glu Val
          170                      175                      180

aac tct cag gtg cag gtc gat gag gtc acc aag gct gct gag cca ctg 691
Asn Ser Gln Val Gln Val Asp Glu Val Thr Lys Ala Ala Glu Pro Leu

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Gly Leu Ser Val Asn Thr Gln Thr Val Thr Thr Val Asn Glu Ile Gln			
200	205	210	
cag gct gtt gaa gct ctc ggc gat gtt gat gtc atc tac gtt cca act	787		
Gln Ala Val Glu Ala Leu Gly Asp Val Asp Val Ile Tyr Val Pro Thr			
215	220	225	
gac aac atg gtt gtt tcc ggt att tct tct ctg gtt cag gtt gct gag	835		
Asp Asn Met Val Val Ser Gly Ile Ser Ser Leu Val Gln Val Ala Glu			
230	235	240	245
cag aag cag atc cct gtg atc ggc gct gag tcc ggc act gtt gag ggt	883		
Gln Lys Gln Ile Pro Val Ile Gly Ala Glu Ser Gly Thr Val Glu Gly			
250	255	260	
ggc gca ctg gca acc ctg ggt atc gat tac acc gag ctt ggc cgc cag	931		
Gly Ala Leu Ala Thr Leu Gly Ile Asp Tyr Thr Glu Leu Gly Arg Gln			
265	270	275	
act ggt gag atg gct ctg cgt att ctg cag gac ggc gaa gac cca gca	979		
Thr Gly Glu Met Ala Leu Arg Ile Leu Gln Asp Gly Glu Asp Pro Ala			
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acc atg cct gtg gag act gca act gag ttc acc tac gtg atc aac gaa	1027		
Thr Met Pro Val Glu Thr Ala Thr Glu Phe Thr Tyr Val Ile Asn Glu			
295	300	305	
gat gca gca gag cgc cag ggc gtg gag atc cct caa gag att ttg gat	1075		
Asp Ala Ala Glu Arg Gln Gly Val Glu Ile Pro Gln Glu Ile Leu Asp			
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Lys Ala Glu Arg Val			
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<211> 330

<212> PRT

<213> Corynebacterium glutamicum

<400> 504

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20 25 30	
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35 40 45	
Leu Val Gln His Pro Ala Leu Asp Ala Ala Thr Thr Gly Phe Lys Glu	
50 55 60	
Ala Phe Glu Glu Ala Gly Val Asp Val Thr Phe Asp Glu Gln Asn Ala	
65 70 75 80	
Asn Gly Glu Gln Gly Thr Ala Leu Thr Ile Ser Gln Gln Phe Ala Ser	

85										90					95				
Asp	Asn	Leu	Asp	Leu	Val	Leu	Ala	Val	Ala	Thr	Pro	Ala	Ala	Gln	Ala				
			100						105					110					
Thr	Ala	Gln	Asn	Ile	Thr	Asp	Ile	Pro	Val	Leu	Phe	Thr	Ala	Val	Thr				
		115					120					125							
Asp	Ala	Val	Ser	Ala	Glu	Leu	Val	Asp	Ser	Asn	Glu	Ala	Pro	Gly	Gly				
		130				135					140								
Asn	Val	Thr	Gly	Thr	Ser	Asp	Ile	Ala	Pro	Ile	Glu	Gln	Gln	Leu	Glu				
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Leu	Leu	Gln	Gln	Leu	Val	Pro	Asp	Ala	Lys	Ser	Ile	Gly	Ile	Val	Tyr				
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Ala	Ser	Gly	Glu	Val	Asn	Ser	Gln	Val	Gln	Val	Asp	Glu	Val	Thr	Lys				
			180					185						190					
Ala	Ala	Glu	Pro	Leu	Gly	Leu	Ser	Val	Asn	Thr	Gln	Thr	Val	Thr	Thr				
		195					200						205						
Val	Asn	Glu	Ile	Gln	Gln	Ala	Val	Glu	Ala	Leu	Gly	Asp	Val	Asp	Val				
		210				215					220								
Ile	Tyr	Val	Pro	Thr	Asp	Asn	Met	Val	Val	Ser	Gly	Ile	Ser	Ser	Leu				
225					230					235					240				
Val	Gln	Val	Ala	Glu	Gln	Lys	Gln	Ile	Pro	Val	Ile	Gly	Ala	Glu	Ser				
				245					250					255					
Gly	Thr	Val	Glu	Gly	Gly	Ala	Leu	Ala	Thr	Leu	Gly	Ile	Asp	Tyr	Thr				
		260					265						270						
Glu	Leu	Gly	Arg	Gln	Thr	Gly	Glu	Met	Ala	Leu	Arg	Ile	Leu	Gln	Asp				
		275					280					285							
Gly	Glu	Asp	Pro	Ala	Thr	Met	Pro	Val	Glu	Thr	Ala	Thr	Glu	Phe	Thr				
		290				295					300								
Tyr	Val	Ile	Asn	Glu	Asp	Ala	Ala	Glu	Arg	Gln	Gly	Val	Glu	Ile	Pro				
305					310					315					320				
Gln	Glu	Ile	Leu	Asp	Lys	Ala	Glu	Arg	Val										
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<212> DNA

<213> Corynebacterium glutamicum

<220>

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<222> (101)..(1240)

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							Val	Ser	Asp	Val	Thr					
							1				5					
gtt	ggc	gat	att	cgc	cgc	att	ttg	gat	gag	gct	tat	ccg	ccg	gcg	ttg	163
Val	Gly	Asp	Ile	Arg	Arg	Ile	Leu	Asp	Glu	Ala	Tyr	Pro	Pro	Ala	Leu	
				10					15					20		
gcg	gaa	agc	tgg	gac	aaa	gtg	ggg	ctg	atc	tgc	ggg	gat	cca	aca	gag	211
Ala	Glu	Ser	Trp	Asp	Lys	Val	Gly	Leu	Ile	Cys	Gly	Asp	Pro	Thr	Glu	
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tcg	gtg	aag	cgt	gtc	ggg	tta	gca	ctc	gat	tgc	acc	cag	gca	gtg	gcc	259
Ser	Val	Lys	Arg	Val	Gly	Leu	Ala	Leu	Asp	Cys	Thr	Gln	Ala	Val	Ala	
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gac	aag	gct	gtg	gac	atg	ggg	ttg	gac	atg	ctg	atc	att	cac	cac	cca	307
Asp	Lys	Ala	Val	Asp	Met	Gly	Leu	Asp	Met	Leu	Ile	Ile	His	His	Pro	
	55					60					65					
ttg	ctg	ctg	cgt	ggg	gtg	acg	tct	gtt	gct	gcg	gat	gag	cca	aaa	ggc	355
Leu	Leu	Leu	Arg	Gly	Val	Thr	Ser	Val	Ala	Ala	Asp	Glu	Pro	Lys	Gly	
70					75					80					85	
aag	gtc	att	cac	acc	cta	att	cgc	ggc	ggg	gtg	gca	ctg	ttt	tcc	gcg	403
Lys	Val	Ile	His	Thr	Leu	Ile	Arg	Gly	Gly	Val	Ala	Leu	Phe	Ser	Ala	
				90					95					100		
cac	act	aat	gcg	gat	tcc	gcg	cgc	cca	ggg	gtc	aac	gat	aaa	ctc	gcc	451
His	Thr	Asn	Ala	Asp	Ser	Ala	Arg	Pro	Gly	Val	Asn	Asp	Lys	Leu	Ala	
			105					110					115			
gag	ctc	gtc	ggc	atc	acg	gcc	ggg	cga	ccc	atc	gcg	aca	cgg	ctt	tta	499
Glu	Leu	Val	Gly	Ile	Thr	Ala	Gly	Arg	Pro	Ile	Ala	Thr	Arg	Leu	Leu	
		120					125					130				
ggc	ggc	atg	gac	aaa	tgg	ggc	gtg	cac	gtt	ctg	ccc	aag	gat	gca	gcg	547
Gly	Gly	Met	Asp	Lys	Trp	Gly	Val	His	Val	Leu	Pro	Lys	Asp	Ala	Ala	
	135					140					145					
tac	cta	aag	aag	atg	ctt	ttc	gac	gca	ggg	gac	ggt	gcg	atc	ggc	gac	595
Tyr	Leu	Lys	Lys	Met	Leu	Phe	Asp	Ala	Gly	Ala	Gly	Ala	Ile	Gly	Asp	
150					155					160				165		
tac	cga	gag	tgt	gcc	ttt	gag	atc	gaa	gga	acc	ggg	cag	ttt	agg	ccc	643
Tyr	Arg	Glu	Cys	Ala	Phe	Glu	Ile	Glu	Gly	Thr	Gly	Gln	Phe	Arg	Pro	
				170					175					180		
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Val	Glu	Gly	Ala	Asn	Pro	Ala	Glu	Gly	Asp	Val	Asp	Lys	Leu	Phe	Lys	
			185					190					195			
tcc	ctt	gag	ctg	cgc	atc	gag	ttt	gtt	gca	ccg	cgc	aac	ctg	cgc	gcc	739
Ser	Leu	Glu	Leu	Arg	Ile	Glu	Phe	Val	Ala	Pro	Arg	Asn	Leu	Arg	Ala	
		200					205					210				
cgg	ctc	acg	tgc	gtg	ctg	cgg	gag	gct	cat	ccg	tat	gag	gag	cct	gcc	787
Arg	Leu	Thr	Ser	Val	Leu	Arg	Glu	Ala	His	Pro	Tyr	Glu	Glu	Pro	Ala	
	215					220				225						
ttc	gat	att	gtt	gaa	atg	cac	agc	gct	gag	agt	tta	gaa	aat	gcg	acc	835

Phe Asp Ile Val Glu Met His Ser Ala Glu Ser Leu Glu Asn Ala Thr
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 gga ttg ggt cgt gtg ggt gaa ttg ccg gag ccg atg cgc ctc gcg gat 883
 Gly Leu Gly Arg Val Gly Glu Leu Pro Glu Pro Met Arg Leu Ala Asp
 250 255 260
 ttc gtg caa caa gtg gcc aac aac ctg cct gtc acc gaa tgg ggc gtg 931
 Phe Val Gln Gln Val Ala Asn Asn Leu Pro Val Thr Glu Trp Gly Val
 265 270 275
 cgc gct acc ggc gat cct gaa caa atg gtg tcc cgt gtg gcg gtt tca 979
 Arg Ala Thr Gly Asp Pro Glu Gln Met Val Ser Arg Val Ala Val Ser
 280 285 290
 tca ggg tcg ggt gac agt ttc tta aac gat gtg att aag ctc gga gtg 1027
 Ser Gly Ser Gly Asp Ser Phe Leu Asn Asp Val Ile Lys Leu Gly Val
 295 300 305
 gac gtt tat gtc act tct gat ctg cgc cac cat cca gtt gat gaa tat 1075
 Asp Val Tyr Val Thr Ser Asp Leu Arg His His Pro Val Asp Glu Tyr
 310 315 320 325
 ctc cga gaa ggt ggc cct gca gta atc gat act gca cac tgg gcc agc 1123
 Leu Arg Glu Gly Gly Pro Ala Val Ile Asp Thr Ala His Trp Ala Ser
 330 335 340
 gaa ttt cca tgg act tcc caa gcc caa gaa att ttg cag gac aaa gcc 1171
 Glu Phe Pro Trp Thr Ser Gln Ala Gln Glu Ile Leu Gln Asp Lys Ala
 345 350 355
 cca cag gtt gaa gtt gat gtg att tcg atc cgc aca gac ccc tgg acc 1219
 Pro Gln Val Glu Val Asp Val Ile Ser Ile Arg Thr Asp Pro Trp Thr
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<212> PRT

<213> Corynebacterium glutamicum

<400> 506

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 20 25 30

Gly Asp Pro Thr Glu Ser Val Lys Arg Val Gly Leu Ala Leu Asp Cys
 35 40 45

Thr Gln Ala Val Ala Asp Lys Ala Val Asp Met Gly Leu Asp Met Leu
 50 55 60

Ile Ile His His Pro Leu Leu Arg Gly Val Thr Ser Val Ala Ala
 65 70 75 80

Asp Glu Pro Lys Gly Lys Val Ile His Thr Leu Ile Arg Gly Gly Val
 85 90 95
 Ala Leu Phe Ser Ala His Thr Asn Ala Asp Ser Ala Arg Pro Gly Val
 100 105 110
 Asn Asp Lys Leu Ala Glu Leu Val Gly Ile Thr Ala Gly Arg Pro Ile
 115 120 125
 Ala Thr Arg Leu Leu Gly Gly Met Asp Lys Trp Gly Val His Val Leu
 130 135 140
 Pro Lys Asp Ala Ala Tyr Leu Lys Lys Met Leu Phe Asp Ala Gly Ala
 145 150 155 160
 Gly Ala Ile Gly Asp Tyr Arg Glu Cys Ala Phe Glu Ile Glu Gly Thr
 165 170 175
 Gly Gln Phe Arg Pro Val Glu Gly Ala Asn Pro Ala Glu Gly Asp Val
 180 185 190
 Asp Lys Leu Phe Lys Ser Leu Glu Leu Arg Ile Glu Phe Val Ala Pro
 195 200 205
 Arg Asn Leu Arg Ala Arg Leu Thr Ser Val Leu Arg Glu Ala His Pro
 210 215 220
 Tyr Glu Glu Pro Ala Phe Asp Ile Val Glu Met His Ser Ala Glu Ser
 225 230 235 240
 Leu Glu Asn Ala Thr Gly Leu Gly Arg Val Gly Glu Leu Pro Glu Pro
 245 250 255
 Met Arg Leu Ala Asp Phe Val Gln Gln Val Ala Asn Asn Leu Pro Val
 260 265 270
 Thr Glu Trp Gly Val Arg Ala Thr Gly Asp Pro Glu Gln Met Val Ser
 275 280 285
 Arg Val Ala Val Ser Ser Gly Ser Gly Asp Ser Phe Leu Asn Asp Val
 290 295 300
 Ile Lys Leu Gly Val Asp Val Tyr Val Thr Ser Asp Leu Arg His His
 305 310 315 320
 Pro Val Asp Glu Tyr Leu Arg Glu Gly Gly Pro Ala Val Ile Asp Thr
 325 330 335
 Ala His Trp Ala Ser Glu Phe Pro Trp Thr Ser Gln Ala Gln Glu Ile
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<211> 1470

<212> DNA

<213> Corynebacterium glutamicum

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<222> (101)..(1447)

<223> RXC00362

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 Met Gly Ile Ile Ala
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ctg ctc gtt ttt atc gca att gcc gtg ata ttg aat gtg ttt ttg aaa 163
 Leu Leu Val Phe Ile Ala Ile Ala Val Ile Leu Asn Val Phe Leu Lys
 10 15 20

cga gat att tca gaa gca ttg cta gtt gga tta gta gga act gcg ctt 211
 Arg Asp Ile Ser Glu Ala Leu Leu Val Gly Leu Val Gly Thr Ala Leu
 25 30 35

gtc ggc ggt gta aat gca ccg aca tta ctg att gat gct gta gtg gat 259
 Val Gly Gly Val Asn Ala Pro Thr Leu Leu Ile Asp Ala Val Val Asp
 40 45 50

gct gct cag tcg gaa gtt act ttc gca ggt atg gcc ttt gtt ttc atg 307
 Ala Ala Gln Ser Glu Val Thr Phe Ala Gly Met Ala Phe Val Phe Met
 55 60 65

ggc atc gtt gtg caa tca act gga ttg att gat cga tta atc gca atc 355
 Gly Ile Val Val Gln Ser Thr Gly Leu Ile Asp Arg Leu Ile Ala Ile
 70 75 80 85

ctt aac tcg att ttt ggt cgg ctt cga ggt ggc gca ggt tat gtt tcc 403
 Leu Asn Ser Ile Phe Gly Arg Leu Arg Gly Gly Ala Gly Tyr Val Ser
 90 95 100

act ctt gga tct gcg ctc att gga ctc atc gct gga tca acg gct gga 451
 Thr Leu Gly Ser Ala Leu Ile Gly Leu Ile Ala Gly Ser Thr Ala Gly
 105 110 115

aac tcc gcg acg gtt ggc tca gtg acg atc cct tgg atg aaa aag acg 499
 Asn Ser Ala Thr Val Gly Ser Val Thr Ile Pro Trp Met Lys Lys Thr
 120 125 130

gga tgg act gct gaa agg tcc gca acg tta gtc gcg ggc aac tct ggc 547
 Gly Trp Thr Ala Glu Arg Ser Ala Thr Leu Val Ala Gly Asn Ser Gly
 135 140 145

ctt ggt gtt gcg ttg cct ccc aat tca aca atg ttc atc att ttg gca 595
 Leu Gly Val Ala Leu Pro Pro Asn Ser Thr Met Phe Ile Ile Leu Ala
 150 155 160 165

ttg cca gct gca gca gct tct tcg gcc tct cag gtg tac att gct ttg 643
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 170 175 180

gct tgt ggt ggt gcg tat gca gtg ctc tac cgc tta gcg gtc gtc ttt 691
 Ala Cys Gly Gly Ala Tyr Ala Val Leu Tyr Arg Leu Ala Val Val Phe
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Val Ser Phe Gly Glu Ala Met Lys Thr Gly Trp Arg Ser Pro Leu Ile	
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ttc ctt gga att ttg atc ccc gta atc ctc aca atc ggc cca ttg tct	835
Phe Leu Gly Ile Leu Ile Pro Val Ile Leu Thr Ile Gly Pro Leu Ser	
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gaa tgg tta aag aca cat gga gtt ggg gag tct ggt gtt aaa tcg atg	883
Glu Trp Leu Lys Thr His Gly Val Gly Glu Ser Gly Val Lys Ser Met	
250 255 260	
tcg atc atc gtg tgg gtg cca att ctg att acg gca att gct ctg att	931
Ser Ile Ile Val Trp Val Pro Ile Leu Ile Thr Ala Ile Ala Leu Ile	
265 270 275	
gaa ggg cgt aaa cga att gct aac aac atg gca cac ttt agg gtt cag	979
Glu Gly Arg Lys Arg Ile Ala Asn Asn Met Ala His Phe Arg Val Gln	
280 285 290	
atc tcc aag gac ttg cca caa ttt gcc acc gta gga att tcg ttg ttt	1027
Ile Ser Lys Asp Leu Pro Gln Phe Ala Thr Val Gly Ile Ser Leu Phe	
295 300 305	
tct gcg ctt gca gca gcg aac atc atg gaa gaa ctg ggt gtt ggc ccg	1075
Ser Ala Leu Ala Ala Ala Asn Ile Met Glu Glu Leu Gly Val Gly Pro	
310 315 320 325	
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Gln Leu Ser Asn Trp Leu Asp Ser Met Asp Leu Pro Lys Ser Val Met	
330 335 340	
gtg atc att gtc tgc atc atg tgc att gtg gtg gca acg cca ctg tcg	1171
Val Ile Ile Val Cys Ile Met Cys Ile Val Val Ala Thr Pro Leu Ser	
345 350 355	
tca aca gca acc gcg gct gcg att ggt gct ccc gct gtc gct gcg ttg	1219
Ser Thr Ala Thr Ala Ala Ala Ile Gly Ala Pro Ala Val Ala Ala Leu	
360 365 370	
gct gcg gta ggt att gat cca act gtg gcg atc gta gtg atc ttg ctg	1267
Ala Ala Val Gly Ile Asp Pro Thr Val Ala Ile Val Val Ile Leu Leu	
375 380 385	
tgc act tcc act gaa ggt gca tcc ccg ccg gtg ggc gcg ccg att tac	1315
Cys Thr Ser Thr Glu Gly Ala Ser Pro Pro Val Gly Ala Pro Ile Tyr	
390 395 400 405	
ctt tct gct gcg atc gcc gat gca aac cca acg aaa atg ttc gta cca	1363
Leu Ser Ala Ala Ile Ala Asp Ala Asn Pro Thr Lys Met Phe Val Pro	
410 415 420	
ctg att acg tac ttt gtt gtc ccc atg att ctg ctt gct tgg cta gtt	1411
Leu Ile Thr Tyr Phe Val Val Pro Met Ile Leu Leu Ala Trp Leu Val	
425 430 435	

gga atg gga ttc tta cca gtg att gtt cct acg ggt taaaggggta 1457
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<211> 449

<212> PRT

<213> Corynebacterium glutamicum

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Val Gly Thr Ala Leu Val Gly Gly Val Asn Ala Pro Thr Leu Leu Ile
 35 40 45

Asp Ala Val Val Asp Ala Ala Gln Ser Glu Val Thr Phe Ala Gly Met
 50 55 60

Ala Phe Val Phe Met Gly Ile Val Val Gln Ser Thr Gly Leu Ile Asp
 65 70 75 80

Arg Leu Ile Ala Ile Leu Asn Ser Ile Phe Gly Arg Leu Arg Gly Gly
 85 90 95

Ala Gly Tyr Val Ser Thr Leu Gly Ser Ala Leu Ile Gly Leu Ile Ala
 100 105 110

Gly Ser Thr Ala Gly Asn Ser Ala Thr Val Gly Ser Val Thr Ile Pro
 115 120 125

Trp Met Lys Lys Thr Gly Trp Thr Ala Glu Arg Ser Ala Thr Leu Val
 130 135 140

Ala Gly Asn Ser Gly Leu Gly Val Ala Leu Pro Pro Asn Ser Thr Met
 145 150 155 160

Phe Ile Ile Leu Ala Leu Pro Ala Ala Ala Ala Ser Ser Ala Ser Gln
 165 170 175

Val Tyr Ile Ala Leu Ala Cys Gly Gly Ala Tyr Ala Val Leu Tyr Arg
 180 185 190

Leu Ala Val Val Phe Tyr Trp Thr Arg Lys Asp Lys Ile Pro Ala Thr
 195 200 205

Pro Asp Asp Gln Arg Val Ser Phe Gly Glu Ala Met Lys Thr Gly Trp
 210 215 220

Arg Ser Pro Leu Ile Phe Leu Gly Ile Leu Ile Pro Val Ile Leu Thr
 225 230 235 240

Ile Gly Pro Leu Ser Glu Trp Leu Lys Thr His Gly Val Gly Glu Ser
 245 250 255

Gly Val Lys Ser Met Ser Ile Ile Val Trp Val Pro Ile Leu Ile Thr
 260 265 270
 Ala Ile Ala Leu Ile Glu Gly Arg Lys Arg Ile Ala Asn Asn Met Ala
 275 280 285
 His Phe Arg Val Gln Ile Ser Lys Asp Leu Pro Gln Phe Ala Thr Val
 290 295 300
 Gly Ile Ser Leu Phe Ser Ala Leu Ala Ala Ala Asn Ile Met Glu Glu
 305 310 315 320
 Leu Gly Val Gly Pro Gln Leu Ser Asn Trp Leu Asp Ser Met Asp Leu
 325 330 335
 Pro Lys Ser Val Met Val Ile Ile Val Cys Ile Met Cys Ile Val Val
 340 345 350
 Ala Thr Pro Leu Ser Ser Thr Ala Thr Ala Ala Ala Ile Gly Ala Pro
 355 360 365
 Ala Val Ala Ala Leu Ala Ala Val Gly Ile Asp Pro Thr Val Ala Ile
 370 375 380
 Val Val Ile Leu Leu Cys Thr Ser Thr Glu Gly Ala Ser Pro Pro Val
 385 390 395 400
 Gly Ala Pro Ile Tyr Leu Ser Ala Ala Ile Ala Asp Ala Asn Pro Thr
 405 410 415
 Lys Met Phe Val Pro Leu Ile Thr Tyr Phe Val Val Pro Met Ile Leu
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 Leu Ala Trp Leu Val Gly Met Gly Phe Leu Pro Val Ile Val Pro Thr
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Gly

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<212> DNA

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<222> (101)..(1180)

<223> RXC00412

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 Val Ser His Thr Ala
 1 5

tcc aca ccg acg cca gag gaa tac tcc gcg cag caa ccc agc acc cag 163
 Ser Thr Pro Thr Glu Glu Tyr Ser Ala Gln Gln Pro Ser Thr Gln
 10 15 20

ggc act cgc gtt gag ttc cgc ggc ata acc aaa gtc ttt agc aac aat	211
Gly Thr Arg Val Glu Phe Arg Gly Ile Thr Lys Val Phe Ser Asn Asn	
25 30 35	
aaa tct gct aaa acc acc gcg ctt gat aat gtc act ctc acc gta gaa	259
Lys Ser Ala Lys Thr Thr Ala Leu Asp Asn Val Thr Leu Thr Val Glu	
40 45 50	
ccc ggt gag gta atc ggc atc atc ggt tac tct ggc gcc ggc aag tcc	307
Pro Gly Glu Val Ile Gly Ile Ile Gly Tyr Ser Gly Ala Gly Lys Ser	
55 60 65	
act ctt gtc cgc ctc atc aat ggc ctt gac tcc ccc acg agc ggt tcg	355
Thr Leu Val Arg Leu Ile Asn Gly Leu Asp Ser Pro Thr Ser Gly Ser	
70 75 80 85	
ttg ctg ctc aac ggc acc gac atc gtc gga atg ccc gag tct aag ctg	403
Leu Leu Leu Asn Gly Thr Asp Ile Val Gly Met Pro Glu Ser Lys Leu	
90 95 100	
cgt aaa ctg cgc agt aat atc ggc atg att ttc cag cag ttc aac ctg	451
Arg Lys Leu Arg Ser Asn Ile Gly Met Ile Phe Gln Gln Phe Asn Leu	
105 110 115	
ttc cag tcg cgt act gcg gct gga aat gtg gag tac ccg ctg gaa gtt	499
Phe Gln Ser Arg Thr Ala Ala Gly Asn Val Glu Tyr Pro Leu Glu Val	
120 125 130	
gcc aag atg gac aag gca gct cgt aaa gct cgc gtg caa gaa atg ctc	547
Ala Lys Met Asp Lys Ala Ala Arg Lys Ala Arg Val Gln Glu Met Leu	
135 140 145	
gag ttc gtc ggc ctg ggc gac aaa ggc aaa aac tac ccc gag cag ctg	595
Glu Phe Val Gly Leu Gly Asp Lys Gly Lys Asn Tyr Pro Glu Gln Leu	
150 155 160 165	
tcg ggc ggc cag aag cag cgc gtc ggc att gcc cgt gca ctg gcc acc	643
Ser Gly Gly Gln Lys Gln Arg Val Gly Ile Ala Arg Ala Leu Ala Thr	
170 175 180	
aat cca acg ctt ttg ctt gcc gac gaa gcc acc tcc gct ttg gac cca	691
Asn Pro Thr Leu Leu Leu Ala Asp Glu Ala Thr Ser Ala Leu Asp Pro	
185 190 195	
gaa acc acc cat gaa gtt ctg gag ctg ctg cgc aag gta aac cgc gaa	739
Glu Thr Thr His Glu Val Leu Glu Leu Leu Arg Lys Val Asn Arg Glu	
200 205 210	
ctg ggc atc acc atc gtt gtg atc acc cac gaa atg gaa gtt gtg cgt	787
Leu Gly Ile Thr Ile Val Val Ile Thr His Glu Met Glu Val Val Arg	
215 220 225	
tcc atc gca gac aag gtt gct gtg atg gaa tcc ggc aaa gtt gtg gaa	835
Ser Ile Ala Asp Lys Val Ala Val Met Glu Ser Gly Lys Val Val Glu	
230 235 240 245	
tac ggc agc gtc tac gag gtg ttc tcc aat cca caa aca cag gtt gct	883
Tyr Gly Ser Val Tyr Glu Val Phe Ser Asn Pro Gln Thr Gln Val Ala	
250 255 260	
caa aag ttc gtg gcc acc gcg ctg cgt aac acc cca gac caa gtg gaa	931

Gln Lys Phe Val Ala Thr Ala Leu Arg Asn Thr Pro Asp Gln Val Glu
 265 270 275

tcg gaa gat ctg ctt agc cat gag gga cgt ctg ttc acc att gat ctg 979
 Ser Glu Asp Leu Leu Ser His Glu Gly Arg Leu Phe Thr Ile Asp Leu
 280 285 290

act gaa acg tcc ggc ttc ttt gca gca acc gct cgt gct gcc gaa caa 1027
 Thr Glu Thr Ser Gly Phe Phe Ala Ala Thr Ala Arg Ala Ala Glu Gln
 295 300 305

ggt gct ttt gtc aac atc gtt cac ggt ggc gtg acc acc ttg caa cgc 1075
 Gly Ala Phe Val Asn Ile Val His Gly Gly Val Thr Thr Leu Gln Arg
 310 315 320 325

caa tca ttt ggc aaa atg act gtt cga ctc acc ggc aac acc gct gcg 1123
 Gln Ser Phe Gly Lys Met Thr Val Arg Leu Thr Gly Asn Thr Ala Ala
 330 335 340

att gaa gag ttc tat caa acc ttg acc aag acc acg acc atc aag gag 1171
 Ile Glu Glu Phe Tyr Gln Thr Leu Thr Lys Thr Thr Thr Ile Lys Glu
 345 350 355

atc acc cga tgaacgagat gatcctcgca gct 1203
 Ile Thr Arg
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<210> 510

<211> 360

<212> PRT

<213> Corynebacterium glutamicum

<400> 510

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Val Phe Ser Asn Asn Lys Ser Ala Lys Thr Thr Ala Leu Asp Asn Val
 35 40 45

Thr Leu Thr Val Glu Pro Gly Glu Val Ile Gly Ile Ile Gly Tyr Ser
 50 55 60

Gly Ala Gly Lys Ser Thr Leu Val Arg Leu Ile Asn Gly Leu Asp Ser
 65 70 75 80

Pro Thr Ser Gly Ser Leu Leu Leu Asn Gly Thr Asp Ile Val Gly Met
 85 90 95

Pro Glu Ser Lys Leu Arg Lys Leu Arg Ser Asn Ile Gly Met Ile Phe
 100 105 110

Gln Gln Phe Asn Leu Phe Gln Ser Arg Thr Ala Ala Gly Asn Val Glu
 115 120 125

Tyr Pro Leu Glu Val Ala Lys Met Asp Lys Ala Ala Arg Lys Ala Arg
 130 135 140

Val Gln Glu Met Leu Glu Phe Val Gly Leu Gly Asp Lys Gly Lys Asn
 145 150 155 160
 Tyr Pro Glu Gln Leu Ser Gly Gly Gln Lys Gln Arg Val Gly Ile Ala
 165 170 175
 Arg Ala Leu Ala Thr Asn Pro Thr Leu Leu Leu Ala Asp Glu Ala Thr
 180 185 190
 Ser Ala Leu Asp Pro Glu Thr Thr His Glu Val Leu Glu Leu Leu Arg
 195 200 205
 Lys Val Asn Arg Glu Leu Gly Ile Thr Ile Val Val Ile Thr His Glu
 210 215 220
 Met Glu Val Val Arg Ser Ile Ala Asp Lys Val Ala Val Met Glu Ser
 225 230 235 240
 Gly Lys Val Val Glu Tyr Gly Ser Val Tyr Glu Val Phe Ser Asn Pro
 245 250 255
 Gln Thr Gln Val Ala Gln Lys Phe Val Ala Thr Ala Leu Arg Asn Thr
 260 265 270
 Pro Asp Gln Val Glu Ser Glu Asp Leu Leu Ser His Glu Gly Arg Leu
 275 280 285
 Phe Thr Ile Asp Leu Thr Glu Thr Ser Gly Phe Phe Ala Ala Thr Ala
 290 295 300
 Arg Ala Ala Glu Gln Gly Ala Phe Val Asn Ile Val His Gly Gly Val
 305 310 315 320
 Thr Thr Leu Gln Arg Gln Ser Phe Gly Lys Met Thr Val Arg Leu Thr
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 Gly Asn Thr Ala Ala Ile Glu Glu Phe Tyr Gln Thr Leu Thr Lys Thr
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 Thr Thr Ile Lys Glu Ile Thr Arg
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 <223> RXC00526

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 Met Ser Leu Ile Glu
 1 5
 atg cga aat att gtc aag acc tac aac att gga tct gaa ggt gaa ctc 163

Met	Arg	Asn	Ile	Val	Lys	Thr	Tyr	Asn	Ile	Gly	Ser	Glu	Gly	Glu	Leu	
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acc	gtg	ttg	cac	ggt	gtg	gat	ttc	cat	gtg	gac	cgt	ggc	gaa	ttc	gtg	211
Thr	Val	Leu	His	Gly	Val	Asp	Phe	His	Val	Asp	Arg	Gly	Glu	Phe	Val	
			25					30					35			
tcg	gtt	gtg	ggt	acg	tcc	ggc	tca	ggt	aaa	tca	acg	atg	atg	aac	atc	259
Ser	Val	Val	Gly	Thr	Ser	Gly	Ser	Gly	Lys	Ser	Thr	Met	Met	Asn	Ile	
		40					45					50				
att	ggg	ttg	ttg	gat	aag	cca	act	gat	ggc	acg	tac	acc	ttg	gat	ggc	307
Ile	Gly	Leu	Leu	Asp	Lys	Pro	Thr	Asp	Gly	Thr	Tyr	Thr	Leu	Asp	Gly	
	55					60					65					
gtg	gat	gtg	ttg	gat	atc	agc	gat	gat	gct	ttg	gcg	agc	cac	cgc	gct	355
Val	Asp	Val	Leu	Asp	Ile	Ser	Asp	Asp	Ala	Leu	Ala	Ser	His	Arg	Ala	
	70				75					80					85	
aaa	tcg	att	ggt	ttt	gtg	ttt	cag	aac	ttc	aat	ctg	att	ggc	cgg	atc	403
Lys	Ser	Ile	Gly	Phe	Val	Phe	Gln	Asn	Phe	Asn	Leu	Ile	Gly	Arg	Ile	
				90					95					100		
gat	gcg	ttg	aag	aat	gtg	gaa	atg	ccc	atg	atg	tat	gcg	ggc	att	ccg	451
Asp	Ala	Leu	Lys	Asn	Val	Glu	Met	Pro	Met	Met	Tyr	Ala	Gly	Ile	Pro	
			105					110					115			
gct	aag	cag	cgg	aga	agt	cgt	gcg	gtt	gaa	tta	ttg	gaa	atg	gtc	ggg	499
Ala	Lys	Gln	Arg	Arg	Ser	Arg	Ala	Val	Glu	Leu	Leu	Glu	Met	Val	Gly	
		120					125					130				
atg	ggt	gag	cgt	ctc	aac	cat	gag	ccc	aat	gag	ctt	tcg	ggt	ggt	cag	547
Met	Gly	Glu	Arg	Leu	Asn	His	Glu	Pro	Asn	Glu	Leu	Ser	Gly	Gly	Gln	
	135					140					145					
aag	cag	cgc	gtg	gcc	att	gct	cgc	gcg	ttg	gcg	aac	gat	cct	gag	atc	595
Lys	Gln	Arg	Val	Ala	Ile	Ala	Arg	Ala	Leu	Ala	Asn	Asp	Pro	Glu	Ile	
	150				155				160						165	
att	ctt	gct	gat	gaa	cca	act	ggt	gcg	ttg	gat	tct	gca	acg	ggc	cgg	643
Ile	Leu	Ala	Asp	Glu	Pro	Thr	Gly	Ala	Leu	Asp	Ser	Ala	Thr	Gly	Arg	
				170					175					180		
atg	gtg	atg	gat	att	ttc	cac	cag	ctc	aac	aag	gag	cag	ggc	aaa	acc	691
Met	Val	Met	Asp	Ile	Phe	His	Gln	Leu	Asn	Lys	Glu	Gln	Gly	Lys	Thr	
			185					190					195			
atc	gtg	ttt	att	act	cac	aac	cct	gag	ctt	gct	gat	gaa	tct	gat	cgg	739
Ile	Val	Phe	Ile	Thr	His	Asn	Pro	Glu	Leu	Ala	Asp	Glu	Ser	Asp	Arg	
		200					205					210				
gtg	gtc	acc	atg	gtt	gac	ggg	cgc	atc	att	ggg	tct	gag	gtg	aaa	cac	787
Val	Val	Thr	Met	Val	Asp	Gly	Arg	Ile	Ile	Gly	Ser	Glu	Val	Lys	His	
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Ser																
230																

<210> 512

<211> 230

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 512

Met Ser Leu Ile Glu Met Arg Asn Ile Val Lys Thr Tyr Asn Ile Gly
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Ser Glu Gly Glu Leu Thr Val Leu His Gly Val Asp Phe His Val Asp
 20 25 30

Arg Gly Glu Phe Val Ser Val Val Gly Thr Ser Gly Ser Gly Lys Ser
 35 40 45

Thr Met Met Asn Ile Ile Gly Leu Leu Asp Lys Pro Thr Asp Gly Thr
 50 55 60

Tyr Thr Leu Asp Gly Val Asp Val Leu Asp Ile Ser Asp Asp Ala Leu
 65 70 75 80

Ala Ser His Arg Ala Lys Ser Ile Gly Phe Val Phe Gln Asn Phe Asn
 85 90 95

Leu Ile Gly Arg Ile Asp Ala Leu Lys Asn Val Glu Met Pro Met Met
 100 105 110

Tyr Ala Gly Ile Pro Ala Lys Gln Arg Arg Ser Arg Ala Val Glu Leu
 115 120 125

Leu Glu Met Val Gly Met Gly Glu Arg Leu Asn His Glu Pro Asn Glu
 130 135 140

Leu Ser Gly Gly Gln Lys Gln Arg Val Ala Ile Ala Arg Ala Leu Ala
 145 150 155 160

Asn Asp Pro Glu Ile Ile Leu Ala Asp Glu Pro Thr Gly Ala Leu Asp
 165 170 175

Ser Ala Thr Gly Arg Met Val Met Asp Ile Phe His Gln Leu Asn Lys
 180 185 190

Glu Gln Gly Lys Thr Ile Val Phe Ile Thr His Asn Pro Glu Leu Ala
 195 200 205

Asp Glu Ser Asp Arg Val Val Thr Met Val Asp Gly Arg Ile Ile Gly
 210 215 220

Ser Glu Val Lys His Ser
 225 230

<210> 513

<211> 1185

<212> DNA

<213> *Corynebacterium glutamicum*

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<222> (101)..(1162)

<223> RXC01004

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tcacccccat caccatgaa gaagcaaagg agtacgaaaa gtg agt att tgg gca 115
                               Val Ser Ile Trp Ala
                               1 5

act gtc ctt cta att atc gtc ctt ctt tcc gcc aac gcc ttc ttc gtg 163
Thr Val Leu Leu Ile Ile Val Leu Leu Ser Ala Asn Ala Phe Phe Val
          10          15          20

gcc gcg gag ttc gca ctg att tcc tcg cgc cgg gac cgc ctg gat tcc 211
Ala Ala Glu Phe Ala Leu Ile Ser Ser Arg Arg Asp Arg Leu Asp Ser
          25          30          35

ctg gta tcc cag ggt aaa aag gga gct gaa aag gtt ctc tac gca acc 259
Leu Val Ser Gln Gly Lys Lys Gly Ala Glu Lys Val Leu Tyr Ala Thr
          40          45          50

gag cac ctc tcc atc atg ttg gcg ggc gct cag ttc ggt att acg gtc 307
Glu His Leu Ser Ile Met Leu Ala Gly Ala Gln Phe Gly Ile Thr Val
          55          60          65

tgt tct ctg att ctg ggt aaa gtc gca gaa cct gcg atc gcc cac ttc 355
Cys Ser Leu Ile Leu Gly Lys Val Ala Glu Pro Ala Ile Ala His Phe
          70          75          80          85

att gag gtg cct ttc acc tcc tgg ggt gtt cca aat gat ttg atc cac 403
Ile Glu Val Pro Phe Thr Ser Trp Gly Val Pro Asn Asp Leu Ile His
          90          95          100

cca att tcc ttc gtc atc gca ctg gcg atc atc acc tgg ttg cac att 451
Pro Ile Ser Phe Val Ile Ala Leu Ala Ile Ile Thr Trp Leu His Ile
          105          110          115

ctc ttt ggt gaa atg gtg cca aag aac atc gct att gct ggc cct gaa 499
Leu Phe Gly Glu Met Val Pro Lys Asn Ile Ala Ile Ala Gly Pro Glu
          120          125          130

acc tta ggc atg tgg ctt gct cca gtg ctc att gcg ttt gtg aag att 547
Thr Leu Gly Met Trp Leu Ala Pro Val Leu Ile Ala Phe Val Lys Ile
          135          140          145

acc cgc ccg ttg atc gag ttc atg aac tgg atc gcc cgt ctg acc ctt 595
Thr Arg Pro Leu Ile Glu Phe Met Asn Trp Ile Ala Arg Leu Thr Leu
          150          155          160          165

cgc gcc ttt ggt gtg gag caa aaa aac gag ctg gat tcc acc gtg gac 643
Arg Ala Phe Gly Val Glu Gln Lys Asn Glu Leu Asp Ser Thr Val Asp
          170          175          180

cca gag cag ctg gca tca atg att tcc gag tcc cgt tcc gaa ggc ctc 691
Pro Glu Gln Leu Ala Ser Met Ile Ser Glu Ser Arg Ser Glu Gly Leu
          185          190          195

ctt gat gct gaa gag cac gcc cgc ctg tcc aag gcg ctg cgc tct gag 739
Leu Asp Ala Glu Glu His Ala Arg Leu Ser Lys Ala Leu Arg Ser Glu
          200          205          210

cag cgt tcc atc aag gaa ctg gtg att aag gat gag gac gtg cgc acg 787
Gln Arg Ser Ile Lys Glu Leu Val Ile Lys Asp Glu Asp Val Arg Thr

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215	220	225	
ctg gcg ttc ggt aaa tct ggc ccg acc ttg cac cag ttg gag gaa gca			835
Leu Ala Phe Gly Lys Ser Gly Pro Thr Leu His Gln Leu Glu Glu Ala			
230	235	240	245
gtc cgc gag acc ggt ttc tcc cgc ttc cct gtc acc ggc cgc gat gga			883
Val Arg Glu Thr Gly Phe Ser Arg Phe Pro Val Thr Gly Arg Asp Gly			
250	255		260
tcc tac ttg ggt tat atc cac atc aag gat att ttg cct cgt ctg gct			931
Ser Tyr Leu Gly Tyr Ile His Ile Lys Asp Ile Leu Pro Arg Leu Ala			
265	270		275
gat cct gag atg gat ccc tcc gag acc att ccg cgt tct gca ctg cgc			979
Asp Pro Glu Met Asp Pro Ser Glu Thr Ile Pro Arg Ser Ala Leu Arg			
280	285		290
cct ttg agc aat gtg gat gcc gac ggc ctc atg gat gac gtc ttg gat			1027
Pro Leu Ser Asn Val Asp Ala Asp Gly Leu Met Asp Asp Val Leu Asp			
295	300		305
ttt atg cac tac cgc tcc gcg cac atg gct cag gtt cgc ctc aaa ggt			1075
Phe Met His Tyr Arg Ser Ala His Met Ala Gln Val Arg Leu Lys Gly			
310	315		320
gag ctt ctc ggc gtg att acg ctg gag gat ctc atc gaa gaa tac gtg			1123
Glu Leu Leu Gly Val Ile Thr Leu Glu Asp Leu Ile Glu Glu Tyr Val			
330	335		340
ggc acc gtc aac gat tgg act cac gaa agc tcc gac gac tagaaatagt			1172
Gly Thr Val Asn Asp Trp Thr His Glu Ser Ser Asp Asp			
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aactgtgttg gac			1185

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<211> 354

<212> PRT

<213> Corynebacterium glutamicum

<400> 514

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20 25 30

Asp Arg Leu Asp Ser Leu Val Ser Gln Gly Lys Lys Gly Ala Glu Lys
35 40 45

Val Leu Tyr Ala Thr Glu His Leu Ser Ile Met Leu Ala Gly Ala Gln
50 55 60

Phe Gly Ile Thr Val Cys Ser Leu Ile Leu Gly Lys Val Ala Glu Pro
65 70 75 80

Ala Ile Ala His Phe Ile Glu Val Pro Phe Thr Ser Trp Gly Val Pro
85 90 95

Asn Asp Leu Ile His Pro Ile Ser Phe Val Ile Ala Leu Ala Ile Ile
 100 105 110
 Thr Trp Leu His Ile Leu Phe Gly Glu Met Val Pro Lys Asn Ile Ala
 115 120 125
 Ile Ala Gly Pro Glu Thr Leu Gly Met Trp Leu Ala Pro Val Leu Ile
 130 135 140
 Ala Phe Val Lys Ile Thr Arg Pro Leu Ile Glu Phe Met Asn Trp Ile
 145 150 155 160
 Ala Arg Leu Thr Leu Arg Ala Phe Gly Val Glu Gln Lys Asn Glu Leu
 165 170 175
 Asp Ser Thr Val Asp Pro Glu Gln Leu Ala Ser Met Ile Ser Glu Ser
 180 185 190
 Arg Ser Glu Gly Leu Leu Asp Ala Glu Glu His Ala Arg Leu Ser Lys
 195 200 205
 Ala Leu Arg Ser Glu Gln Arg Ser Ile Lys Glu Leu Val Ile Lys Asp
 210 215 220
 Glu Asp Val Arg Thr Leu Ala Phe Gly Lys Ser Gly Pro Thr Leu His
 225 230 235 240
 Gln Leu Glu Glu Ala Val Arg Glu Thr Gly Phe Ser Arg Phe Pro Val
 245 250 255
 Thr Gly Arg Asp Gly Ser Tyr Leu Gly Tyr Ile His Ile Lys Asp Ile
 260 265 270
 Leu Pro Arg Leu Ala Asp Pro Glu Met Asp Pro Ser Glu Thr Ile Pro
 275 280 285
 Arg Ser Ala Leu Arg Pro Leu Ser Asn Val Asp Ala Asp Gly Leu Met
 290 295 300
 Asp Asp Val Leu Asp Phe Met His Tyr Arg Ser Ala His Met Ala Gln
 305 310 315 320
 Val Arg Leu Lys Gly Glu Leu Leu Gly Val Ile Thr Leu Glu Asp Leu
 325 330 335
 Ile Glu Glu Tyr Val Gly Thr Val Asn Asp Trp Thr His Glu Ser Ser
 340 345 350
 Asp Asp

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<211> 732

<212> DNA

<213> Corynebacterium glutamicum

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<222> (101)..(709)

<223> RXC01017

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agtgtggatt gctagaaaac tttaagaaag aggaaataat atg gct caa aaa gta 115
                                         Met Ala Gln Lys Val
                                         1 5

acc ttc tgg ttc gat acc acc tgc cca ttc tgc tgg gtc acc tcc cgc 163
Thr Phe Trp Phe Asp Thr Thr Cys Pro Phe Cys Trp Val Thr Ser Arg
                        10 15 20

tgg att aag gaa gtc gaa caa gtc cgc gat att gaa atc cag tgg gtt 211
Trp Ile Lys Glu Val Glu Gln Val Arg Asp Ile Glu Ile Gln Trp Val
                        25 30 35

cca atg agc ctc gct gtc cta aac gaa ggc cgt gat ctc cca gag gat 259
Pro Met Ser Leu Ala Val Leu Asn Glu Gly Arg Asp Leu Pro Glu Asp
                        40 45 50

tac aag gag cgc atg aag gct gca tgg gga cca gca cgc gtt ttc gca 307
Tyr Lys Glu Arg Met Lys Ala Ala Trp Gly Pro Ala Arg Val Phe Ala
                        55 60 65

gct gtc gcc acc gac cat gct gac aag ctc ggc gac ctg tac acc gca 355
Ala Val Ala Thr Asp His Ala Asp Lys Leu Gly Asp Leu Tyr Thr Ala
70 75 80 85

atg ggt acc cgc atc cac aac gac ggt cgc gga cca atc gaa ggt tcc 403
Met Gly Thr Arg Ile His Asn Asp Gly Arg Gly Pro Ile Glu Gly Ser
90 95 100

ttc aat gat gtc atc gca gag gca ctt gaa gag gtc ggc cta gac gct 451
Phe Asn Asp Val Ile Ala Glu Ala Leu Glu Glu Val Gly Leu Asp Ala
105 110 115

gca ctt ggt gaa gtt gca gac acc acc gaa tgg gac gac gca ctt cgc 499
Ala Leu Gly Glu Val Ala Asp Thr Thr Glu Trp Asp Asp Ala Leu Arg
120 125 130

gca ttc cac cag acc gca atg gac gag gtc ggc aac gat gtc gga acc 547
Ala Phe His Gln Thr Ala Met Asp Glu Val Gly Asn Asp Val Gly Thr
135 140 145

cca gtg gtc aag ctc ggc gac acc gct ttc ttc ggc cca gtg ctc acc 595
Pro Val Val Lys Leu Gly Asp Thr Ala Phe Phe Gly Pro Val Leu Thr
150 155 160 165

cgc atc cca cgc ggc gag gaa gca gga gag atc ttc gac gct tcc ttc 643
Arg Ile Pro Arg Gly Glu Glu Ala Gly Glu Ile Phe Asp Ala Ser Phe
170 175 180

aag ctc gca agc tat ccc cac ttc ttt gaa atc aag cgc agc cgc act 691
Lys Leu Ala Ser Tyr Pro His Phe Phe Glu Ile Lys Arg Ser Arg Thr
185 190 195

gag aac cca cag ttc gac taattaacgc tgtctctgct tat 732
Glu Asn Pro Gln Phe Asp
200

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<400> 516															
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			20					25					30		
Glu	Ile	Gln	Trp	Val	Pro	Met	Ser	Leu	Ala	Val	Leu	Asn	Glu	Gly	Arg
		35					40					45			
Asp	Leu	Pro	Glu	Asp	Tyr	Lys	Glu	Arg	Met	Lys	Ala	Ala	Trp	Gly	Pro
	50					55					60				
Ala	Arg	Val	Phe	Ala	Ala	Val	Ala	Thr	Asp	His	Ala	Asp	Lys	Leu	Gly
65					70					75					80
Asp	Leu	Tyr	Thr	Ala	Met	Gly	Thr	Arg	Ile	His	Asn	Asp	Gly	Arg	Gly
				85					90					95	
Pro	Ile	Glu	Gly	Ser	Phe	Asn	Asp	Val	Ile	Ala	Glu	Ala	Leu	Glu	Glu
			100					105					110		
Val	Gly	Leu	Asp	Ala	Ala	Leu	Gly	Glu	Val	Ala	Asp	Thr	Thr	Glu	Trp
		115					120					125			
Asp	Asp	Ala	Leu	Arg	Ala	Phe	His	Gln	Thr	Ala	Met	Asp	Glu	Val	Gly
	130					135					140				
Asn	Asp	Val	Gly	Thr	Pro	Val	Val	Lys	Leu	Gly	Asp	Thr	Ala	Phe	Phe
145					150					155					160
Gly	Pro	Val	Leu	Thr	Arg	Ile	Pro	Arg	Gly	Glu	Glu	Ala	Gly	Glu	Ile
			165						170					175	
Phe	Asp	Ala	Ser	Phe	Lys	Leu	Ala	Ser	Tyr	Pro	His	Phe	Phe	Glu	Ile
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Lys	Arg	Ser	Arg	Thr	Glu	Asn	Pro	Gln	Phe	Asp					
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738

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cgc cgt gct gat tca acg ggg gct cct gcg gca gct tcc aag gaa gct			211
Arg Arg Ala Asp Ser Thr Gly Ala Pro Ala Ala Ala Ser Lys Glu Ala			
	25	30	35
tcc caa caa atg gac gct gcc gga gtt ctt gag tgg gcc agg acc gct			259
Ser Gln Gln Met Asp Ala Ala Gly Val Leu Glu Trp Ala Arg Thr Ala			
	40	45	50
gtc gag cag ctt tct gaa cgt cgt gca gag atc aat gca ctg aat gtc			307
Val Glu Gln Leu Ser Glu Arg Arg Ala Glu Ile Asn Ala Leu Asn Val			
	55	60	65
ttt cct gtt cca gat gca gac act gga tca aac atg acc tac acc atg			355
Phe Pro Val Pro Asp Ala Asp Thr Gly Ser Asn Met Thr Tyr Thr Met			
	70	75	80
aca gct gcg ttg gat gaa gcg ctg aaa ctg ggg gag ttg ggt gat gtc			403
Thr Ala Ala Leu Asp Glu Ala Leu Lys Leu Gly Glu Leu Gly Asp Val			
	90	95	100
gca agg att act gag gct ttg gct gtt ggt tct gtg cgt gga gcc cga			451
Ala Arg Ile Thr Glu Ala Leu Ala Val Gly Ser Val Arg Gly Ala Arg			
	105	110	115
gga aat tct gga gta gtc ctt agt cag gtc ctt cgc gct att gct cag			499
Gly Asn Ser Gly Val Val Leu Ser Gln Val Leu Arg Ala Ile Ala Gln			
	120	125	130
gca gct gct gac ggg gtt att gat ggc cac aca atc caa gaa gcg cta			547
Ala Ala Ala Asp Gly Val Ile Asp Gly His Thr Ile Gln Glu Ala Leu			
	135	140	145
tcc att gct cgc tcc cta gtt gat cgc gca att aca gat cct gtg gag			595
Ser Ile Ala Arg Ser Leu Val Asp Arg Ala Ile Thr Asp Pro Val Glu			
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ggc act gtt gtc act gtg ttg cgt tct			622
Gly Thr Val Val Thr Val Leu Arg Ser			
	170		

<210> 518

<211> 174

<212> PRT

<213> Corynebacterium glutamicum

<400> 518

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 20 25 30

Ala Ser Lys Glu Ala Ser Gln Gln Met Asp Ala Ala Gly Val Leu Glu
 35 40 45

Trp Ala Arg Thr Ala Val Glu Gln Leu Ser Glu Arg Arg Ala Glu Ile
 50 55 60
 Asn Ala Leu Asn Val Phe Pro Val Pro Asp Ala Asp Thr Gly Ser Asn
 65 70 75 80
 Met Thr Tyr Thr Met Thr Ala Ala Leu Asp Glu Ala Leu Lys Leu Gly
 85 90 95
 Glu Leu Gly Asp Val Ala Arg Ile Thr Glu Ala Leu Ala Val Gly Ser
 100 105 110
 Val Arg Gly Ala Arg Gly Asn Ser Gly Val Val Leu Ser Gln Val Leu
 115 120 125
 Arg Ala Ile Ala Gln Ala Ala Ala Asp Gly Val Ile Asp Gly His Thr
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 Ile Gln Glu Ala Leu Ser Ile Ala Arg Ser Leu Val Asp Arg Ala Ile
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 Thr Asp Pro Val Glu Gly Thr Val Val Thr Val Leu Arg Ser
 165 170

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 <212> DNA
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 <223> RXC01212

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 Met Pro Met Thr Thr
 1 5
 aca cca gca atc gac gta aca gac ctc gtg aga acc tac ggc gac tac 163
 Thr Pro Ala Ile Asp Val Thr Asp Leu Val Arg Thr Tyr Gly Asp Tyr
 10 15 20
 acc gca gtc aag ggc ctg aat ttc cat gta cag cgc ggt gaa gta ttt 211
 Thr Ala Val Lys Gly Leu Asn Phe His Val Gln Arg Gly Glu Val Phe
 25 30 35
 ggt ctg ctc ggc acc aac ggg gcc ggc aaa acc tcc acc ttg gaa gtc 259
 Gly Leu Leu Gly Thr Asn Gly Ala Gly Lys Thr Ser Thr Leu Glu Val
 40 45 50
 atc gaa gga ctt tcc gca ccc agc tcc ggc acc gtg cgc atc tcc ggg 307
 Ile Glu Gly Leu Ser Ala Pro Ser Ser Gly Thr Val Arg Ile Ser Gly
 55 60 65
 ctt gac ccc gtt gcc gac cgc gcg atc ctg cgc ccc gag ctc ggc atc 355
 Leu Asp Pro Val Ala Asp Arg Ala Ile Leu Arg Pro Glu Leu Gly Ile

70	75	80	85	
atg ctg caa tca ggc ggc ctg cca tca cag ctc acc gtc gcc gaa acc				403
Met Leu Gln Ser Gly Gly Leu Pro Ser Gln Leu Thr Val Ala Glu Thr	90	95	100	
atg gac atg tgg cac ggc acc tgc acg tat ccg cgc gcc att aaa gat				451
Met Asp Met Trp His Gly Thr Cys Thr Tyr Pro Arg Ala Ile Lys Asp	105	110	115	
gtg ctt gcc gac gtc gac ctc cta cac cgc gaa aac gtc aag gtc ggc				499
Val Leu Ala Asp Val Asp Leu Leu His Arg Glu Asn Val Lys Val Gly	120	125	130	
gcg ctt tcc gga ggc gaa caa cga cgc ctt gat ttg gcc tgc gca ctg				547
Ala Leu Ser Gly Gly Glu Gln Arg Arg Leu Asp Leu Ala Cys Ala Leu	135	140	145	
ctt ggc gac ccc tca att ttg ttc ctc gac gaa ccc acc acc ggc ctc				595
Leu Gly Asp Pro Ser Ile Leu Phe Leu Asp Glu Pro Thr Thr Gly Leu	150	155	160	165
gac cca gaa tct agg cgc cac acc tgg caa ctc ctg ctg gac ctg aaa				643
Asp Pro Glu Ser Arg Arg His Thr Trp Gln Leu Leu Leu Asp Leu Lys	170	175	180	
cag cgc ggc gtc acc atg atg ctg acc acc cac tac ctg gag gaa gcc				691
Gln Arg Gly Val Thr Met Met Leu Thr Thr His Tyr Leu Glu Glu Ala	185	190	195	
gaa ttc ctc tgc gac cgg att gcc atc atg aac gcc ggt gag atc gca				739
Glu Phe Leu Cys Asp Arg Ile Ala Ile Met Asn Ala Gly Glu Ile Ala	200	205	210	
gtg gaa ggc acc ttg gat gaa ctg gtg gcc cgc gag aag tcg atc atc				787
Val Glu Gly Thr Leu Asp Glu Leu Val Ala Arg Glu Lys Ser Ile Ile	215	220	225	
agt ttc gtg ctg cgt ggc ggg cag gtg gag ttg ccg gtc ttg agt ggg				835
Ser Phe Val Leu Arg Gly Gly Gln Val Glu Leu Pro Val Leu Ser Gly	230	235	240	245
gct gaa atc atc cgc gac aac aac cac gtc cgc atc gcc acc acc acc				883
Ala Glu Ile Ile Arg Asp Asn Asn His Val Arg Ile Ala Thr Thr Thr	250	255	260	
ctg cag cag cac acc tta gaa ata ctt acc tgg gct gca gag acc ggg				931
Leu Gln Gln His Thr Leu Glu Ile Leu Thr Trp Ala Ala Glu Thr Gly	265	270	275	
atc gcg ctg gaa ggc ttc gct gca aaa ccc gcc acc ttg gaa tcc gta				979
Ile Ala Leu Glu Gly Phe Ala Ala Lys Pro Ala Thr Leu Glu Ser Val	280	285	290	
ttc atg gac atc gcc tca ctc gag aac acc tcg ctg caa acc gcc				1024
Phe Met Asp Ile Ala Ser Leu Glu Asn Thr Ser Leu Gln Thr Ala	295	300	305	
tagaatcttt aaggagacca caa				1047

<210> 520
 <211> 308
 <212> PRT
 <213> Corynebacterium glutamicum

<400> 520

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Arg Gly Glu Val Phe Gly Leu Leu Gly Thr Asn Gly Ala Gly Lys Thr
      35              40              45

Ser Thr Leu Glu Val Ile Glu Gly Leu Ser Ala Pro Ser Ser Gly Thr
 50              55              60

Val Arg Ile Ser Gly Leu Asp Pro Val Ala Asp Arg Ala Ile Leu Arg
 65              70              75              80

Pro Glu Leu Gly Ile Met Leu Gln Ser Gly Gly Leu Pro Ser Gln Leu
      85              90              95

Thr Val Ala Glu Thr Met Asp Met Trp His Gly Thr Cys Thr Tyr Pro
      100             105             110

Arg Ala Ile Lys Asp Val Leu Ala Asp Val Asp Leu Leu His Arg Glu
      115             120             125

Asn Val Lys Val Gly Ala Leu Ser Gly Gly Glu Gln Arg Arg Leu Asp
 130             135             140

Leu Ala Cys Ala Leu Leu Gly Asp Pro Ser Ile Leu Phe Leu Asp Glu
 145             150             155             160

Pro Thr Thr Gly Leu Asp Pro Glu Ser Arg Arg His Thr Trp Gln Leu
      165             170             175

Leu Leu Asp Leu Lys Gln Arg Gly Val Thr Met Met Leu Thr Thr His
 180             185             190

Tyr Leu Glu Glu Ala Glu Phe Leu Cys Asp Arg Ile Ala Ile Met Asn
      195             200             205

Ala Gly Glu Ile Ala Val Glu Gly Thr Leu Asp Glu Leu Val Ala Arg
      210             215             220

Glu Lys Ser Ile Ile Ser Phe Val Leu Arg Gly Gly Gln Val Glu Leu
 225             230             235             240

Pro Val Leu Ser Gly Ala Glu Ile Ile Arg Asp Asn Asn His Val Arg
      245             250             255

Ile Ala Thr Thr Thr Leu Gln Gln His Thr Leu Glu Ile Leu Thr Trp
      260             265             270

Ala Ala Glu Thr Gly Ile Ala Leu Glu Gly Phe Ala Ala Lys Pro Ala
      275             280             285

Thr Leu Glu Ser Val Phe Met Asp Ile Ala Ser Leu Glu Asn Thr Ser

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290 295 300

Leu Gln Thr Ala
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<212> DNA
<213> *Corynebacterium glutamicum*

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<222> (101)..(1108)
<223> RXC01306

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Met Thr Glu Trp Tyr
1 5
gtc gtt tta ccc gcc act att cta ctc atc gcg ctg tct gcg ttt ttc 163
Val Val Leu Pro Ala Thr Ile Leu Leu Ile Ala Leu Ser Ala Phe Phe
10 15 20
gtc atc att gag ttc gct ttg ctt gca gct agg cgg aac cgg tta gag 211
Val Ile Ile Glu Phe Ala Leu Leu Ala Ala Arg Arg Asn Arg Leu Glu
25 30 35
gag act gtg gaa acc tcg cgg tct tcc cgc gct gcg ttg cga agc ctc 259
Glu Thr Val Glu Thr Ser Arg Ser Ser Arg Ala Ala Leu Arg Ser Leu
40 45 50
aat gaa ctt act ctc atg ctc gcg ggc gcg cag ttg gga atc acc atg 307
Asn Glu Leu Thr Leu Met Leu Ala Gly Ala Gln Leu Gly Ile Thr Met
55 60 65
gtg act ttc gcg ttg ggt gct atc acg aag ccg tgg gtt cat tat gct 355
Val Thr Phe Ala Leu Gly Ala Ile Thr Lys Pro Trp Val His Tyr Ala
70 75 80 85
ttg atg ccg ctc ttc gaa tgg gcg cgt ata ccg ctg gtt atg gca gat 403
Leu Met Pro Leu Phe Glu Trp Ala Arg Ile Pro Leu Val Met Ala Asp
90 95 100
gtc att gcg ttt att ttg tcg ctg ttt atc gta acg ttt ctg cac ttg 451
Val Ile Ala Phe Ile Leu Ser Leu Phe Ile Val Thr Phe Leu His Leu
105 110 115
gtc atc ggc gaa atg gct ccg aaa tcc tgg gca atc gcg cat ccg gag 499
Val Ile Gly Glu Met Ala Pro Lys Ser Trp Ala Ile Ala His Pro Glu
120 125 130
acg gca ctt cga act atc gcg att ccc gca cgg ggc ttc att aac ctg 547
Thr Ala Leu Arg Thr Ile Ala Ile Pro Ala Arg Gly Phe Ile Asn Leu
135 140 145
ttt cgt cca ttg ctg cag tgg atc aac aaa atg gcg aac gat ttg gtc 595
Phe Arg Pro Leu Leu Gln Trp Ile Asn Lys Met Ala Asn Asp Leu Val

150	155	160	165	
cgc aaa gtt ggt gaa act ccc gtt gat cga gct gca gct ggt ggc tat				643
Arg Lys Val Gly Glu Thr Pro Val Asp Arg Ala Ala Ala Gly Gly Tyr				
	170	175	180	
gac acc gat acc ctc cat gcc ctc att gag cat tcc cga gaa act ggc				691
Asp Thr Asp Thr Leu His Ala Leu Ile Glu His Ser Arg Glu Thr Gly				
	185	190	195	
gct ctg gat cag caa tcc gcc gcc caa atc agc gga att atc aag ctg				739
Ala Leu Asp Gln Ser Ala Ala Gln Ile Ser Gly Ile Ile Lys Leu				
	200	205	210	
gat aaa atc acg gtc ggt caa acc ctg acc gca tct cca ttt acg cac				787
Asp Lys Ile Thr Val Gly Gln Thr Leu Thr Ala Ser Pro Phe Thr His				
	215	220	225	
agc gcc agc gcc acg gtt gct gag gtg caa gcc gca gct cag cgc agt				835
Ser Ala Ser Ala Thr Val Ala Glu Val Gln Ala Ala Ala Gln Arg Ser				
	230	235	240	245
ggc agc ttg cgt gtg ctt atc gac gcc ccc tcc cac ctt ttc cca cac				883
Gly Ser Leu Arg Val Leu Ile Asp Ala Pro Ser His Leu Phe Pro His				
	250	255	260	
gtc att cat gtg cga gac acc ctt ggt gcc tcg cca gac gag aag gct				931
Val Ile His Val Arg Asp Thr Leu Gly Ala Ser Pro Asp Glu Lys Ala				
	265	270	275	
tcg aag tgg tct cgc cca atc ctc acc gtt gct gag acc gac acg tta				979
Ser Lys Trp Ser Arg Pro Ile Leu Thr Val Ala Glu Thr Asp Thr Leu				
	280	285	290	
cac caa gcg ctg gaa tac atg cgg gag cat aac gag cag atc agt gcg				1027
His Gln Ala Leu Glu Tyr Met Arg Glu His Asn Glu Gln Ile Ser Ala				
	295	300	305	
gtg ctt tcc gct gat ggg aaa acg gtg ctt ggt gta ata act tgg gat				1075
Val Leu Ser Ala Asp Gly Lys Thr Val Leu Gly Val Ile Thr Trp Asp				
	310	315	320	325
cac atc ttg aaa tac ctg tgg cct gca tcg gtg tagctaattt gaggtgcgct				1128
His Ile Leu Lys Tyr Leu Trp Pro Ala Ser Val				
	330	335		
gaa				1131
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<213> Corynebacterium glutamicum				
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20 25 30				

Arg Asn Arg Leu Glu Glu Thr Val Glu Thr Ser Arg Ser Ser Arg Ala
 35 40 45
 Ala Leu Arg Ser Leu Asn Glu Leu Thr Leu Met Leu Ala Gly Ala Gln
 50 55 60
 Leu Gly Ile Thr Met Val Thr Phe Ala Leu Gly Ala Ile Thr Lys Pro
 65 70 75 80
 Trp Val His Tyr Ala Leu Met Pro Leu Phe Glu Trp Ala Arg Ile Pro
 85 90 95
 Leu Val Met Ala Asp Val Ile Ala Phe Ile Leu Ser Leu Phe Ile Val
 100 105 110
 Thr Phe Leu His Leu Val Ile Gly Glu Met Ala Pro Lys Ser Trp Ala
 115 120 125
 Ile Ala His Pro Glu Thr Ala Leu Arg Thr Ile Ala Ile Pro Ala Arg
 130 135 140
 Gly Phe Ile Asn Leu Phe Arg Pro Leu Leu Gln Trp Ile Asn Lys Met
 145 150 155 160
 Ala Asn Asp Leu Val Arg Lys Val Gly Glu Thr Pro Val Asp Arg Ala
 165 170 175
 Ala Ala Gly Gly Tyr Asp Thr Asp Thr Leu His Ala Leu Ile Glu His
 180 185 190
 Ser Arg Glu Thr Gly Ala Leu Asp Gln Gln Ser Ala Ala Gln Ile Ser
 195 200 205
 Gly Ile Ile Lys Leu Asp Lys Ile Thr Val Gly Gln Thr Leu Thr Ala
 210 215 220
 Ser Pro Phe Thr His Ser Ala Ser Ala Thr Val Ala Glu Val Gln Ala
 225 230 235 240
 Ala Ala Gln Arg Ser Gly Ser Leu Arg Val Leu Ile Asp Ala Pro Ser
 245 250 255
 His Leu Phe Pro His Val Ile His Val Arg Asp Thr Leu Gly Ala Ser
 260 265 270
 Pro Asp Glu Lys Ala Ser Lys Trp Ser Arg Pro Ile Leu Thr Val Ala
 275 280 285
 Glu Thr Asp Thr Leu His Gln Ala Leu Glu Tyr Met Arg Glu His Asn
 290 295 300
 Glu Gln Ile Ser Ala Val Leu Ser Ala Asp Gly Lys Thr Val Leu Gly
 305 310 315 320
 Val Ile Thr Trp Asp His Ile Leu Lys Tyr Leu Trp Pro Ala Ser Val
 325 330 335


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  1             5             10             15
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Val Ala Thr Leu Thr Tyr Ala Tyr Ser Asp Ser Thr Ala Val Val Gly
 20 25 30

Pro Leu Ala Pro Ala Ala Glu Pro His Ser Trp Asp Leu Cys Glu His
 35 40 45

His Ala Glu Arg Ile Thr Ala Pro Leu Gly Trp Glu Met Leu Arg Val
 50 55 60

Asn Asp Ile Lys Val Asp Asp Asp Glu Asp Leu Thr Ala Leu Ala Gln
 65 70 75 80

Ala Val Arg Glu Ala Gly Arg Thr Val Ser Gly Leu Val Pro Glu Asp
 85 90 95

Glu Val Gly Gly Asn His Pro Val Asn Arg Ser Ala Arg Ile Ala Glu
 100 105 110

Gln Lys Val His Arg Arg Gly His Leu Tyr Val Val Pro Asp Gln Asp
 115 120 125

Glu Ser
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<210> 525
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 <212> DNA
 <213> Corynebacterium glutamicum

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 <222> (1)..(591)
 <223> RXC01372

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cct gcc cgc atc gtg gcg tcg ata agc act ctt tta gat ctt tta gaa 96
 Pro Ala Arg Ile Val Ala Ser Ile Ser Thr Leu Leu Asp Leu Leu Glu
 20 25 30

gca gac ccc agc att att tcc gac cgc ttg gaa cac ctc gcc gac tgc 144
 Ala Asp Pro Ser Ile Ile Ser Asp Arg Leu Glu His Leu Ala Asp Cys
 35 40 45

att gat gag gaa gtg gaa tcg cta tcg ccg gaa cgt gac gaa cta gtc 192
 Ile Asp Glu Glu Val Glu Ser Leu Ser Pro Glu Arg Asp Glu Leu Val
 50 55 60

aat ccc ggc cga aaa ctg cgc gca tac gta gat cac gca cgg atc gtg 240
 Asn Pro Gly Arg Lys Leu Arg Ala Tyr Val Asp His Ala Arg Ile Val
 65 70 75 80

cat acc ggc cga act gat gtg gga ctc gcg att gcc aac gtt atc gcc 288
 His Thr Gly Arg Thr Asp Val Gly Leu Ala Ile Ala Asn Val Ile Ala
 85 90 95

cca atc tgg acc cga cga ggc ctg gta tca gcc gtg ctg gat ttt ccc 336

Pro Ile Trp Thr Arg Arg Gly Leu Val Ser Ala Val Leu Asp Phe Pro
 100 105 110

gag ctc atg gaa tca ttg ccg gaa ctc cgc gga ccc gag cca att acc 384
 Glu Leu Met Glu Ser Leu Pro Glu Leu Arg Gly Pro Glu Pro Ile Thr
 115 120 125

gac gat ata ttc cat gac cca ttc ata gat gac gaa ccc ggg gtg gta 432
 Asp Asp Ile Phe His Asp Pro Phe Ile Asp Asp Glu Pro Gly Val Val
 130 135 140

ccg ttt agg gct gtt gtc tgg gcc gaa gag gaa ccc gga atc ccc gat 480
 Pro Phe Arg Ala Val Val Trp Ala Glu Glu Glu Pro Gly Ile Pro Asp
 145 150 155 160

gcc atg gcg caa agc tgc gac gga cct agc aaa ggg gcg ctg aca caa 528
 Ala Met Ala Gln Ser Cys Asp Gly Pro Ser Lys Gly Ala Leu Thr Gln
 165 170 175

gca ctg cgt ttg ctg gtg cgc gga cag tca gcc acg acc tat tcc att 576
 Ala Leu Arg Leu Leu Val Arg Gly Gln Ser Ala Thr Thr Tyr Ser Ile
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 Glu Glu Lys Asp Leu
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<210> 526
 <211> 197
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 <213> Corynebacterium glutamicum

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 20 25 30

Ala Asp Pro Ser Ile Ile Ser Asp Arg Leu Glu His Leu Ala Asp Cys
 35 40 45

Ile Asp Glu Glu Val Glu Ser Leu Ser Pro Glu Arg Asp Glu Leu Val
 50 55 60

Asn Pro Gly Arg Lys Leu Arg Ala Tyr Val Asp His Ala Arg Ile Val
 65 70 75 80

His Thr Gly Arg Thr Asp Val Gly Leu Ala Ile Ala Asn Val Ile Ala
 85 90 95

Pro Ile Trp Thr Arg Arg Gly Leu Val Ser Ala Val Leu Asp Phe Pro
 100 105 110

Glu Leu Met Glu Ser Leu Pro Glu Leu Arg Gly Pro Glu Pro Ile Thr
 115 120 125

Asp Asp Ile Phe His Asp Pro Phe Ile Asp Asp Glu Pro Gly Val Val
 130 135 140

Pro Phe Arg Ala Val Val Trp Ala Glu Glu Glu Pro Gly Ile Pro Asp
 145 150 155 160

Ala Met Ala Gln Ser Cys Asp Gly Pro Ser Lys Gly Ala Leu Thr Gln
 165 170 175

Ala Leu Arg Leu Leu Val Arg Gly Gln Ser Ala Thr Thr Tyr Ser Ile
 180 185 190

Glu Glu Lys Asp Leu
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<210> 527
 <211> 669
 <212> DNA
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 <222> (101)..(646)
 <223> RXC01659

<400> 527

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 Val Ala Gly Val Ala
 1 5

cag cgt ttt gtc gac gag cgc att cac gtc ggt ttg gat tcc atg cca 163
 Gln Arg Phe Val Asp Glu Arg Ile His Val Gly Leu Asp Ser Met Pro
 10 15 20

gaa gct gtg act gct gtg tgg atg gaa tct gat tgg gtg ttg gcg gaa 211
 Glu Ala Val Thr Ala Val Trp Met Glu Ser Asp Trp Val Leu Ala Glu
 25 30 35

acc atc aag ggt tcc acg cct tcc gat tgg gaa gag att ttg cgg ccg 259
 Thr Ile Lys Gly Ser Thr Pro Ser Asp Trp Glu Glu Ile Leu Arg Pro
 40 45 50

ttg gcg ctg ctc acg gac gcg tct ttc acg ttg cca cct cgt tcc acg 307
 Leu Ala Leu Leu Thr Asp Ala Ser Phe Thr Leu Pro Pro Arg Ser Thr
 55 60 65

cgt gcg caa acc ttg gat ttg aag cat ttg gaa cca agc cgt ctg aag 355
 Arg Ala Gln Thr Leu Asp Leu Lys His Leu Glu Pro Ser Arg Leu Lys
 70 75 80 85

ccg gag cag cca gaa aag cca gcg ttt act ccc aat gct tcg gaa gaa 403
 Pro Glu Gln Pro Glu Lys Pro Ala Phe Thr Pro Asn Ala Ser Glu Glu
 90 95 100

gat ttg tct cag ccg ttg gtg atc cgc ccc gag gag ccg ttg cag atg 451
 Asp Leu Ser Gln Pro Leu Val Ile Arg Pro Glu Glu Pro Leu Gln Met
 105 110 115

ccg gtt cgc ggt gtg cag gaa agc cgc gga gtg gtc gag cca cgg tca 499
 Pro Val Arg Gly Val Gln Glu Ser Arg Gly Val Val Glu Pro Arg Ser
 120 125 130

ttg ggt gcg gat gat gtg gag tcg att gcg gag ggc gat cca gag cgt 547
 Leu Gly Ala Asp Asp Val Glu Ser Ile Ala Glu Gly Asp Pro Glu Arg
 135 140 145
 ccg agc gat ctt tat ggc acg cgt gtg ctg cgt gat ctc aat ggt cag 595
 Pro Ser Asp Leu Tyr Gly Thr Arg Val Leu Arg Asp Leu Asn Gly Gln
 150 155 160 165
 tcc agt att ttc caa gat tcc acc gac gcg gat gag cca cca aaa aag 643
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 170 175 180
 tgg tagaaaactg gtgtttttcg gcc 669
 Trp

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 <212> PRT
 <213> Corynebacterium glutamicum

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 Trp Val Leu Ala Glu Thr Ile Lys Gly Ser Thr Pro Ser Asp Trp Glu
 35 40 45
 Glu Ile Leu Arg Pro Leu Ala Leu Leu Thr Asp Ala Ser Phe Thr Leu
 50 55 60
 Pro Pro Arg Ser Thr Arg Ala Gln Thr Leu Asp Leu Lys His Leu Glu
 65 70 75 80
 Pro Ser Arg Leu Lys Pro Glu Gln Pro Glu Lys Pro Ala Phe Thr Pro
 85 90 95
 Asn Ala Ser Glu Glu Asp Leu Ser Gln Pro Leu Val Ile Arg Pro Glu
 100 105 110
 Glu Pro Leu Gln Met Pro Val Arg Gly Val Gln Glu Ser Arg Gly Val
 115 120 125
 Val Glu Pro Arg Ser Leu Gly Ala Asp Asp Val Glu Ser Ile Ala Glu
 130 135 140
 Gly Asp Pro Glu Arg Pro Ser Asp Leu Tyr Gly Thr Arg Val Leu Arg
 145 150 155 160
 Asp Leu Asn Gly Gln Ser Ser Ile Phe Gln Asp Ser Thr Asp Ala Asp
 165 170 175
 Glu Pro Pro Lys Lys Trp
 180